

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2003, 16:03:18 ; Search time 13.2661 Seconds  
(without alignments)  
927.898 Million cell updates/sec

Title: US-10-019-455A-6

Perfect score: 676

Sequence: 1 MARILLFLPGLVAVCAVHG.....RVQEATKEVPTTIDDFCE 128

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_76:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	257.5	38.1	131	2 I38019	melanoma-derived g
2	86.5	12.8	839	1 TVHUVV	transforming prote
3	85.5	12.6	844	1 TVNSVV	transforming prote
4	81.5	12.1	878	2 I51940	gene VAV2 protei
5	78.5	11.6	1589	1 AG4YCS	cell division cont
6	76.5	11.3	295	2 F90113	cell division cycl
7	74.5	11.0	1215	2 T32734	myosin-IA - Acanth
8	74	10.9	308	2 T48525	hypothetical prote
9	71.5	10.6	541	2 C64439	asparagine synthas
10	71.5	10.6	671	1 C69621	fructose-bisphosph
11	71	10.5	283	2 A23516	Balbani ring 1 ch
12	71	10.5	585	2 G96995	ATP-dependent RNA
13	71	10.5	722	2 G86746	hypothetical prote
14	71	10.5	769	2 G90186	AAA family ATPase
15	70.5	10.4	84	2 AG0693	probable lipoprote
16	70.5	10.4	444	1 A64417	phosphoribosylamin
17	70.5	10.4	669	2 D72278	endo-1,4-beta-mann
18	70.5	10.4	678	2 C97114	recG helicase [imp
19	70	10.4	209	2 D86758	cratate phosphorib
20	70	10.4	259	2 C64427	hypothetical prote
21	69.5	10.3	1199	2 T47442	disease resistance
22	69	10.2	328	2 E86714	quinone oxidoreduc
23	69	10.2	392	2 I39521	rubredoxin-NAD+ re
24	69	10.2	670	2 S67383	probable signal tr
25	69	10.2	2193	2 S52919	polyprotein (IA, 1
26	69	10.2	2541	2 T29340	hypothetical prote
27	68.5	10.1	461	2 AF2340	sugar ABC transpor
28	68.5	10.1	505	1 S24550	protein-tyrosine k
29	68.5	10.1	506	1 S24553	protein-tyrosine k

30 68 10.1 162 2 B29662  
31 68 10.1 234 2 AE3482  
32 68 10.1 332 2 T04200  
33 68 10.1 359 2 B29960  
34 68 10.1 366 2 G90951  
35 68 10.1 366 2 C85800  
36 68 10.1 782 2 B83966  
37 67.5 10.0 374 2 B97258  
38 67.5 10.0 839 2 G96719  
39 67.5 10.0 1072 2 AD1280  
40 67 9.9 142 2 C75325  
41 67 9.9 373 2 T39655  
42 67 9.9 383 2 S24156  
43 67 9.9 509 2 G82104  
44 67 9.9 518 1 P2WL8  
45 67 9.9 524 2 S36483

#### ALIGNMENTS

##### RESULT 1

I38019  
melanoma-derived growth regulatory protein MIA - human  
C;Species: Homo sapiens (man)  
C;Date: 17-May-1996 #sequence\_revision 17-May-1996 #text\_change 04-Mar-2000  
C;Accession: I38019; S40238  
R;Blesch, A.; Bosserhoff, A.K.; Apfel, R.; Behl, C.; Hoesdoerfer, B.; Schmitt, A.; Jac  
Cancer Res. 54, 5695-5701, 1994  
A;Title: Cloning of a novel malignant melanoma-derived growth-regulatory protein, MIA.  
A;Reference number: I38019; MUID:95007612; PMID:7923218  
A;Accession: I38019  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-131 <RES>  
A;Cross-references: EMBL:X75450; NID:g438057; PIDN:CAA53203.1; PID:g438058  
C;Genetics:  
A;Gene: mia  
C;Superfamily: human melanoma-derived growth regulatory protein MIA

Query Match 38.1%; Score 257.5; DB 2; Length 131;  
Best Local Similarity 41.2%; Pred. No. 4.7e-19;  
Matches 56; Conservative 26; Mismatches 41; Indels 13; Gaps 5;  
Qy 1 MARILLFLPGLVAVCA-----VHGIFMDRLASKKLCADDECVYTISLSAQEDNAPD 54  
Db 1 MARSIVCL--GVIIILSAFSGPGVGRGPMFKLADRLKCADQEGSHPTISMAVALQDYNAPD 58  
Qy 55 CRFINVKKGOIYVYYSKLVKENGAGE-FWAGSVYVGQDDEMGV-VGYFPRNLVKEORVYQ 112  
Db 59 CRFTLTHRGQVYVYVFSKL---KGRGLFWGSGVQGDYIGDLAARLGFPPSSIVREDQTLK 115  
Qy 113 EATKEVPTTIDIFFCE 128  
Db 116 PGKVDVKTDRKDFVCQ 131

##### RESULT 2

TVHUVV  
transforming protein vav - human (fragments)  
N;Alternate names: finger protein vav  
C;Species: Homo sapiens (man)  
C;Date: 31-Mar-1991 #sequence\_revision 03-May-1996 #text\_change 18-Jun-1999  
C;Accession: B39576; S05382  
R;Katzav, S.; Cleveland, J.H.; Heslop, H.E.; Pulido, D.  
Mol. Cell. Biol. 11, 1912-1920, 1991  
A;Title: Loss of the amino-terminal helix-loop-helix domain of the vav proto-oncogene  
A;Reference number: A39576; MUID:91172176; PMID:2005887  
A;Accession: B39576  
A;Molecule type: mRNA  
A;Residues: 1-61 <KAT>  
A;Cross-references: GB:M59834; NID:g340189; PIDN:AAA63267.1; PID:g340190  
A;Note: the authors translated the codon CAA for residue 6 as Glu, CAG for residue 13

R;Katzav, S.; Martin-Zanca, D.; Barbacid, M.  
EMBO J. 8, 2283-2290, 1989  
A;Title: vav, a novel human oncogene derived from a locus ubiquitously expressed in hematopoietic cells  
A;Reference number: S05382; MUID:90005432; PMID:2477241  
A;Accession: S05382  
A;Molecule type: mRNA  
A;Residues: 62-839 <KAT2>  
A;Cross-references: EMBL:X16316  
R;Adams, J.M.; Houston, H.; Allen, J.; Linta, T.; Harvey, R.  
Oncogene 7, 611-618, 1992  
A;Title: The hematopoietically expressed vav proto-oncogene shares homology with the dbl oncogene  
A;Reference number: S23669; MUID:92228488; PMID:1565462  
A;Contents: annotation  
A;Note: in the sequence from mouse the authors find three additional nucleotides that predicted in the published human sequences  
C;Comment: In comparing these sequences with the mouse (see PIR:TWMSV), there appear to be three additional nucleotides in the human sequence  
C;Genetics:  
A;Gene: GDB:VAV1; VAV  
A;Cross-references: GDB:127112; OMIM:164875  
A;Map position: 19p13.3-19p13.3  
A;Superfamily: vav transforming protein; CDC24 homology; protein kinase C zinc-binding repeat homology <K22>  
C;Keywords: phosphoprotein; transforming protein; zinc finger  
F;126-170/Region: acidic  
F;188-452/Domain: CDC24 homology <CD24>  
F;509-557/Domain: protein kinase C zinc-binding repeat homology <K22>  
F;522-542/Region: zinc finger CCCC motif  
F;547-560/Region: zinc finger HCCH motif  
F;598-648/Domain: SH3 homology <SH3A>  
F;664-756/Domain: SH2 homology <SH2>  
F;783-831/Domain: SH3 homology <SH3B>  
F;433/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

Query Match 12.8%; Score 86.5; DB 1; Length 839;  
Best Local Similarity 32.9%; Pred. No. 1;  
Matches 23; Conservative 13; Mismatches 21; Indels 13; Gaps 3;

QY 44 ASAQEDYNAPDPCRFINVKKQOIYVYSLVKENGAGFEWAGSVYGDQEMGVGYPPRN 103  
DB 781 AKARYDFCARDRLSLSKEGDI-----KILNKKQQGQWVRGEIYGR-----VGMFPAN 829  
QY 104 LVKEQRYVQE 113  
DB 830 YVEED--YSE 837

RESULT 3  
TWMSV  
C;Species: Mus musculus (house mouse)  
C;Date: 03-May-1994 #sequence revision 16-Feb-1996 #text\_change 18-Jun-1999  
C;Accession: A61187; A39576; S36941; S23669  
R;Coppola, J.; Bryant, S.; Koda, T.; Conway, D.; Barbacid, M.  
Cell Growth Differ. 2, 95-105, 1991  
A;Title: Mechanism of activation of the vav protooncogene.  
A;Reference number: A61187; MUID:91299578; PMID:2069873  
A;Accession: A61187  
A;Status: not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-844 <COP>  
R;Katzav, S.; Cleveland, J.L.; Heslop, H.E.; Pulido, D.  
Mol. Cell. Biol. 11, 1912-1920, 1991  
A;Title: Loss of the amino-terminal helix-loop-helix domain of the vav proto-oncogene affects its transforming activity  
A;Reference number: A39576; MUID:91172176; PMID:2005887  
A;Accession: A39576  
A;Molecule type: mRNA  
A;Residues: 1-28, 'E', '30-93 <KAT>  
A;Cross-references: GB:M59833; NID:9202343; PIDN:AAA63402.1; PID:G202344  
R;Adams, J.M.  
submitted to the EMBL Data Library, January 1992  
A;Reference number: S36941  
A;Accession: S36941  
A;Molecule type: mRNA  
A;Residues: 1-323, 'DLLMVMQRYVLYKHLLOELVK', '346-347, 'QDAT', '352, 'K', '354, 'N', '355-453, 'R', '45

A;Cross-references: EMBL:X64361; NID:955220; PIDN:CAA45713.1; PID:955221  
R;Adams, J.M.; Houston, H.; Allen, J.; Linta, T.; Harvey, R.  
Oncogene 7, 611-618, 1992  
A;Title: The hematopoietically expressed vav proto-oncogene shares homology with the d dbl oncogene  
A;Reference number: S23669; MUID:92228488; PMID:1565462  
A;Contents: annotation; the authors note the frameshift difference with sequence in A6  
A;Note: the complete sequence was submitted to Genbank; see S36941  
C;Genetics:  
A;Gene: vav  
C;Superfamily: vav transforming protein; CDC24 homology; protein kinase C zinc-binding repeat homology <K22>  
C;Keywords: phosphoprotein; transforming protein; zinc finger  
F;132-102/Region: leucine-rich  
F;132-176/Region: acidic  
F;194-458/Domain: CDC24 homology <CD24>  
F;336-340/Region: proline-rich  
F;486-493/Region: nuclear location signal  
F;513-563/Domain: protein kinase C zinc-binding repeat homology <K21>  
F;528-548/Region: zinc finger CCCC motif  
F;553-566/Region: zinc finger HCCH motif  
F;575-582/Region: nuclear location signal  
F;604-654/Domain: SH3 homology <SH3A>  
F;606-609/Region: proline-rich  
F;670-761/Domain: SH2 homology <SH2>  
F;788-836/Domain: SH3 homology <SH3B>  
F;433/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

Query Match 12.6%; Score 85.5; DB 1; Length 844;  
Best Local Similarity 31.4%; Pred. No. 1.3;  
Matches 22; Conservative 14; Mismatches 21; Indels 13; Gaps 3;

QY 44 ASAQEDYNAPDPCRFINVKKQOIYVYSLVKENGAGFEWAGSVYGDQEMGVGYPPRN 103  
DB 786 AKARYDFCARDRLSLSKEGDI-----KILNKKQQGQWVRGEIYGR-----IGWFPNS 834  
QY 104 LVKEQRYVQE 113  
DB 835 YVEED--YSE 842

RESULT 4  
IS1940  
gene VAV2 protein - human  
C;Species: Homo sapiens (man)  
C;Date: 01-Nov-1996 #sequence\_revision 01-Nov-1996 #text\_change 16-Jul-1999  
C;Accession: IS1940  
R;Henske, E.P.; Short, M.P.; Jozwiak, S.; Bovey, C.M.; Ramakrishnan, S.; Haines, J.L.; K.  
Ann. Hum. Genet. 59, 25-37, 1995  
A;Title: Identification of VAV2 on 9q34 and its exclusion as the tuberous sclerosis gene  
A;Reference number: IS1940; MUID:95283235; PMID:7762982  
A;Accession: IS1940  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-878 <RES>  
A;Cross-references: GB:S76992; NID:9913345; PIDN:AAB34377.1; PID:9913346  
C;Genetics:  
A;Gene: GDB:VAV2  
A;Cross-references: GDB:370880; OMIM:600428  
A;Map position: 9q34-9q34  
C;Superfamily: vav transforming protein; CDC24 homology; protein kinase C zinc-binding repeat homology <CD24>  
F;198-462/Domain: CDC24 homology <CD24>  
F;524-572/Domain: protein kinase C zinc-binding repeat homology <K22>  
F;673-764/Domain: SH2 homology <SH2>  
F;823-872/Domain: SH3 homology <SH3>

Query Match 12.1%; Score 81.5; DB 2; Length 878;  
Best Local Similarity 26.3%; Pred. No. 3.4;  
Matches 20; Conservative 21; Mismatches 22; Indels 13; Gaps 3;

QY 38 VVT---ISLASAODYNAPDPCRFINVKKQOIYVYSLVKENGAGFEWAGSVYGDQEM 94  
DB 812 VFTPRVIGTAVRYNFAARDMLSLREGDVVRIYRIGGDOG---WKKG-----ETN 861  
QY 95 GVVGYPRLVKEQRY 110



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Db      862 GRIGWFPSTVVEEGI 877
      |.:|:| |.:|:|
RESULT 5
RGBCYS
cell division control protein CDC25 - yeast (Saccharomyces cerevisiae)
N/Alternate names: protein L2142.6; protein YLR310C
C/Species: Saccharomyces cerevisiae
C/Date: 31-Mar-1988 #sequence revision 31-Mar-1993 #text_change 21-Jul-2000
C/Accession: A26596; S51442; A23444; S43051; S47990
R/Broek, D.; Toda, T.; Michaeli, T.; Levin, L.; Birchmeier, C.; Zoller, M.; Powers, S.;
Cell 48, 789-799, 1987
A/Title: The S. cerevisiae CDC25 gene product regulates the RAS/adenylate cyclase pathway
A/Reference number: A26596; MUID:87131091; PMID:3545497
A/Accession: A26596
A/Molecule type: DNA
A/Residues: 1-1589 <BRO>
A/Cross-references: EMBL:M15458; NID:gl711184; PIDN:AAA34478.1; PID:gl711185
R/Pauley, A.
submitted to the EMBL Data Library, November 1994
A/Description: The sequence of S. cerevisiae cosmid L2142.
A/Reference number: S51437
A/Accession: S51442
A/Molecule type: DNA
A/Residues: 1-1589 <PAU>
A/Cross-references: EMBL:U17247; NID:g577216; PIDN:AAB67360.1; PID:g577222; GSPDB:GN0001
R/Camonis, J.H.; Kalekine, M.; Gondre, B.; Garreau, H.; Boy-Marcotte, E.; Jacquet, M.
EMBO J. 5, 375-380, 1986
A/Title: Characterization, cloning and sequence analysis of the CDC25 gene which controls
A/Reference number: A23444; MUID:86220116; PMID:3011405
A/Accession: A23444
A/Molecule type: DNA
A/Residues: 1-496, 'Y', 498-953, 'LSVWNLGR', 964-1589 <CAM>
A/Cross-references: EMBL:X03579; NID:g3483; PIDN:CAA27259.1; PID:g3484
R/Daniel, J.H.
Curr. Genet. 10, 879-885, 1986
A/Title: The CDC25 "Start" gene of Saccharomyces cerevisiae: sequencing of the active C-
A/Reference number: S43051; MUID:88194639; PMID:3329037
A/Accession: S43051
A/Molecule type: DNA
A/Residues: 877-1589 <DAN>
A/Cross-references: EMBL:X03579
C/Genetics:
A/Gene: SGD:CDC25; CTN1; MIPS:YLR310C
A/Cross-references: SGD:S0004301; MIPS:YLR310C
A/Map position: 12R
C/Function:
A/Description: positive control of level of cellular cAMP at the stage at which the cell
C/Superfamily: budding yeast CDC25; CDC25-type guanine nucleotide exchange activator hom
C/Keywords: cell cycle control; transmembrane protein
F:1301-1542/Domain: CDC25-type guanine nucleotide exchange activator homology <SOS>
Query Match 11.6%; Score 78.5; DB 1; Length 1589;
Best Local Similarity 25.8%; Pred. No. 13;
Matches 23; Conservative 21; Mismatches 34; Indels 11; Gaps 4;
QY 26 LASKKLCADECVYTISLASAEDYNAP-----DCRFNVKKGQIYVYVSKLVKENGAGE 80
|.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:|
Db 45 LSSSPSTSLTIRPIGIVVAAYDFNYPFKDSSQLLSVQOGETIYLNK-----NSSG- 99
|.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:|
QY 81 FWAGSYVGQDGMGVGVYPPRNLVKEQR 109
|.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:|
Db 100 WNDGLVIDDSNGKVN-RGVFPQNFGRPLR 127
|.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:|
RESULT 6
F90113
cell division cycle 2 homolog [imported] - Guillardia theta nucleomorph
C/Species: nucleomorph Guillardia theta
A/Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 15-Jun-2001
C/Accession: F90113
R;Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; R;
Nature 410, 1091-1096, 2001
A/Title: The highly reduced genome of an enslaved algal nucleus.
A/Reference number: A99082; MUID:11323671; PMID:11323671
A/Accession: F90113
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-295 <DOU>
A/Cross-references: GB:AJ010592; NID:gl2580757; PIDN:CAC27075.1; GSPDB:GN00151
C/Genetics:
A/Map position: 2
A/Genome: nucleomorph
A/Superfamily: kinase-related transforming protein; protein kinase homology
C/Keywords: nucleomorph
Query Match 11.3%; Score 76.5; DB 2; Length 295;
Best Local Similarity 28.4%; Pred. No. 3.5;
Matches 33; Conservative 16; Mismatches 36; Indels 31; Gaps 8;
QY 11 GLVAVCAV-HGIFMDRLASKKLCADDECYVYTISLASAEDYNAPDCRFNVKKGQIYVY 69
|.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:|
Db 144 GIVKICDFGMGTF---LCSKKICLSKIV-TLW-----YRAPE-----ILLGQHFDY 187
|.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:|
QY 70 SKLVKNGA--GFVWAGSVVGQDGMGVGVYPPRNLVKEQRVYQVQATKEVPTTDI 123
|.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:|
Db 188 SVDWMSFGCVIGELITGEILFQKSLDQL-----NKLFQ--TIGTPTTEI 231
|.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:|
RESULT 7
T32734
myosin-1A - Acanthamoeba castellanii
C/Species: Acanthamoeba castellanii
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 08-Sep-2000
C/Accession: T32734
R/Lee, W.L.; Ostap, E.M.; Zot, H.G.; Pollard, T.D.
submitted to the EMBL Data Library, August 1998
A/Description: Hydrodynamic and ligand binding properties of Acanthamoeba myosin-1A GP
A/Reference number: Z21216
A/Accession: T32734
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-1215 <LEE>
A/Cross-references: EMBL:AF085185; NID:g3599477; PID:g3599478; PIDN:AAC35357.1
A/Experimental source: strain Neff
C/Genetics:
A/Gene: MIA
A/Introns: 1/3; 41/3; 72/2; 103/2; 162/3; 184/1; 217/1; 296/1; 340/3; 390/3; 447/3; 50
C/Superfamily: protozoan myosin heavy chain IB; myosin motor domain homology; SH3 homo
F:14-674/Domain: myosin motor domain homology <MMO>
Query Match 11.0%; Score 74.5; DB 2; Length 1215;
Best Local Similarity 28.6%; Pred. No. 25;
Matches 20; Conservative 12; Mismatches 25; Indels 13; Gaps 2;
QY 38 VYITISLASAEDYNAPDCRFNVKKGQIYVYVSKLVKENGAGEFWAGSYVGQDGMGVY 97
|.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:|
Db 1158 VPTVGRCRALDYCAOBADELTLREGDVIDVIQK-----SGHWBGTILNGK-----T 1204
|.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:|
QY 98 GYFPRNLVKE 107
|.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:|
Db 1205 GVFPANLYVED 1214
|.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:| |.:|:|
RESULT 8
T48525
hypothetical protein T22p22.50 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C/Accession: T48525
R/Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft
submitted to the Protein Sequence Database, April 2000
A/Reference number: Z24490

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Tue Dec 30 10:20:54 2003

Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetel Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Ser akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpsira, P.; Tognoni, A.; Tosato, V.; Uchiyam T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, A.; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A.; Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis* A; Reference number: A69580; MUID:98044033; PMID:9384377

A; Accession: C69621  
A; Status: nucleic acid sequence not shown; translation not shown  
A; Molecule type: DNA  
A; Residues: 1-671 <KUN>  
A; Cross-references: GB:Z99124; GB:AL009126; NID:g2636442; PIDN:CAB16056.1; PID:g263656  
A; Experimental source: strain 168  
C; Genetics:  
A; Gene: fbp; yydE  
C; Function:  
A; Description: catalyzes the hydrolysis of fructose-1,6-bisphosphate to fructose-6-phosphate  
A; Pathway: gluconeogenesis  
A; Note: requires manganese ion for stability and phosphoenolpyruvate for activation  
C; Superfamily: *Bacillus subtilis* fructose-bisphosphatase; phosphatase core homolog  
C; Keywords: carbohydrate metabolism; gluconeogenesis; metalloprotein; phosphoric monoe

Query Match 10.6%; Score 71.5; DB 1; Length 671;  
Best Local Similarity 22.8%; Pred. No. 27; Mismatches 21; Indels 29; Gaps 4;  
Matches 26; Conservative

Qy 22 FMDRLASKKLCADDECVYTITSLASQEDYNAPDCRFINVKKGQIYVYS-----KLV 73  
Db 35 YLDLLAQKYDCEKVVTEILKA-----ILNLPKGFHFVSLHGEYQAFQHV 83  
Qy 74 KENGAG-----EFWAGSYGQDGMGVGYPFRN---LVKEQRYQYQATKE 117  
Db 84 LRNGSGRVKEKIRDFSGVIYDREIDELAAALVYTPEDKLIKHDFAKEALNE 137

RESULT 11  
A23516  
Balbiani ring 1 chain - midge (*Chironomus tentans*) (fragment)  
C; Species: *Chironomus tentans*  
C; Date: 23-Aug-1987 #sequence\_revision 23-Aug-1987 #text\_change 21-Jul-2000  
C; Accession: A23516  
R; Hoog, C.; Engberg, C.; Wieslander, L.  
Nucleic Acids Res. 14, 703-719, 1986  
A; Title: A BR 1 gene in *Chironomus tentans* has a composite structure: a large repetiti  
A; Reference number: A23516; MUID:86120366; PMID:3003693  
A; Accession: A23516  
A; Molecule type: DNA  
A; Residues: 1-383 <HOO>  
A; Cross-references: GB:X03490; NID:g7043; PIDN:CAA27206.1; PID:g769785  
A; Note: the authors translated the codon GAA for residue 118 as Gly and TTC for residu  
C; Genetics:  
A; Introns: 273/1  
C; Superfamily: unassigned Balbiani ring proteins

Query Match 10.5%; Score 71; DB 2; Length 383;  
Best Local Similarity 28.0%; Pred. No. 17; Mismatches 37; Indels 20; Gaps 3;  
Matches 26; Conservative

Qy 24 DRLASKKLCADDECVYTITSLASQEDYNAPDCRFINVKKGQIYVYSKLVKENGAGEFWA 83  
Db 303 DKDCCKNCNCDGAKF-----PECESNSKQSGMDFILAKLFPQGG-GDFFA 348  
Qy 84 GSVYGDGQDGMGVGYPFRNLVKEQRYQYQATK 116  
Db 349 GSVEVDGKK-----LSPEKKEFGKALQDAVK 375

RESULT 12  
G96995  
ATP-dependent RNA helicase, superfamily II [imported] - *Clostridium acetobutylicum*  
C; Species: *Clostridium acetobutylicum*  
C; Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 14-Sep-2001

A; Accession: T48525  
A; Status: preliminary  
A; Molecule type: DNA  
A; Residues: 1-308 <BEV>  
A; Cross-references: EMBL:AL163814  
A; Experimental source: cultivar Columbia; BAC clone T22P22  
C; Genetics:  
A; Map position: 5  
A; Introns: 63/3; 117/3; 135/3; 180/3  
A; Note: T22P22.50

Query Match 10.9%; Score 74; DB 2; Length 308;  
Best Local Similarity 37.2%; Pred. No. 6; Mismatches 17; Indels 2; Gaps 1;  
Matches 16; Conservative

Qy 62 KQCIYVTSKLVKENGAGEFWAGSYGQDGMGVGYPFRNL 104  
Db 168 KGGERAVYASIVQEXDIGNWVTVDRYDPDVH--IGYWPKEK 208

RESULT 9  
C64439  
asparagine synthase (glutamine-hydrolyzing) (EC 6.3.5.4) [similarity] - *Methanococcus ja*  
C; Species: *Methanococcus jannaschii*  
C; Date: 13-Sep-1996 #sequence\_revision 09-Jun-2000 #text\_change 19-Jul-2002  
C; Accession: C64439  
R; Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.; Reich, C.J.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Ison, J.D.; Sadov, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1038-1073, 1996  
A; Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C. A; Title: Complete genome sequence of the methanogenic archaeon, *Methanococcus jannaschii* A; Reference number: A64300; MUID:96337999; PMID:8688087  
A; Accession: C64439  
A; Status: nucleic acid sequence not shown; translation not shown  
A; Molecule type: DNA  
A; Residues: "MRD", 1-541 <BUL>  
A; Cross-references: GB:U67554; GB:L77117; NID:g2826365; PIDN:AAB99117.1; PID:g1591755; T  
A; Note: an incorrect initiation codon was used  
C; Genetics:  
A; Map position: REV1058315-1056681  
C; Superfamily: asparagine synthase (glutamine-hydrolyzing)  
C; Keywords: asparagine biosynthesis; ligase  
F; 2-541/Product: asparagine synthase (glutamine-hydrolyzing) #status predicted <MAT>  
F; 2/Active site: Cys #status predicted

Query Match 10.6%; Score 71.5; DB 2; Length 541;  
Best Local Similarity 25.7%; Pred. No. 22; Mismatches 33; Indels 23; Gaps 6;  
Matches 27; Conservative

Qy 21 IFMDRLAS-----KKLCADDECVYTITSLASQEDYNAPDCRFINVKKGQIYVYSKL 72  
Db 298 IYAERLAKNLKLRKKIISEEYEVFPKAKADEVD-----LKKGVGIPYIVASEM 352  
Qy 73 VKENGAGEFWAGSYGQDGMGVGYPFRNLVKEQRYQYQATKE 117  
Db 353 ANEDGLKVV-----LSQGADEL-FGGY-----ARHERIVRERGE 387

RESULT 10  
C69621  
fructose-bisphosphatase (EC 3.1.3.11) [validated] - *Bacillus subtilis*  
C; Species: *Bacillus subtilis*  
C; Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 03-Jun-2002  
C; Accession: C69621  
R; Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertez C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, S. Nature 390, 249-256, 1997  
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallez iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koester, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel

C;Accession: G96995  
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 193, 4823-4838, 2001  
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum ATCC824  
A;Reference number: A96900; MUID:21359325; PMID:21359325  
C;Accession: G96995  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-585 <KUR>  
A;Cross-references: GB:AE001437; PIDN:AAK78754.1; PID:gl5023664; GSPDB:GN00168  
A;Experimental source: Clostridium acetobutylicum ATCC824  
C;Genetics:  
A;Gene: CAC0778

Query Match 10.5%; Score 71; DB 2; Length 585;  
Best Local Similarity 29.4%; Pred. No. 26;  
Matches 30; Conservative 13; Mismatches 37; Indels 22; Gaps 5;

QY 30 KLCADD----ECVYTISLASAQAEDYNAPDCRFNVKGGQIYVYSK-----LVKENGAGE 80  
DB 272 KCDEVEIKYKRAIPLEVEDSEFNKD-----IKEGDAVVVFSKRVLEIAQSVSARG 326

QY 81 FWAGSVGCDQDGVGVGVPFRNLVKEQRYVQBATKEVPTTD 122  
DB 327 IKASIIYGDLPPEV-----RMLQYEQFIKKE--TKVLVTTD 360

RESULT 13  
G86746  
hypothetical protein nrde [imported] - Lactococcus lactis subsp. lactis (strain IL1403)  
C;Species: Lactococcus lactis subsp. lactis  
C;Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 03-Aug-2001  
C;Accession: G86746  
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissensbach, J.; Ehrlich, S.; Moulé, S.; O'Gaora, P.  
Genome Res. 11, 731-753, 2001  
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis strain IL1403  
A;Reference number: A86625; MUID:21235186; PMID:11337471  
A;Accession: G86746  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-722 <STO>  
A;Cross-references: GB:AB005176; PID:gl2723918; PIDN:AAK05073.1; GSPDB:GN00146  
A;Experimental source: strain IL1403  
C;Genetics:  
A;Gene: nrde  
C;Superfamily: Salmonella typhimurium ribonucleoside-diphosphate reductase

Query Match 10.5%; Score 71; DB 2; Length 722;  
Best Local Similarity 26.2%; Pred. No. 33;  
Matches 28; Conservative 21; Mismatches 52; Indels 6; Gaps 2;

QY 11 GLVAVCAVHGIFMDRLASKKLCADDEC-VYTISLASAQAEDYNAPDCRFNVKGGQIYVY 69  
DB 249 GVVYLSLFHPDIMEFLSTKKENADEKIRVKTSLG-----VTVPKFVELVKKGTMVLF 303

QY 70 SKLVKENGAGFWAGSVGCDQDGVGVGVPFRNLVKEQRYVQBATK 116  
DB 304 EPYFVEKYGKPFPAEVDITAEYDKMVPANPEIRKTSINARELEQELSK 350

RESULT 14  
C90186  
AAA family ATPase [imported] - Sulfolobus solfataricus  
C;Species: Sulfolobus solfataricus  
C;Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 15-Jun-2001  
C;Accession: C90186  
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-  
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.  
arrett, R.A.; Ragan, M.A.; Sersen, C.W.; Van der Oost, J.  
submitted to GenBank, April 2001  
A;Description: Sulfolobus solfataricus complete genome.  
A;Reference number: A99139

A;Accession: C90186  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-769 <KUR>  
A;Cross-references: GB:AE006641; NID:gl13813572; PIDN:AAK40746.1; GSPDB:GN00155  
C;Genetics:  
A;Gene: SSO0421  
C;Superfamily: transitional endoplasmic reticulum ATPase; FtsH/SEC18/CDC48-type ATP-bi

Query Match 10.5%; Score 71; DB 2; Length 769;  
Best Local Similarity 35.0%; Pred. No. 35;  
Matches 28; Conservative 10; Mismatches 20; Indels 22; Gaps 5;

QY 67 YVYSKLVKENG-----AGFWAGSVGCDG--QDEMVGVGYPFRNL-----VKE 107  
DB 51 YTISRLGIENGVDVEIIGPSGSAQAALIGDGAADNEIRVDGIYRSIGVGIGDEVTVKR 110

QY 108 QRVYQBATKEV--PTTDIDF 125  
DB 111 AQV-QDATKVVLAQTQPISF 129

RESULT 15  
AG0693  
probable lipoprotein ydha [imported] - Salmonella enterica subsp. enterica serovar Typhi  
C;Species: Salmonella enterica subsp. enterica serovar Typhi  
A;Note: this species has also been called Salmonella typhi  
C;Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C;Accession: AG0693  
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church-  
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farra  
S.; Moule, S.; O'Gaora, P.  
Nature 413, 848-852, 2001  
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K  
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica ser  
A;Reference number: AB0502; MUID:21534947; PMID:11677608  
A;Accession: AG0693  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-84 <PAR>  
A;Cross-references: GB:AL513382; PIDN:CAD01920.1; PID:gl6502762; GSPDB:GN00176  
C;Genetics:  
A;Gene: ydha

Query Match 10.4%; Score 70.5; DB 2; Length 84;  
Best Local Similarity 26.8%; Pred. No. 3.8;  
Matches 22; Conservative 20; Mismatches 25; Indels 15; Gaps 4;

QY 1 MARILLFLPGLVAVCAVHGIFMDRLASKKL---CADDECYVTISLASAQAEDYN-APDCR 56  
DB 3 MKKIAIMFLPVLITGCSVYQQFVERMQTDTLEYQC--DEKPLTVKANNPREEVSFYDNK 60

QY 57 FINVKKG-----QQIYVY 69  
DB 61 LLTLKQGIFASGARYTDGIYVF 82

Search completed: December 29, 2003, 16:10:38  
Job time : 15.2661 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2003, 16:03:18 ; Search time 5.01961 Seconds  
(without alignments)  
1199,181 Million cell updates/sec

Title: US-10-019-455a-6  
Perfect score: 676  
Sequence: 1 MARILLFLPLVAVCAVHG.....RVYQEAKEVPTTIDFFCE 128

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	676	100.0	128	1	Q9nrc9 homo sapien
2	602	89.1	128	1	OTOR_MOUSE
3	480	71.0	132	1	OTOR_CHICK
4	390	57.7	133	1	OTOR_RANCA
5	257.5	38.1	131	1	MIA_HUMAN
6	256.5	37.9	130	1	MIA_BOVIN
7	254	37.6	130	1	MIA_RAT
8	235.5	34.8	130	1	MIA_MOUSE
9	88.5	13.1	847	1	VAV3_MOUSE
10	86.5	12.8	845	1	VAV3_HUMAN
11	85.5	12.8	847	1	VAV3_HUMAN
12	85.5	12.6	843	1	VAV_RAT
13	85.5	12.6	845	1	VAV_MOUSE
14	82.5	12.2	868	1	VAV2_MOUSE
15	81.5	12.1	878	1	VAV2_HUMAN
16	78.5	11.6	1589	1	CC25 YEAST
17	78	11.5	625	1	TR11_MOUSE
18	75	11.1	1721	1	ITN1_HUMAN
19	74	10.9	2161	1	SHK1_HUMAN
20	73	10.8	1217	1	ITN1_RAT
21	71.5	10.6	541	1	ASNH_METJA
22	71	10.5	1714	1	ITN1_MOUSE
23	71	10.5	2167	1	SHK1_RAT
24	70.5	10.4	444	1	PUR2_METJA
25	70.5	10.4	905	1	ZO3_MOUSE
26	70	10.4	209	1	PYR2_LACLA
27	70	10.4	209	1	PYR2_STRP3
28	70	10.4	209	1	PYR2_STRPY
29	70	10.4	259	1	YA20_METJA
30	70	10.4	1815	1	SHK3_RAT
31	69	10.2	392	1	RUBE_ACICA
32	69	10.2	670	1	YBV2_SCHPO
33	69	10.2	2193	1	POLG_EC09H

RESULT 1

ID	OTOR_HUMAN	STANDARD;	PRT;	128 AA.
AC	Q9NRC9;	2203	1	POLG_EC09B
DT	16-OCT-2001 (Rel. 40, Created)	505	1	SRK1_SPOLA
DT	16-OCT-2001 (Rel. 40, last sequence update)	506	1	SRK4_SPOLA
DT	28-FEB-2003 (Rel. 41, last annotation update)	162	1	BAR2_CHIPA
DE	Otoraplin precursor (Fibrocyte-derived protein) (Melanoma inhibitory activity like protein).	366	1	TORY_ECO57
GN	OTOR OR FDP OR MIAL.	534	1	VL2_HPV37
OS	Homo sapiens (Human).	383	1	PGI3_ASPNG
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	474	1	SYE_VIBCH
OX	NCBI_TaxID=9606;	518	1	VL2_HPV08
EN	SEQUENCE FROM N.A.	524	1	VL2_HPV17
RP	TISSUE=Cochlea;	809	1	DCML_OLICA
RX	MEDLINE=20334619; PubMed=10873378;	209	1	PYRE_LISMO
RA	Robertson N.G., Heller S., Lin J.S., Resendes B.L., Weremowicz S., Denis C.S., Bell A.M., Hudspeth A.J., Morton C.C.;			
RT	"A novel conserved cochlear gene, OTOR: identification, expression analysis, and chromosomal mapping.";			
RL	Genomics 66:242-248 (2000).			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Cochlea;			
RX	MEDLINE=20568254; PubMed=10998416;			
RA	Cohen-Salmon M., Frenz D., Liu W., Verpy E., Voegelings S., Petit C.;			
RT	"Fdp, a new fibrocyte-derived protein related to MIA/CD-RAP, has an in vitro effect on the early differentiation of the inner ear mesenchyme.";			
RL	J. Biol. Chem. 275:40036-40041 (2000).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain and Cochlea;			
RX	MEDLINE=21100875; PubMed=11161796;			
RA	Rendtorff N.D., Frodin M., Attie-Bitach T., Vekemans M., Tommerup N.;			
RT	"Identification and characterization of an inner ear-expressed human melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent polymorphism that abolishes translation.";			
RL	Genomics 71:40-52 (2001).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	MEDLINE=21638749; PubMed=11780052;			
RA	Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R., Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L., Bailey J., Barlow K.F., Bates K.N., Bead L.M., Beare D.M., Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M., Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R., Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M., Ellington A.G., Frankland J.A., Fraser A., French L., Garner P., Grahman D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E., Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,			

Q66577 e genome po  
P42686 spongilla 1  
P42690 spongilla 1  
P08725 chironomus  
P58361 escherichia  
Q80905 human papil  
Q12554 aspergillus  
O31153 vibrio chol  
P06419 human papil  
P19919 oligotropa  
Q85688 listeria mo



Tue Dec 30 10:20:54 2003

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OTOR_CHICK STANDARD; PRT; 132 AA.
AC Q918P6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Otoraplin precursor.
GN OTOR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20334619; PubMed=10873378;
RA Robertson N.G., Heller S., Lin J.S., Resendes B.L., Weremowicz S.,
RA Denis C.S., Bell A.M., Hudspeth A.J., Morton C.C.;
RT "A novel conserved cochlear gene, OTOR: identification, expression
RT analysis, and chromosomal mapping.";
RL Genomics 66:242-248(2000).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN COCHLEA.
CC -!- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-----
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DR EMBL; AF233518; AAF82727.1; -.
DR HSP; Q16674; 111J.
DR InterPro; IPR001452; SH3.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS00002; SH3; 1.
KW Signal; SH3 domain.
FT SIGNAL 1 23
FT CHAIN 24 132
FT DOMAIN 42 114
FT DISULFID 35 40
FT DISULFID 58 131
FT DISULFID 58 131
SQ SEQUENCE 132 AA; 15177 MW; 9D1CB07FD353CE1C CRC64;

Query Match 71.0%; Score 480; DB 1; Length 132;
Best Local Similarity 73.8%; Pred. No. 1e-42; Mismatches 20; Indels 2; Gaps 2;
Matches 93; Conservative 11;

QY 4 ILLFLPGLVAVCAVHGIFMDRLASKKLCADDECVYTTISLASAQEDYNAPDCRFINVKKG 63
DB 8 IVLFLCFLMNPFTAT-GIFMDKLSKLCADDDCVYTTISLVRABEDYNAPDCRFINIKKG 66

QY 64 QOIYVYKLVKNGAGFWAGSVYGDG-QDEMGVVGYPRLVKEQRYQVQATKEVPTTD 122
DB 67 QLIYVYKLVKNGESGEFWAGSVYGEYEDHMGTVGYPFRSLVSEHQHYQANKTIPTID 126

QY 123 IDFCCE 128
DB 127 IDFCCE 132

RESULT 4
OTOR_RANCA STANDARD; PRT; 133 AA.
AC Q918P5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Otoraplin precursor.
GN OTOR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20334619; PubMed=10873378;
RA Robertson N.G., Heller S., Lin J.S., Resendes B.L., Weremowicz S.,
RA Denis C.S., Bell A.M., Hudspeth A.J., Morton C.C.;
RT "A novel conserved cochlear gene, OTOR: identification, expression
RT analysis, and chromosomal mapping.";
RL Genomics 66:242-248(2000).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN COCHLEA.
CC -!- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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DR EMBL; AF233518; AAF82727.1; -.
DR HSP; Q16674; 111J.
DR InterPro; IPR001452; SH3.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS00002; SH3; 1.
KW Signal; SH3 domain.
FT SIGNAL 1 23
FT CHAIN 24 132
FT DOMAIN 42 114
FT DISULFID 35 40
FT DISULFID 58 131
FT DISULFID 58 131
SQ SEQUENCE 132 AA; 15177 MW; 9D1CB07FD353CE1C CRC64;

Query Match 71.0%; Score 480; DB 1; Length 132;
Best Local Similarity 73.8%; Pred. No. 1e-42; Mismatches 20; Indels 2; Gaps 2;
Matches 93; Conservative 11;

QY 4 ILLFLPGLVAVCAVHGIFMDRLASKKLCADDECVYTTISLASAQEDYNAPDCRFINVKKG 63
DB 8 IVLFLCFLMNPFTAT-GIFMDKLSKLCADDDCVYTTISLVRABEDYNAPDCRFINIKKG 66

QY 64 QOIYVYKLVKNGAGFWAGSVYGDG-QDEMGVVGYPRLVKEQRYQVQATKEVPTTD 122
DB 67 QLIYVYKLVKNGESGEFWAGSVYGEYEDHMGTVGYPFRSLVSEHQHYQANKTIPTID 126

QY 123 IDFCCE 128
DB 127 IDFCCE 132

RESULT 4
OTOR_RANCA STANDARD; PRT; 133 AA.
AC Q918P5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Otoraplin precursor.
GN OTOR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20334619; PubMed=10873378;
RA Robertson N.G., Heller S., Lin J.S., Resendes B.L., Weremowicz S.,
RA Denis C.S., Bell A.M., Hudspeth A.J., Morton C.C.;
RT "A novel conserved cochlear gene, OTOR: identification, expression
RT analysis, and chromosomal mapping.";
RL Genomics 66:242-248(2000).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN COCHLEA.
CC -!- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-----
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-----
DR EMBL; AF233519; AAF82728.1; -.
DR HSP; Q16674; 111J.
DR InterPro; IPR001452; SH3.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS00002; SH3; 1.
KW Signal; SH3 domain.
FT SIGNAL 1 23
FT CHAIN 24 133
FT DOMAIN 48 115
FT DISULFID 35 40
FT DISULFID 58 132
FT DISULFID 58 132
SQ SEQUENCE 133 AA; 15243 MW; 25440C1A3CF911AE CRC64;

Query Match 57.7%; Score 390; DB 1; Length 133;
Best Local Similarity 58.9%; Pred. No. 2.1e-33;
Matches 66; Conservative 26; Mismatches 18; Indels 2; Gaps 2;

QY 19 HGIFMDRLASKKLCADDECVYTTISLASAQEDYNAPDCRFINVKKGQOIYVYKLVKNG-G 77
DB 22 YGVYVYKLVKSKKLCADDECVYTTISLASAQEDYNAPDCRFINVKKGELVYITKLVKEND 81

QY 78 AGEFWAGSVYGDG-QDEMGVVGYPRLVKEQRYQVQATKEVPTTDIDFCCE 128
DB 82 AGEFWAGSVYSDQYRDQGLVGYFPSSLVTLTVYKQELQELPTTAVDFYCD 133

RESULT 5
MIA_HUMAN STANDARD; PRT; 131 AA.
AC Q16674;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Melanoma derived growth regulatory protein precursor (Melanoma
DE inhibitory activity).
GN MIA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=95007612; PubMed=7923218;
RA Blesch A., Bosscherhoff A.-K., Apfel R., Behl C., Hessdoerfer B.,
RA Schmitt A., Jachimczak P., Lottspeich F., Buettner R., Bogdahn U.;
RT "Cloning of a novel malignant melanoma-derived growth-regulatory
RT protein, MIA.";
RL Cancer Res. 54:5695-5701(1994).

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OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20334619; PubMed=10873378;
RA Robertson N.G., Heller S., Lin J.S., Resendes B.L., Weremowicz S.,
RA Denis C.S., Bell A.M., Hudspeth A.J., Morton C.C.;
RT "A novel conserved cochlear gene, OTOR: identification, expression
RT analysis, and chromosomal mapping.";
RL Genomics 66:242-248(2000).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-----
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-----
DR EMBL; AF233519; AAF82728.1; -.
DR HSP; Q16674; 111J.
DR InterPro; IPR001452; SH3.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS00002; SH3; 1.
KW Signal; SH3 domain.
FT SIGNAL 1 23
FT CHAIN 24 133
FT DOMAIN 48 115
FT DISULFID 35 40
FT DISULFID 58 132
FT DISULFID 58 132
SQ SEQUENCE 133 AA; 15243 MW; 25440C1A3CF911AE CRC64;

Query Match 57.7%; Score 390; DB 1; Length 133;
Best Local Similarity 58.9%; Pred. No. 2.1e-33;
Matches 66; Conservative 26; Mismatches 18; Indels 2; Gaps 2;

QY 19 HGIFMDRLASKKLCADDECVYTTISLASAQEDYNAPDCRFINVKKGQOIYVYKLVKNG-G 77
DB 22 YGVYVYKLVKSKKLCADDECVYTTISLASAQEDYNAPDCRFINVKKGELVYITKLVKEND 81

QY 78 AGEFWAGSVYGDG-QDEMGVVGYPRLVKEQRYQVQATKEVPTTDIDFCCE 128
DB 82 AGEFWAGSVYSDQYRDQGLVGYFPSSLVTLTVYKQELQELPTTAVDFYCD 133

RESULT 5
MIA_HUMAN STANDARD; PRT; 131 AA.
AC Q16674;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Melanoma derived growth regulatory protein precursor (Melanoma
DE inhibitory activity).
GN MIA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=95007612; PubMed=7923218;
RA Blesch A., Bosscherhoff A.-K., Apfel R., Behl C., Hessdoerfer B.,
RA Schmitt A., Jachimczak P., Lottspeich F., Buettner R., Bogdahn U.;
RT "Cloning of a novel malignant melanoma-derived growth-regulatory
RT protein, MIA.";
RL Cancer Res. 54:5695-5701(1994).

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KW	Growth factor; Signal;	
FT	SIGNAL	1 24

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CC -1- SIMILARITY: Contains 1 SH3 domain.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U51437; AAC48523.1; -.
CC DR HSP; Q16674; 111J.
CC DR InterPro; IPR001452; SH3.
CC DR Pfam; PF00018; SH3; 1.
CC DR SMART; SM00326; SH3; 1.
CC DR PROSITE; PS00002; SH3; 1.
CC KW Growth factor; Signal; SH3 domain.
CC FT SIGNAL 1 22
CC FT CHAIN 23 130
CC FT DOMAIN 42 112
CC FT DISULFID 35 40
CC FT DISULFID 58 129
CC FT DISULFID 58 129
CC FT CONFLICT 46 47
CC SQ SEQUENCE 130 AA; 14353 MW; 95D153161C78E02A CRC64;

Query Match 37.9%; Score 256.5; DB 1; Length 130;
Best Local Similarity 43.1%; Pred. No. 1.3e-19;
Matches 56; Conservative 23; Mismatches 36; Indels 15; Gaps 5;

Qy 4 ILLFLPGLVAVCAVHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFNVKKG 63
Db 11 VLLSATFPFGSA-----GGRPMPLADRMCADECSHPISVAVALQDYVAPDREFLTIHQG 66

Qy 64 QQIVYVSKLVKENGAGE-FWAGSV---YGDGDEMVGVSQGYDYGDAARL---GYFPSSIVREDQTLKPAKTDV 118
Db 67 QVVYVFSKL---KGRGLFWGSGVQGYDYGDAARL---GYFPSSIVREDQTLKPAKTDV 120

Qy 119 PTTDIDFFCE 128
Db 121 KTDIWDIFYCQ 130

RESULT 7
MIA_RAT ID MIA_RAT STANDARD; PRT; 130 AA.
AC Q62946; P97591;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Melanoma derived growth regulatory protein precursor (Melanoma
DE inhibitory activity) (Cartilage-derived retinoic acid-sensitive
DE protein) (CD-RAP).
DE MIA OR CDAP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Mammary gland;
RA Lu J.X.;
RT "Gene expression changes associated with chemically-induced rat
RT mammary carcinogenesis.";
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE OF 34-124 FROM N.A.
RC TISSUE=Cartilage;
RX MEDLINE=96216414; PubMed=8621736;
RA Dietz U.H., Sandell L.J.;
RT "Cloning of a retinoic acid-sensitive mRNA expressed in cartilage and
RT during chondrogenesis.";
RL J. Biol. Chem. 271:3311-3316(1996).
CC -1- FUNCTION: MAY FUNCTION DURING CARTILAGE DEVELOPMENT AND

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CC MAINTENANCE.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: CARTILAGE PRIMORDIA AND CARTILAGE.
CC -1- INDUCTION: Repressed by retinoic acid.
CC -1- PM: MAY POSSES TWO INTRAMOLECULAR DISULFIDE BONDS.
CC -1- SIMILARITY: BELONGS TO THE MIA / OFOR FAMILY.
CC -1- SIMILARITY: Contains 1 SH3 domain.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U51438; AAC52481.1; -.
CC DR EMBL; U67884; AAB4659.1; -.
CC DR HSP; Q16674; 111J.
CC DR InterPro; IPR001452; SH3.
CC DR Pfam; PF00018; SH3; 1.
CC DR SMART; SM00326; SH3; 1.
CC DR PROSITE; PS00002; SH3; FALSE NEG.
CC KW Growth factor; Signal; SH3 domain.
CC FT SIGNAL 1 22
CC FT CHAIN 23 130
CC FT DOMAIN 42 112
CC FT DISULFID 35 40
CC FT DISULFID 58 129
CC FT CONFLICT 46 47
CC SQ SEQUENCE 130 AA; 14536 MW; 5F99149AECF74501 CRC64;

Query Match 37.6%; Score 254; DB 1; Length 130;
Best Local Similarity 40.9%; Pred. No. 2.4e-19;
Matches 52; Conservative 26; Mismatches 39; Indels 10; Gaps 4;

Qy 9 LPGLVAVCAVHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFNVKKG 63
Db 7 LLGIVILSVFSGLSRADRMPLADRLKCADECSHPISMAVALQDYVAPDREFLTIYRG 66

Qy 64 QQIVYVSKLVKENGAGE-FWAGSVYGDGQDEMVG-VGYFPRLNVRKQRYQATKEVPTT 121
Db 67 QVVYVFSKL---KGRGLFWGSGVQGYDYGDAARL---GYFPSSIVREDQTLKPGKVDKMTD 123

Qy 122 DIDDFCE 128
Db 124 EWDIFYCQ 130

RESULT 8
MIA_MOUSE ID MIA_MOUSE STANDARD; PRT; 130 AA.
AC Q61865; O09086; P97495;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Melanoma derived growth regulatory protein precursor (Melanoma
DE inhibitory activity) (Cartilage-derived retinoic acid-sensitive
DE protein) (CD-RAP).
DE MIA OR CDAP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=95007612; PubMed=7923218;
RA Blesch A., Bossenroff A.-K., Apfel R., Behl C., Hesseoerfer B.,
RA Schmitt A., Jachimczak P., Lottspeich F., Buettnner R., Bogdahn U.;
RT "Cloning of a novel malignant melanoma-derived growth-regulatory
RT protein, MIA.";

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Tue Dec 30 10:20:54 2003

us-10-019-455a-6.rsp

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Cancer Res. 54:5695-5701(1994).
[2]
SEQUENCE FROM N.A.
STRAIN=129/SV;
MEDLINE=97251341; PubMed=9097023;
Bossenroff A.K., Kondo S., Moser M., Dietz U., Copeland N.G.,
Trenkle T., McClelland M., Adlkofer K., Welsh J.;
Gilbert D.J., Jenkins N.A., Buettner R., Sandell L.J.;
"Mouse CD-RAP/MIA gene: structure, chromosomal localization, and
expression in cartilage and chondrosarcoma.";
Dev. Dyn. 208:516-525(1997).
INHIBITION ON MELANOMA CELLS IN VITRO AS
WELL AS SOME OTHER NEUROECTODERMAL TUMORS, INCLUDING GLIOMAS (BY
SIMILARITY).
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: ALL MALIGNANT MELANOMA CELL LINES TESTED AND
INFREQUENTLY IN GLIOMA CELL LINES.
-!- PTM: MAY POSSESS TWO INTRAMOLECULAR DISULFIDE BONDS.
-!- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
-!- SIMILARITY: Contains 1 SH3 domain.
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EMBL; X94322; CAA63983.1; -.
EMBL; U85612; AAB42082.1; -.
EMBL; X97965; CAA66608.1; -.
HSSP; Q16674; 111J.
MCD; MGI:109615; Mia.
GO; GO:0007160; P:cell-matrix adhesion; IMP.
GO; GO:0030198; P:extracellular matrix organization and bioge. . .; IMP.
InterPro; IPR001452; SH3.
Pfam; PF00018; SH3; 1.
SMART; SM00326; SH3; 1.
PROSITE; PS50002; SH3; FALSE NEG.
Growth factor; Signal; SH3 domain.
POTENTIAL.
SIGNAL 1 22
CHAIN 23 130
MELANOMA DERIVED GROWTH REGULATORY
PROTEIN.
DOMAIN 42 112
DISULFID 35 40
BY SIMILARITY.
DISULFID 58 129
BY SIMILARITY.
CONFLICT 112 113
TL -> NS (IN REF. 1).
SEQUENCE 130 AA; 14593 MW; 16C957459C5BBSF9 CRC64;
Query Match 34.8%; Score 235.5; DB 1; Length 130;
Best Local Similarity 43.5%; Pred. No. 2e-17;
Matches 47; Conservative 21; Mismatches 35; Indels 5; Gaps 3;
QY 23 MDRLASKKLCADDECVYTTSLASAEQEDYNAPDCRFINVKKGQOIVYVSKLVKENGAGE-F 81
Db 26 MPKLADWKLKADCECHPSHPSMAVALQDYVAPDCRFLTIYRGQVYVFSKL---KGRGLP 82
QY 82 WAGSVYGDQDENGCV-VGYFPRNLVKEQRVYQVQATKEVPTTIDFPCE 128
Db 83 WGSVQGGYGDLAARLGYFPSSIVREDTLKPKIDMKTDQWDFYQ 130
RESULT 9
VAV3 MOUSE STANDARD; PRT; 847 AA.
AC Q9R0C8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Vav-3 protein.
GN VAV3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
KW Phorbol-ester binding; Zinc; SH2 domain; SH3 domain; Repeat;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20179693; PubMed=10713454;
RA Trenkle T., McClelland M., Adlkofer K., Welsh J.;
RT "Major transcript variants of VAV3, a new member of the VAV family of
guanine nucleotide exchange factors.";
RL Gene 2451139-149 (2000). FACTOR FOR GTP-BINDING PROTEINS RHOA, RHOG AND,
CC -!- FUNCTION: EXCHANGE. FACTOR FOR GTP-BINDING PROTEINS RHOA, RHOG AND,
CC TO A LESSER EXTENT, RAC-1. BINDS PHYSICALLY TO THE NUCLEOTIDE-FREE
CC STATES OF THOSE GTPASES (BY SIMILARITY).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Alpha;
CC IsoId=Q9R0C8-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=Q9R0C8-2; Sequence=Not described;
CC -!- SIMILARITY: Contains 1 calponin-homology (CH) domain.
CC -!- SIMILARITY: Contains 1 DBL-homology (DH) domain.
CC -!- SIMILARITY: Contains 1 PH domain.
CC -!- SIMILARITY: Contains 1 zinc-dependent phorbol-ester and DAG
CC binding domain.
CC -!- SIMILARITY: Contains 1 SH2 domain.
CC -!- SIMILARITY: Contains 2 SH3 domains.
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EMBL; AF067816; AAF09171.1; -.
HSSP; P29355; 1SEM.
MCD; MGI:188518; Vav3.
InterPro; IPR001715; Calponin-like.
InterPro; IPR003247; CH type.
InterPro; IPR002219; DAG_PE-bind.
InterPro; IPR001331; GDS_CDC24.
InterPro; IPR001849; PH.
InterPro; IPR000219; RhoGEF.
InterPro; IPR000980; SH2.
InterPro; IPR001452; SH3.
InterPro; IPR003096; SM22_calponin.
Pfam; PF00130; DAG_PE-bind; 1.
Pfam; PF00169; PH; 1.
Pfam; PF00621; RhoGEF; 1.
Pfam; PF00017; SH2; 1.
Pfam; PF00018; SH3; 1.
PRINTS; PR00401; SH2DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
PRINTS; PR00888; SM22CALPONIN.
ProDom; PD001527; CH type; 1.
ProDom; PD000093; SH2; 1.
ProDom; PD000066; SH3; 1.
SMART; SM00109; CH; 1.
SMART; SM00033; CH; 1.
SMART; SM00233; PH; 1.
SMART; SM00325; RhoGEF; 1.
SMART; SM00252; SH2; 1.
SMART; SM00326; SH3; 2.
PROSITE; PS50021; CH; 1.
PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
PROSITE; PS50010; DH_2; 1.
PROSITE; PS50074; DH_1; 1.
PROSITE; PS50043; PH_DOMAIN; 1.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 2.
KW Phorbol-ester binding; Zinc; SH2 domain; SH3 domain; Repeat;

```

KW Guanine-nucleotide releasing factor; Alternative splicing.  
 FT DOMAIN 1 119 CH.  
 FT DOMAIN 192 371 DH.  
 FT DOMAIN 400 502 EH.  
 FT DOMAIN 514 562 FH.  
 FT DOMAIN 592 660 GH.  
 FT DOMAIN 672 766 IH.  
 FT DOMAIN 788 847 JH.  
 SQ SEQUENCE 847 AA; 97946 MW; 9AGB63F0D9E60F8F CRC64;  
 Query Match 13.1%; Score 88.5; DB 1; Length 847;  
 Best Local Similarity 31.3%; Pred. No. 0.24;  
 Matches 21; Conservative 14; Mismatches 21; Indels 11; Gaps 2;  
 QY 41 ISLSAQEDYNAPDCRFNVKKGQIYVYVYKLVKENGAGFVAGSVYGDQDENGWVGVF 100  
 DB LGIARARDFCFARDRELKLLKGMVKIYTKM-----SANGWVRGEVNGR-----VGNVF 838  
 QY 101 PRNLYKE 107  
 DB 839 PSTYVEE 845  
 RESULT 10  
 VAV HUMAN STANDARD; PRT: 845 AA.  
 AC P15498; Q15860;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Vav proto-oncogene.  
 GN VAV1 OR VAV.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Denninger D.J., Borges C.R., Shaw C.L., Cushman A.M., Kawahara R.S.;  
 RT "Transcriptional regulation of the vav proto-oncogene."  
 RL Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP SEQUENCE OF 62-845 FROM N.A.  
 RX MEDLINE=90005432; PubMed=2477241;  
 RA Katrav S., Martin-Zanca D., Barbacid M.;  
 RT "vav, a novel human oncogene derived from a locus ubiquitously  
 expressed in hematopoietic cells."  
 RL EMBO J. 8:2283-2290(1989).  
 RN [3]  
 RP SEQUENCE OF 1-61 FROM N.A.  
 RX MEDLINE=91172176; PubMed=2005887;  
 RA Katrav S., Cleveland J.L., Heslop H.E., Pulido D.;  
 RT "Loss of the amino-terminal helix-loop-helix domain of the vav proto-  
 oncogene activates its transforming potential."  
 RL Mol. Cell. Biol. 11:1912-1920(1991).  
 RN [4]  
 RP SEQUENCE OF 299-837 FROM N.A.  
 RA Romero F.;  
 RT Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.  
 RN [5]  
 RP SEQUENCE OF 299-334 FROM N.A.  
 RX MEDLINE=96038895; PubMed=7478592;  
 RA Ramos-Morales F., Romero F., Schweighoffer F., Bismuth G., Camonis J.,  
 RA Tortolero M., Fischer S.;  
 RT "The proline-rich region of Vav binds to Grb2 and Grb3-3."  
 RL Oncogene 11:1665-1669(1995).  
 RN [6]  
 RP SIMILARITY TO CDC24 FAMILY.  
 RX MEDLINE=92228488; PubMed=1565462;  
 RA Adams J.M., Houston H., Allen J., Lints T., Harvey R.;  
 RT "The hematopoietically expressed vav proto-oncogene shares homology  
 with the dhl GDP-GTP exchange factor, the bcr gene and a yeast gene  
 (CDC24) involved in cytoskeletal organization.";

Oncogene 7:611-618(1992).  
 CC -i- FUNCTION: Couples tyrosine kinase signals with the activation of  
 the Rho/Rac GTPases, thus leading to cell differentiation and/or  
 proliferation.  
 CC -i- SUBUNIT: Interacts with SLA (By similarity). Interacts with Grb2  
 and Grb3.  
 CC -i- TISSUE SPECIFICITY: WIDELY EXPRESSED IN HEMATOPOIETIC CELLS BUT  
 NOT IN OTHER CELL TYPES.  
 CC -i- PTM: Phosphorylated on tyrosine residues.  
 CC -i- MISCELLANEOUS: 'Vav' stands for the sixth letter of the Hebrew  
 alphabet.  
 CC -i- SIMILARITY: Contains 1 calponin-homology (CH) domain.  
 CC -i- SIMILARITY: Contains 1 DEL-homology (DH) domain.  
 CC -i- SIMILARITY: Contains 1 PH domain.  
 CC -i- SIMILARITY: Contains 1 zinc-dependent phorbol-ester and DAG  
 binding domain.  
 CC -i- SIMILARITY: Contains 1 SH2 domain.  
 CC -i- SIMILARITY: Contains 2 SH3 domains.  
 CC -i- CAUTION: Ref.2 sequence differs from that shown due to frameshifts  
 in position 322 and 355.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC EMBL; AF030227; AAC25011.1; JOINED.  
 CC EMBL; AF030201; AAC25011.1; JOINED.  
 CC EMBL; AF030202; AAC25011.1; JOINED.  
 CC EMBL; AF030203; AAC25011.1; JOINED.  
 CC EMBL; AF030204; AAC25011.1; JOINED.  
 CC EMBL; AF030205; AAC25011.1; JOINED.  
 CC EMBL; AF030206; AAC25011.1; JOINED.  
 CC EMBL; AF030207; AAC25011.1; JOINED.  
 CC EMBL; AF030208; AAC25011.1; JOINED.  
 CC EMBL; AF030209; AAC25011.1; JOINED.  
 CC EMBL; AF030210; AAC25011.1; JOINED.  
 CC EMBL; AF030211; AAC25011.1; JOINED.  
 CC EMBL; AF030212; AAC25011.1; JOINED.  
 CC EMBL; AF030213; AAC25011.1; JOINED.  
 CC EMBL; AF030214; AAC25011.1; JOINED.  
 CC EMBL; AF030215; AAC25011.1; JOINED.  
 CC EMBL; AF030216; AAC25011.1; JOINED.  
 CC EMBL; AF030217; AAC25011.1; JOINED.  
 CC EMBL; AF030218; AAC25011.1; JOINED.  
 CC EMBL; AF030219; AAC25011.1; JOINED.  
 CC EMBL; AF030220; AAC25011.1; JOINED.  
 CC EMBL; AF030221; AAC25011.1; JOINED.  
 CC EMBL; AF030222; AAC25011.1; JOINED.  
 CC EMBL; AF030223; AAC25011.1; JOINED.  
 CC EMBL; AF030224; AAC25011.1; JOINED.  
 CC EMBL; AF030225; AAC25011.1; JOINED.  
 CC EMBL; AF030226; AAC25011.1; JOINED.  
 CC EMBL; X16316; CAA34383.1; ALT\_FRAME.  
 CC EMBL; M59834; AAA63267.1; --  
 CC EMBL; X83931; CAA58783.1; --  
 CC PIR; B39576; TVHUVV.  
 CC HSSP; P29354; IGRI.  
 CC TRANSFAC; T00880; --  
 CC Genew; HGNC:12657; VAV1.  
 CC MIM; 164875; --  
 CC GO; GO:0003700; P:transcription factor activity; TAS.  
 CC GO; GO:0007048; P:oncogenesis; TAS.  
 CC InterPro; IPR001715; Calponin-like.  
 CC InterPro; IPR003247; CH type.  
 CC InterPro; IPR002219; DAG PE-bind.  
 CC InterPro; IPR001331; GDS\_CDC24.  
 CC InterPro; IPR001849; PH\_--  
 CC InterPro; IPR000219; Rhogef.  
 CC InterPro; IPR000980; SH2.

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DR InterPro; IPR001452; SH3.
DR InterPro; IPR003096; SM22_calponin.
DR Pfam; PF00307; CH; 1.
DR Pfam; PF00130; DAG_PE-bind; 1.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00621; RhoGEF; 1.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 2.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR PRINTS; PR00888; SM22CALPONIN.
DR ProDom; PD001527; CH type; 1.
DR ProDom; PD000093; SH2; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00109; C1; 1.
DR SMART; SM00033; CH; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00325; RhoGEF; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 2.
DR PROSITE; PS00021; CH; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS0010; DH_1; 1.
DR PROSITE; PS00741; DH_1; 1.
DR PROSITE; PS00003; PH DOMAIN; 1.
DR PROSITE; PS00002; SH2; 1.
DR PROSITE; PS00002; SH3; 2.
DR PROSITE; PS00002; SH3; 2.
KW Proto-oncogene; Phorbol-ester binding; Zinc; SH2 domain; SH3 domain;
KW Guanine-nucleotide releasing factor; Repeat; Phosphorylation.
FT DOMAIN 1 119
FT DOMAIN 194 373
FT DOMAIN 402 504
FT DOMAIN 516 564
FT DOMAIN 617 660
FT DOMAIN 671 765
FT DOMAIN 782 842
FT DOMAIN 264 264
FT CONFLICT 718 718
FT CONFLICT 718 718
FT CONFLICT 718 718
SQ SEQUENCE 845 AA; 98313 MW; AC3BC9736FD2F138 CRC64;

Query Match 12.8%; Score 86.5; DB 1; Length 845;
Best Local Similarity 32.9%; Pred. No. 0.38;
Matches 23; Conservative 13; Mismatches 21; Indels 13; Gaps 3;

Qy 44 ASAEQYDNPDCRFVNVKQGIYVYSLVKNKENGAFWAGSVGGQDQEMGVGVFPAN 103
Db 787 AKARYDFCARDSELSKEGDII---KILNKKQGGQWWRGEIYGR-----VGWFFPAN 835

Qy 104 LVKEQRVYQE 113
Db 836 YVEED--YSE 843

RESULT 11
ID VAV3 HUMAN STANDARD; PRT; 847 AA.
AC Q9UKW4; Q95230; Q9Y5X8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vav-3 protein.
GN VAV3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE=94455043; PubMed=10523675;
Movilla N., Bustelo X.R.;
RT "Biological and regulatory properties of Vav-3, a new member of the
RT Vav family of oncoproteins."

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RL Mol. Cell. Biol. 19:7870-7885(1999).
RN [2].
RP SEQUENCE FROM N.A.
RC TISSUE=Breast, and Colon carcinoma;
RX MEDLINE=98371222; PubMed=9705494;
RA Trenkle T., Welsh J., Jung B., Mathieu-Daude F., McClelland M.;
RT "Non-stoichiometric reduced complexity probes for cDNA arrays.";
RL Nucleic Acids Res. 26:3883-3891(1998).
CC -!- FUNCTION: EXCHANGE FACTOR FOR GTP-BINDING PROTEINS RHOA, RHOG AND,
CC TO A LESSER EXTENT, RAC-1. BINDS PHYSICALLY TO THE NUCLEOTIDE-FREE
CC STATES OF THOSE GTPASES.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Alpha;
CC IsoId=Q9UKW4-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=Q9UKW4-2; Sequence=VSP_001820;
CC -!- SIMILARITY: Contains 1 calponin-homology (CH) domain.
CC -!- SIMILARITY: Contains 1 DEL-homology (DH) domain.
CC -!- SIMILARITY: Contains 1 PH domain.
CC -!- SIMILARITY: Contains 1 zinc-dependent phorbol-ester and DAG
CC binding domain.
CC -!- SIMILARITY: Contains 1 SH2 domain.
CC -!- SIMILARITY: Contains 2 SH3 domains.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
CC EMBL; AF118887; AAD20349.1; -.
CC EMBL; AF118886; AAD20348.1; -.
CC EMBL; AF067817; AAC79695.1; -.
CC HSSP; P29355; 1SEM.
CC GENE; HGNC:12659; VAV3.
CC MIM; 605541; -.
CC GO; GO:0005096; F:GTPase activator activity; TAS.
CC GO; GO:0005070; F:SH3/SH2 adaptor protein activity; TAS.
CC GO; GO:0007264; P:small GTPase mediated signal transduction; TAS.
CC InterPro; IPR001715; Calponin-like.
CC InterPro; IPR003247; CH type.
CC InterPro; IPR002219; DAG_PE-bind.
CC InterPro; IPR001331; GDS_CDC24.
CC InterPro; IPR001849; PH.
CC InterPro; IPR000219; RhoGEF.
CC InterPro; IPR000980; SH2.
CC InterPro; IPR001452; SH3.
CC InterPro; IPR003096; SM22_calponin.
CC Pfam; PF00307; CH; 1.
CC Pfam; PF00130; DAG_PE-bind; 1.
CC Pfam; PF00169; PH; 1.
CC Pfam; PF00621; RhoGEF; 1.
CC Pfam; PF00017; SH2; 1.
CC Pfam; PF00018; SH3; 1.
CC PRINTS; PR00401; SH2DOMAIN.
CC PRINTS; PR00452; SH3DOMAIN.
CC PRINTS; PR00888; SM22CALPONIN.
CC ProDom; PD001527; CH type; 1.
CC ProDom; PD000093; SH2; 1.
CC ProDom; PD000066; SH3; 1.
CC SMART; SM00109; C1; 1.
CC SMART; SM00033; CH; 1.
CC SMART; SM00233; PH; 1.
CC SMART; SM00325; RhoGEF; 1.
CC SMART; SM00252; SH2; 1.
CC SMART; SM00326; SH3; 2.
CC PROSITE; PS00021; CH; 1.
CC PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
CC PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.
CC PROSITE; PS0010; DH_1; 1.
CC PROSITE; PS00741; DH_1; 1.
CC PROSITE; PS00003; PH DOMAIN; 1.
CC PROSITE; PS00002; SH2; 1.
CC PROSITE; PS00002; SH3; 2.

```





DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Vav proto-oncogene.  
OS VAV1 OR VAV.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92228488; PubMed=1565462;  
RA Adams J.A., Houston H., Allen J., Lints T., Harvey R.;  
RT "The hematopoietically expressed vav proto-oncogene shares homology  
RT with the dbi GTP-exchange factor, the bcr gene and a yeast gene  
RT (CDC24) involved in cytoskeletal organization.";  
RL Oncogene 7:611-618(1992).  
RN [2]  
RP SEQUENCE OF 1-93 FROM N.A.  
RX MEDLINE=91172176; PubMed=2005887;  
RA Katav S., Cleveland J.L., Heslop H.E., Pulido D.;  
RT "Loss of the amino-terminal helix-loop-helix domain of the vav proto-  
RT oncogene activates its transforming potential.";  
RL Mol. Cell. Biol. 11:1912-1920(1991).  
RN [3]  
RP INTERACTION WITH SLA.  
RX MEDLINE=20130290; PubMed=10662792;  
RA Sosinowski T., Pandey A., Dixit V.M., Weiss A.;  
RT "Grc-like adaptor protein (SLAP) is a negative regulator of T cell  
RT receptor signaling.";  
RL J. Exp. Med. 191:463-474(2000).  
CC -!- FUNCTION: Couples tyrosine kinase signals with the activation of  
CC the Rho/Rac GTPases, thus leading to cell differentiation and/or  
CC proliferation.  
CC -!- SUBUNIT: Interacts with SLA.  
CC -!- TISSUE SPECIFICITY: Widely expressed in hematopoietic cells but  
CC not in other cell types.  
CC -!- PTM: Phosphorylated on tyrosine residues (By similarity).  
CC -!- SIMILARITY: Contains 1 calponin-homology (CH) domain.  
CC -!- SIMILARITY: Contains 1 DSL-homology (DH) domain.  
CC -!- SIMILARITY: Contains 1 PH domain.  
CC -!- SIMILARITY: Contains 1 zinc-dependent phorbol-ester and DAG  
CC binding domain.  
CC -!- SIMILARITY: Contains 1 SH3 domain.  
CC -!- SIMILARITY: Contains 2 SH3 domains.  
CC  
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CC or send an email to [license@sb-sib.ch](mailto:license@sb-sib.ch)).  
CC  
CC EMBL; X64361; CAA45713.1; -;  
CC EMBL; M59833; AAG63402.1; -;  
CC PIR; A61187; TVMSV.  
CC PDB; 1F5X; 15-SEP-00.  
CC PDB; 1GCP; 28-JAN-03.  
CC PDB; 1GCO; 28-JAN-03.  
CC PDB; 1X1Z; 18-DEC-02.  
CC TRANSFAC; T01230; -;  
CC MGD; MGI:98923; Vavl.  
CC InterPro; IPR001715; Calponin-like.  
CC InterPro; IPR003247; CH type.  
CC InterPro; IPR002219; DAG PE-bind.  
CC InterPro; IPR001331; GDS\_CDC24.  
CC InterPro; IPR001849; PH\_CDC24.  
CC InterPro; IPR000219; RhoGEF.  
CC InterPro; IPR000980; SH2.  
CC InterPro; IPR001452; SH3.  
CC InterPro; IPR003096; SM22\_calponin.  
CC Pfam; PF00307; CH; 1.  
CC Pfam; PF00130; DAG PE-bind; 1.  
CC Pfam; PF00169; PH; 1.  
  
DR Pfam; PF00621; RhoGEF; 1.  
DR Pfam; PF00017; SH2; 1.  
DR Pfam; PF00018; SH3; 2.  
DR PRINTS; PR00401; SH2DOMAIN.  
DR PRINTS; PR00452; SH3DOMAIN.  
DR PRINTS; PR00888; SM22CALPONIN.  
DR ProDom; PD001527; CH type; 1.  
DR ProDom; PD000093; SH2; 1.  
DR ProDom; PD000066; SH3; 1.  
DR SMART; SM00109; C1; 1.  
DR SMART; SM00033; CH; 1.  
DR SMART; SM00233; PH; 1.  
DR SMART; SM00325; RhoGEF; 1.  
DR SMART; SM00252; SH2; 1.  
DR SMART; SM00326; SH3; 2.  
DR PROSITE; PS00021; CH; 1.  
DR PROSITE; PS00479; DAG PE BIND DOM 1; 1.  
DR PROSITE; PS00081; DAG PE BIND DOM 2; 1.  
DR PROSITE; PS00101; DH 2; 1.  
DR PROSITE; PS00741; DH 1; 1.  
DR PROSITE; PS00003; PH DOMAIN; 1.  
DR PROSITE; PS00001; SH2; 1.  
DR PROSITE; PS00002; SH3; 2.  
KW Proto-oncogene; Phorbol-ester binding; Zinc; SH2 domain; SH3 domain;  
KW Guanine-nucleotide releasing factor; Repeat; Phosphorylation;  
FT 3D-structure.  
FT DOMAIN 1 119 CH.  
FT DOMAIN 194 373 DH.  
FT DOMAIN 402 504 PH.  
FT DOMAIN 516 564 PHORBOL-ESTER AND DAG BINDING.  
FT DOMAIN 617 660 SH3 1.  
FT DOMAIN 671 765 SH2.  
FT DOMAIN 782 842 SH3 2.  
FT CONFLICT 29 29 Q -> E (IN REF. 2).  
SQ SEQUENCE 845 AA; 98136 MW; 3666DCDD1C5229DA CRC64;  
  
Query Match 12.6%; Score 85.5; DB 1; Length 845;  
Best Local Similarity 31.4%; Pred. No. 0.49;  
Matches 22; Conservative 14; Mismatches 21; Indels 13; Gaps 3;  
  
QY 44 ASAGEDYNAPDCRFNVKKGQIIYYVSKLVKENGAGFVAGSVYGDQDEGVGVYFPRN 103  
DB 787 AKARYDFCDARSRSLKSGDII-----KILNKGQGGWRRGEIYGR-----IGWFFPSN 835  
QY 104 LVKGRVYQVE 113  
DB 836 YVEED--YSE 843  
  
RESULT 14  
VAV2\_MOUSE  
ID VAV2\_MOUSE STANDARD; PRT; 868 AA.  
AC Q60392;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Vav-2 protein.  
GN VAV2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=C57BL/6;  
RX MEDLINE=96313271; PubMed=8710375;  
RA Schuebel K.E., Bustelo X.R., Nielsen D.A., Song B.J., Barbacid M.,  
RA Goldman D., Lee I.J.;  
RT "Isolation and characterization of murine vav2, a member of the vav  
RT family of proto-oncogenes.";  
RL Oncogene 13:363-371(1996).  
CC -!- FUNCTION: Guanine nucleotide exchange factor for the Rho family  
CC of Ras-related GTPases (By similarity).  
CC

CC --!- SIMILARITY: Contains 1 calponin-homology (CH) domain.  
CC --!- SIMILARITY: Contains 1 DBL-homology (DH) domain.  
CC --!- SIMILARITY: Contains 1 PH domain.  
CC --!- SIMILARITY: Contains 1 zinc-dependent phorbol-ester and DAG binding domain.  
CC --!- SIMILARITY: Contains 1 SH2 domain.  
CC --!- SIMILARITY: Contains 2 SH3 domains.  
CC -----  
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CC -----  
CC EMBL; U37017; AAC52761.1; --  
CC HSSP; Q60631; IGBQ.  
CC MGD; MGI:102718; Vav2.  
CC InterPro; IPR001715; Calponin-like.  
CC InterPro; IPR003247; CH type.  
CC InterPro; IPR002219; DAG\_PE-bind.  
CC InterPro; IPR001331; GDS\_CDC24.  
CC InterPro; IPR001849; PH.  
CC InterPro; IPR000219; RhoGEF.  
CC InterPro; IPR000980; SH2.  
CC InterPro; IPR001452; SH3.  
CC Pfam; PF00307; CH; 1.  
CC Pfam; PF00130; DAG\_PE-bind; 1.  
CC Pfam; PF00169; PH; 1.  
CC Pfam; PF00621; RhoGEF; 1.  
CC Pfam; PF00017; SH2; 1.  
CC Pfam; PF00018; SH3; 2.  
CC PRINTS; PR00401; SH2DOMAIN.  
CC PRODOM; PD000527; CH\_type; 1.  
CC PRODOM; PD000093; SH2; 1.  
CC PRODOM; PD000066; SH3; 2.  
CC SMART; SM00109; C1; 1.  
CC SMART; SM00033; CH; 1.  
CC SMART; SM00233; PH; 1.  
CC SMART; SM00325; RhoGEF; 1.  
CC SMART; SM00252; SH2; 1.  
CC SMART; SM00326; SH3; 2.  
CC PROSITE; PS00021; CH; 1.  
CC PROSITE; PS00479; DAG\_PE\_BIND\_DOM\_1; 1.  
CC PROSITE; PS00081; DAG\_PE\_BIND\_DOM\_2; 1.  
CC PROSITE; PS00010; DH\_2; 1.  
CC PROSITE; PS00741; DH\_1; 1.  
CC PROSITE; PS50003; PH DOMAIN; 1.  
CC PROSITE; PS50001; SH2; 1.  
CC PROSITE; PS50002; SH3; 2.  
KW Phorbol-ester binding; Zinc; SH2 domain; SH3 domain;  
KW Guanine-nucleotide releasing factor; Repeat; Phosphorylation.  
FT DOMAIN 1 119  
FT DOMAIN 193 371  
FT DOMAIN 400 502  
FT DOMAIN 514 562  
FT DOMAIN 576 642  
FT DOMAIN 663 757  
FT DOMAIN 806 867  
FT MOD\_RES 142 142  
FT MOD\_RES 159 159  
FT MOD\_RES 172 172  
FT SEQUENCE 868 AA; 99915 MW; D18581E7EB2DBC2 CRC64;  
Query Match 12.2%; Score 82.5; DB 1; Length 868;  
Best Local Similarity 27.6%; Pred. No. 1;  
Matches 21; Conservative 20; Mismatches 22; Indels 13; Gaps 3;

QY 38 VYT---ISLASAQEDYNAPDCRFINVKKQQQIYVYVSKLVKENGAGFWAGSVYGDQDEM 94  
Db 802 VTFPRVIGTAVARYNFARDFMRLELSREGDVVKIYRIGGDOG---WVKG-----ETN 851  
QY 95 GVVGYPFRNLVKEQV 110  
Db 852 GRIGWFPSTYVEEGV 867  
RESULT 15  
ID VAV2 HUMAN STANDARD; PRT; 878 AA.  
AC P52735;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Vav-2 protein.  
GN VAV2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=95283235; PubMed=7762982;  
RA Henske E.P., Short M.P., Jozwiak S., Bovey C.M., Ramlakhan S.,  
RA Haines J.L., Kwiatkowski D.J.;  
RT "Identification of VAV2 on 9q34 and its exclusion as the tuberous  
RT sclerosis gene TSC1";  
RL Ann. Hum. Genet. 59:25-37(1995).  
RN [2]  
RP PHOSPHORYLATION OF TYR-142; TYR-159 AND TYR-172.  
RX MEDLINE=22464432; PubMed=12454019;  
RA Tamás P., Solti Z., Bauer P., Illes A., Sipeki S., Bauer A.,  
RA Farago A., Downard J., Buday L.;  
RT "Mechanism of epidermal growth factor regulation of Vav2, a guanine  
RT nucleotide exchange factor for Rac";  
RL J. Biol. Chem. 278:5163-5171(2003).  
CC --!- FUNCTION: Guanine nucleotide exchange factor for the Rho family  
CC of Ras-related GTPases.  
CC --!- TISSUE SPECIFICITY: Widely expressed.  
CC --!- SIMILARITY: Contains 1 calponin-homology (CH) domain.  
CC --!- SIMILARITY: Contains 1 DBL-homology (DH) domain.  
CC --!- SIMILARITY: Contains 1 PH domain.  
CC --!- SIMILARITY: Contains 1 zinc-dependent phorbol-ester and DAG binding domain.  
CC --!- SIMILARITY: Contains 1 SH2 domain.  
CC --!- SIMILARITY: Contains 2 SH3 domains.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; S76992; AAB34377.1; --  
CC PIR; I51940; I51940.  
CC HSSP; P08631; 1BU1.  
CC Genew; HGNC:12658; VAV2.  
CC MIM; 600428; --  
CC InterPro; IPR001715; Calponin-like.  
CC InterPro; IPR003247; CH type.  
CC InterPro; IPR002219; DAG\_PE-bind.  
CC InterPro; IPR001331; GDS\_CDC24.  
CC InterPro; IPR001849; PH.  
CC InterPro; IPR000219; RhoGEF.  
CC InterPro; IPR000980; SH2.  
CC InterPro; IPR001452; SH3.  
CC Pfam; PF00307; CH; 1.  
CC Pfam; PF00130; DAG\_PE-bind; 1.

DR Pfam; PF00169; PH; 1.  
 DR Pfam; PF00621; RHOGEF; 1.  
 DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00018; SH3; 2.  
 DR PRINTS; PR00401; SH2DOMAIN.  
 DR PRINTS; PR00452; SH3DOMAIN.  
 DR ProDom; PD001527; CH type; 1.  
 DR ProDom; PD000093; SH2; 1.  
 DR ProDom; PD000066; SH3; 2.  
 DR SMART; SM00109; CH; 1.  
 DR SMART; SM00033; CH; 1.  
 DR SMART; SM00233; PH; 1.  
 DR SMART; SM00325; RHOGEF; 1.  
 DR SMART; SM00252; SH2; 1.  
 DR SMART; SM00326; SH3; 2.  
 DR PROSITE; PS50021; CH; 1.  
 DR PROSITE; PS00479; DAG\_PE\_BIND\_DOM\_1; 1.  
 DR PROSITE; PS50081; DAG\_PE\_BIND\_DOM\_2; 1.  
 DR PROSITE; PS50010; DH\_2; 1.  
 DR PROSITE; PS00741; DH\_1; 1.  
 DR PROSITE; PS50003; PH DOMAIN; 1.  
 DR PROSITE; PS50001; SH2; 1.  
 DR PROSITE; PS50002; SH3; 2.  
 KW Phorbol-ester binding; Zinc; SH2 domain; SH3 domain;  
 KW Guanine-nucleotide releasing factor; Repeat; Phosphorylation.  
 FT DOMAIN 1 119  
 FT DOMAIN 198 376  
 FT DOMAIN 405 512  
 FT DOMAIN 524 572  
 FT DOMAIN 586 652  
 FT DOMAIN 673 767  
 FT DOMAIN 816 877  
 FT MOD\_RES 142 142  
 FT MOD\_RES 159 159  
 FT MOD\_RES 172 172  
 SQ SEQUENCE 878 AA; 101256 MW; C8PF7681032146B4 CRC64;

Query Match 12.1%; Score 81.5; DB 1; Length 878;  
 Best Local Similarity 26.3%; Pred. No. 1.3;  
 Matches 20; Conservative 21; Mismatches 22; Indels 13; Gaps 3;  
 QY 38 VYT---ISLASAQEDYNAPDCRFNVKGGQIYVYKLVKENGAGEFWAGSVYGDQDEM 94  
 Db 812 VFTPRVIGTAVARYNFAARDMRELSRLREGDVVRIYSRIGGDG---WNKG-----ETN 861  
 QY 95 GVVGYPFRNLVKEQRV 110  
 Db 862 GRIGWFPFTVVEEGI 877

Search completed: December 29, 2003, 16:04:12  
 Job time : 7.01961 secs



RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,  
 RA Ballaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,  
 RA Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Hernandez J.R., Houck J.,  
 RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarri C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Williams S.M., Woodage T., Worley K.C., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RA "The genome sequence of Drosophila melanogaster."  
 RL Science 287:2185-2195(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Celinker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,  
 RA Evans C.A., Gocayne J.D., Hoskins R.A., Galle R.F.,  
 RA Banzone J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,  
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,  
 RA Dodson K., Dorset V., Doup L.E., Doyle C., Dresnek D., Farfan D.,  
 RA Ferrera S., Frise E., Galle R.F., Garg N.S., George R.A.,  
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,  
 RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,  
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,  
 RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., Schemel F.,  
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,  
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,  
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;  
 RA "Sequencing of Drosophila melanogaster genome."  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Prochnick S.B., Smith C.D.,  
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celinker S.E.,  
 RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,  
 RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,  
 RA Searle S.M.J., Smith E., Shu S., Smutnák F., Whitfield E.,  
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;  
 RA "Annotation of Drosophila melanogaster genome."  
 RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Adams M.D., Celinker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA FlyBase;  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AE003614; AA052413.2; -;  
 DR FlyBase; FBgn0051635; CG31635;  
 SQ SEQUENCE 1257 AA; 139136 MW; 5843F0540E9A511 CRC64;

Query Match 13.2%; Score 89; DB 5; Length 1257;  
 Best Local Similarity 27.4%; Pred. NO. 1.2;  
 Matches 32; Conservative 18; Mismatches 55; Indels 12; Gaps 3;  
 6 LLFLPLVAVCAVHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPCRFINVKKGQ 65  
 17 LALVGLLICCLPTLTWATLSDKRLCADPKCEQIISMGIAKITYAIGEGILSFINSP 76  
 66 IYVYSKLKENGAGFFAGSVGGQDEMGVVPFRLNVKEQVY---QEATKEVP 119  
 77 IRLVLSKAGSN--MOLW-----GVDINGRGYANKDFINEKKILVRDKLLYEVP 124  
 RESULT 10  
 ID Q9VMA7 PRELIMINARY; PRT; 1430 AA.  
 AC Q9VMA7;  
 DT 01-MAY-2000 (TREMELrel. 13, Created)  
 DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)  
 DE CG11098 protein.  
 GN CG11098.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OC NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkeley;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Fandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,  
 RA Ballaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,  
 RA Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarri C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Williams S.M., Woodage T., Worley K.C., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RA "The genome sequence of Drosophila melanogaster."  
 RL Science 287:2185-2195(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Adams M.D., Celinker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,  
 RA Celinker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

ProDom: PD000066; SH3; 1.  
DR SMART; SM00252; SH2; 1.  
DR SMART; SM00326; SH3; 2.  
DR PROSITE; PS00001; SH2; 1.  
DR PROSITE; PS00002; SH3; 2.  
KW Hypothetical protein.  
SQ SEQUENCE 287 AA; 32662 MW; BF2850B8F921F048 CRC64;

Query Match 13.1%; Score 88.5; DB 11; Length 287;  
Best Local Similarity 31.3%; Pred. No. 0.22; Indels 11; Gaps 2;  
Matches 21; Conservative 14; Mismatches 21; Last annotation update)

QY 41 ISLASAQEDYNAPDCRFINVKQQOQIVVYSKLKENGAGEFWAGSVYGDGQDEMGVVG YF 100  
Db 230 LGAIARYDFCARDRELSLKGMVKIYTKM-----SANGWRGEVNGR-----VGPF 278  
QY 101 PRLNVKE 107  
Db 279 PSTYVEE 285

RESULT 12

Q8UUK6 PRELIMINARY; PRT; 846 AA.

ID Q8UUK6 PRELIMINARY; PRT; 846 AA.

AC Q8UUK6; 2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE GDP/GTP exchange factor VAV3.

GN VAV3.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.

OX NCBI\_TaxID=9031;

RP [1]

RP SEQUENCE FROM N.A.

RX PubMed=11805146;

RA Inabe K., Ishiai M., Scharenberg A.M., Freshney N., Downward J.,  
RT Kurosaki T.;  
RT "Vav3 Modulates B Cell Receptor Responses by Regulating  
RT Phosphoinositide 3-Kinase Activation.";  
J. Exp. Med. 195:189-200(2002). DOMAINS.  
CC -1- SIMILARITY: CONTAINS 2 SH3 DOMAINS.  
CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.  
DR EMBL; AY046915; AAL06249.1; -;  
DR InterPro; IPR001715; Calponin-like.  
DR InterPro; IPR003247; CH type.  
DR InterPro; IPR002219; DAG-PE-bind.  
DR InterPro; IPR001331; GDS\_CDC24.  
DR InterPro; IPR001849; PH.  
DR InterPro; IPR000219; RhoGEF.  
DR InterPro; IPR000980; SH2.  
DR InterPro; IPR001452; SH3.  
DR InterPro; IPR003096; SM22\_calponin.  
DR Pfam; PF00307; CH; 1.  
DR Pfam; PF00130; DAG-PE-bind; 1.  
DR Pfam; PF00169; PH; 1.  
DR Pfam; PF00621; RhoGEF; 1.  
DR Pfam; PF00017; SH2; 1.  
DR Pfam; PF00018; SH3; 1.  
DR PRINTS; PR00401; SH2DOMAIN.  
DR PRINTS; PR00452; SH3DOMAIN.  
DR PRINTS; PR00888; SM22CALPONIN.  
DR ProDom; PD001527; CH type; 1.  
DR ProDom; PD000093; SH2; 1.  
DR ProDom; PD000066; SH3; 1.  
DR SMART; SM00109; C1; 1.  
DR SMART; SM00033; CH; 1.  
DR SMART; SM00233; PH; 1.  
DR SMART; SM00325; RhoGEF; 1.  
DR SMART; SM00252; SH2; 1.  
DR SMART; SM00326; SH3; 2.



DR PROSITE; PS00021; CH; 1.  
DR PROSITE; PS00479; DAG PE BIND DOM\_1; 1.  
DR PROSITE; PS00081; DAG PE BIND DOM\_2; 1.  
DR PROSITE; PS00741; DH 1; 1.  
DR PROSITE; PS00010; DH 2; 1.  
DR PROSITE; PS00003; PH DOMAIN; 1.  
DR PROSITE; PS00001; SH2; 1.  
DR PROSITE; PS00002; SH3; 2.  
KW SH3 domain.  
SQ SEQUENCE 846 AA; 97815 MW; C47EE949D873921B CRC64;  
  
Query Match 13.1%; Score 88.5; DB 13; Length 846;  
Best Local Similarity 32.8%; Pred. No. 0.84;  
Matches 22; Conservative 13; Mismatches 21; Indels 11; Gaps 2;  
  
QY 41 ISLASAQEDYNAPDCRFINVKKGQOIYVYSLKVENKAGFEWAGSVYGDQDGMGVV 100  
Db 789 IGIAIARYDFCARDRELKLLKGDVVVKIYTKM-----SANGWNRGEVNGR-----VGWF 837  
  
QY 101 PRNLVKE 107  
Db 838 PSTYVEE 844  
  
RESULT 13  
Q9H0H2 PRELIMINARY; PRT; 1196 AA.  
ID Q9H0H2 (T-EMBLrel. 16, Created)  
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)  
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)  
DE Hypothetical protein.  
GN DKFP434N031.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Testis;  
RX MEDLINE=21154917; PubMed=1230166;  
RA Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,  
RA Ansoer W., Boecker M., Bloeker H., Bauersachs S., Blum H.,  
RA Lauber J., Duesterhoeft A., Beyer A., Koehler K., Strack N.,  
RA Mewes H.W., Oesterwelder B., Obermaier B., Tampe J., Heubner D.,  
RA Wambutt R., Korn B., Klein M., Rostk A.,  
RA "Towards a Catalog of Human Genes and Proteins: Sequencing and  
RT Analysis of 500 Novel Complete Protein Coding Human cDNAs."  
RL Genome Res. 11:422-435(2001).  
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
DR EMBL; AL136797; CAB66731.1; -.  
DR HSP; P06241; LSHE.  
DR InterPro; IPR001452; SH3.  
DR InterPro; IPR001680; WD40.  
DR Pfam; PF00018; SH3; 1.  
DR Pfam; PF00400; WD40; 6.  
DR PRINTS; PR00452; SH3DOMAIN.  
DR ProDom; PD000066; SH3; 1.  
DR SMART; SM00326; SH3; 1.  
DR SMART; SM00320; WD40; 5.  
DR PROSITE; PS00002; SH3; 1.  
DR PROSITE; PS00082; WD\_REPEATS\_2; 4.  
DR PROSITE; PS0294; WD\_REPEATS\_REGION; 1.  
KW Hypothetical protein; Repeat; SH3 domain; WD repeat.  
SQ SEQUENCE 1196 AA; 137114 MW; E27E3EB1D7932024 CRC64;  
  
Query Match 13.1%; Score 88.5; DB 4; Length 1196;  
Best Local Similarity 33.3%; Pred. No. 1.3;  
Matches 27; Conservative 12; Mismatches 31; Indels 11; Gaps 4;  
  
QY 38 VYTISLASAQEDYNAPDCRFINVKKGQOIYVYSLKVENKAGFEWAGSVYGDQDGMGVV 97  
Db 1050 VDTAPTVALYDYTANRSDLTIRGDIIRVF---FKDN--EDWYGS1-GKQGE-----1098

QY 98 GYFPRNLVKEORVYQEAATKEV 118  
Db 1099 GYFPAHVASELYQELPPEI 1119  
  
RESULT 14  
Q8N157 PRELIMINARY; PRT; 1196 AA.  
ID Q8N157 (T-EMBLrel. 22, Created)  
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)  
DE Hypothetical protein FLJ34943.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,  
RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,  
RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,  
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,  
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,  
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,  
RA Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,  
RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.,  
RT "NEDO human cDNA sequencing project."  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Close J.P., Game I.G., Clark B., Thein S.L.;  
RT "An integrated physical and transcript map of human 6q23 encompassing  
RT a quantitative trait loci for foetal haemoglobin expression."  
RL Thesis (2002), Department of Clinical medicine, University of Oxford,  
RL Oxford, United Kingdom.  
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
DR EMBL; AK022622; BAC03840.1; -.  
DR EMBL; AJ459824; CAD30871.1; -.  
DR InterPro; IPR001452; SH3.  
DR InterPro; IPR001680; WD40.  
DR Pfam; PF00400; WD40; 5.  
DR PRINTS; PR00452; SH3DOMAIN.  
DR ProDom; PD000066; SH3; 1.  
DR SMART; SM00326; SH3; 1.  
DR PROSITE; PS00002; SH3; 1.  
DR PROSITE; PS00082; WD\_REPEATS\_2; 4.  
DR PROSITE; PS0294; WD\_REPEATS\_REGION; 1.  
KW Hypothetical protein; Repeat; SH3 domain; WD repeat.  
SQ SEQUENCE 1196 AA; 137114 MW; 16A237C915DABF0F CRC64;  
  
Query Match 13.1%; Score 88.5; DB 4; Length 1196;  
Best Local Similarity 33.3%; Pred. No. 1.3;  
Matches 27; Conservative 12; Mismatches 31; Indels 11; Gaps 4;  
  
QY 38 VYTISLASAQEDYNAPDCRFINVKKGQOIYVYSLKVENKAGFEWAGSVYGDQDGMGVV 97  
Db 1050 VDTAPTVALYDYTANRSDLTIRGDIIRVF---FKDN--EDWYGS1-GKQGE-----1098  
  
QY 98 GYFPRNLVKEORVYQEAATKEV 118  
Db 1099 GYFPAHVASELYQELPPEI 1119  
  
RESULT 15  
Q96D37 PRELIMINARY; PRT; 719 AA.  
ID Q96D37 (T-EMBLrel. 19, Created)  
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)  
DE Hypothetical protein.

Search completed: December 29, 2003, 16:06:24  
Job time : 22.7199 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2003, 16:03:18 ; Search time 25.098 Seconds  
(without alignments)  
809.506 Million cell updates/sec

Title: US-10-019-455A-6  
Perfect score: 676  
Sequence: 1 MARILLFLPGLNCAVHG.....RVQEAKEVPTTIDFFCE 128

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq 19Jun03.\*  
1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*  
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*  
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9: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.\*  
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12: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*  
13: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.\*  
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23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*  
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	676	100.0	128	22	Human growth regul
2	676	100.0	128	22	Human MLP protein
3	676	100.0	128	23	Human angiogenesis
4	676	100.0	128	23	Human PRO9873 prot
5	676	100.0	128	23	Human PRO protein,
6	676	100.0	128	23	Novel human secret
7	602	89.1	128	22	Mouse MLP protein
8	600	88.8	128	22	Rat MLP protein se
9	590	87.3	110	22	Human MLP protein

10	561	83.0	105	22	AA82672	Human growth regul
11	547	80.9	110	22	AA82671	Mouse MLP protein
12	541	80.0	110	22	AA82671	Rat MLP protein se
13	417	61.7	87	22	AA82671	Rat MLP protein se
14	257.5	38.1	131	16	AA82671	Melanoma inhibitor
15	257.5	38.1	131	22	AA82671	Human MIA protein
16	255.5	37.8	137	22	AA82671	Recombinant human
17	231.5	34.2	130	16	AA82671	Melanoma inhibitor
18	236.5	33.5	138	22	AA82671	Human protein sequ
19	225.5	33.4	125	23	AA82671	Human TANGO 130 MI
20	225.5	33.4	410	21	AA82671	Human TANGO 130 pr
21	225.5	33.4	410	23	AA82671	Human TANGO 130 pa
22	225.5	33.4	1907	23	AA82671	Human TANGO 130 po
23	217	32.1	499	22	AA82671	Human PRO polypept
24	217	32.1	499	24	AA82671	Human secreted/tra
25	217	32.1	499	24	AA82671	Novel human secret
26	217	32.1	499	24	AA82671	Human secreted/tra
27	217	32.1	499	24	AA82671	Human PRO polypept
28	217	32.1	499	24	AA82671	Human PRO polypept
29	217	32.1	499	24	AA82671	Human secreted/tra
30	217	32.1	499	24	AA82671	Human PRO polypept
31	217	32.1	499	24	AA82671	Human secreted/tra
32	217	32.1	499	24	AA82671	Human TANGO 130 MI
33	215	31.8	125	23	AA82671	Mouse TANGO 130 MI
34	215	31.8	303	22	AA82671	Human PRO polypept
35	215	31.8	303	22	AA82671	Human secreted/tra
36	215	31.8	303	23	AA82671	Human angiogenesis
37	215	31.8	303	23	AA82671	Human PRO19670 pro
38	215	31.8	303	23	AA82671	Human secreted pol
39	215	31.8	303	24	AA82671	Human secreted/tra
40	215	31.8	303	24	AA82671	Human PRO19670 pro
41	215	31.8	303	24	AA82671	Human secreted/tra
42	215	31.8	303	24	AA82671	Human PRO polypept
43	215	31.8	303	24	AA82671	Human secreted/tra
44	215	31.8	303	24	AA82671	Novel human secret
45	215	31.8	303	24	AA82671	Human secreted/tra

ALIGNMENTS

RESULT 1  
AA82671  
ID AA82671 standard; Protein; 128 AA.  
AC AA82671;  
XX  
XX 02-OCT-2001 (first entry)  
XX  
XX Human growth regulatory-like polypeptide.  
XX  
XX Growth regulatory-like polypeptide; human; cartilage; melanoma;  
XX neuroectodermal tumour; glioma; cancer; therapy; diagnosis.  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX Peptide 1..23  
XX FT /label= Signal\_peptide  
XX FT Protein 24..128  
XX FT /label= Mature\_protein  
XX FT /note= "separately claimed in Claim 10"  
XX  
XX WO200155332-A2.  
XX  
XX 02-AUG-2001.  
XX  
XX 25-JAN-2001; 2001WO-US02455.  
XX  
XX 25-JAN-2000; 2000US-0491404.  
XX 02-MAY-2000; 2000US-0563786.  
XX (HYSE-) HYSEQ INC.  
XX

XX Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;  
PI Drmanac RT;  
XX WPI; 2001-483233/52.  
DR N-PSDB; AAH26343.  
XX Isolated human growth regulatory-like polypeptide useful for treating  
XX e.g. Alzheimer's disease, cancer, autoimmune disorders,  
PT hyperproliferative disorders, coagulation disorders, and nervous system  
PT disorders -  
XX Claim 10; Page 116-117; 119pp; English.  
XX The present sequence is that of a novel human growth regulatory-like  
XX polypeptide (GRLP). The amino acid sequence is predicted from a  
XX novel assembled cDNA (see AAH26343) based on Hyseq clone number  
XX 1637272. The protein has a mol.wt. of 14 kDa unglycosylated. GRLP  
XX belongs to the same protein family as growth regulatory proteins,  
XX growth factors, human melanoma derived growth regulatory protein  
XX precursor (64% similarity and 45% identity over 111 amino acids)  
XX or melanoma inhibitory activity, cattle cartilage-derived  
XX retinoic acid sensitive protein (CD-RAP, 44% identity and 64%  
XX similarity over 126 amino acids) and other retinoic acid-sensitive  
XX proteins. GRLP polypeptides and polynucleotides of the invention  
XX can be used in the prophylaxis, treatment (including gene therapy)  
XX and diagnosis of disorders and diseases caused by, or involving,  
XX cartilage development and maintenance, inhibition of melanoma cell  
XX growth and tumours, including neuroectodermal tumours such as  
XX gliomas. The polypeptides, which include the GRLP mature protein,  
XX may also have nutritional uses, cytokine and cell proliferation  
XX or differentiation activity, stem cell growth factor activity,  
XX haematopoiesis regulating activity, tissue growth activity,  
XX immunosuppressive or immunostimulant activity, activin/inhibin  
XX activity, chemotactic/chemokinetic activity, haemostatic and  
XX thrombolytic activity, use in cancer diagnosis and therapy,  
XX drug screening, receptor/ligand activity, antiinflammatory  
XX activity, and treatment of leukaemia, nervous system disorders,  
XX arthritis and inflammation.  
XX Sequence 128 AA;  
Query Match 100.0%; Score 676; DB 22; Length 128;  
Best Local Similarity 100.0%; Pred. No. 7.9e-80;  
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECYVTISLASAQEDYNAPDCRFINV 60  
Db 1 MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECYVTISLASAQEDYNAPDCRFINV 60  
QY 61 KKGQIYVYVKLVKENGAGFEWAGSVYGDGQDENGWVGYPFRNLVKQRVYQEAATKEVPT 120  
Db 61 KKGQIYVYVKLVKENGAGFEWAGSVYGDGQDENGWVGYPFRNLVKQRVYQEAATKEVPT 120  
QY 121 TDIDFFCE 128  
Db 121 TDIDFFCE 128  
RESULT 2  
AAB69123  
ID AAB69123 standard; Protein; 128 AA.  
XX AAB69123;  
XX 23-APR-2001 (first entry)  
XX Human MLP protein sequence SEQ ID NO:6.  
XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
XX joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
KW cardiac; gene therapy; secretory cell function regulator; promoter;  
KW inhibitor.

XX Homo sapiens.  
XX WO200102564-A1.  
XX 11-JAN-2001.  
XX 29-JUN-2000; 2000WO-JP04278.  
XX 30-JUN-1999; 99JP-0186718.  
XX (TAKE ) TAKEDA CHEM IND LTD.  
XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
PI Tanaka H;  
XX WPI; 2001-159271/16.  
DR N-PSDB; AAF59065.  
XX Safe, low-toxicity secretory cell function-regulatory protein and  
XX encoded DNA, applicable as drugs, in diagnosis and development of  
XX promoters and inhibitors for preventing or treating e.g. bone and joint  
XX diseases -  
XX Claim 2; Page 91-92; 111pp; Japanese.  
XX The present invention describes novel MLP proteins and their encoding  
XX DNAs. The MLP proteins and DNAs have antiinflammatory and cardiac  
XX activities, and can be used in gene therapy and as secretory cell  
XX function regulators. The MLP proteins and DNAs can be used in drugs, in  
XX the diagnosis and development of promoters and inhibitors for preventing  
XX or treating bone and joint diseases as well as pathologic angiogenesis.  
XX AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
XX in the exemplification of the present invention.  
XX Sequence 128 AA;  
Query Match 100.0%; Score 676; DB 22; Length 128;  
Best Local Similarity 100.0%; Pred. No. 7.9e-80;  
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECYVTISLASAQEDYNAPDCRFINV 60  
Db 1 MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECYVTISLASAQEDYNAPDCRFINV 60  
QY 61 KKGQIYVYVKLVKENGAGFEWAGSVYGDGQDENGWVGYPFRNLVKQRVYQEAATKEVPT 120  
Db 61 KKGQIYVYVKLVKENGAGFEWAGSVYGDGQDENGWVGYPFRNLVKQRVYQEAATKEVPT 120  
QY 121 TDIDFFCE 128  
Db 121 TDIDFFCE 128  
RESULT 3  
AAB95602  
ID AAB95602 standard; Protein; 128 AA.  
XX AAB95602;  
XX 19-JUL-2002 (first entry)  
XX Human angiogenesis related protein PRO9873 SEQ ID NO: 360.  
XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
XX atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
KW cardiac; cytostatic; antiangiogenic; hypotensive; vulnery;  
KW antiarteriosclerotic.  
XX Homo sapiens.  
XX WO200208284-A2.  
XX

PD 31-JAN-2002.  
 XX 09-JUL-2001; 2001WO-US21735.  
 XX 20-JUL-2000; 2000US-219556P.  
 PR 25-JUL-2000; 2000US-220624P.  
 PR 25-JUL-2000; 2000US-220624P.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 02-AUG-2000; 2000US-222695P.  
 PR 17-AUG-2000; 2000US-0643657.  
 PR 23-AUG-2000; 2000WO-US23328.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 07-SEP-2000; 2000US-230978P.  
 PR 15-SEP-2000; 2000US-000000P.  
 PR 18-SEP-2000; 2000US-0664610.  
 PR 18-SEP-2000; 2000US-0665350.  
 PR 24-OCT-2000; 2000US-242922P.  
 PR 08-NOV-2000; 2000US-0709238.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 10-NOV-2000; 2000WO-US30873.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000US-0747259.  
 PR 20-DEC-2000; 2000WO-US34956.  
 PR 22-JAN-2001; 2001US-0767609.  
 PR 28-FEB-2001; 2001US-0796498.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 01-MAR-2001; 2001WO-US06566.  
 PR 09-MAR-2001; 2001US-0802706.  
 PR 14-MAR-2001; 2001US-0808689.  
 PR 22-MAR-2001; 2001US-0816744.  
 PR 05-APR-2001; 2001US-0828366.  
 PR 10-MAY-2001; 2001US-0854208.  
 PR 10-MAY-2001; 2001US-0854280.  
 PR 25-MAY-2001; 2001US-0866034.  
 PR 25-MAY-2001; 2001WO-US17092.  
 PR 30-MAY-2001; 2001US-0870574.  
 PR 30-MAY-2001; 2001WO-US17443.  
 PR 01-JUN-2001; 2001WO-US17800.  
 PR 20-JUN-2001; 2001WO-US19692.  
 PR 28-JUN-2001; 2001WO-US00000.  
 XX (GETH ) GENENTECH INC.  
 PA (BAKE/) BAKER K P.  
 PA (FERE/) FERARA N.  
 PA (GERB/) GERBER H.  
 PA (GERR/) GERRITSEN M E.  
 PA (GODD/) GODDARD A.  
 PA (GODO/) GODOWSKI P J.  
 PA (GURN/) GURNEY A L.  
 PA (HILL/) HILLAN K J.  
 PA (MARS/) MARSTERS S A.  
 PA (PANJ/) PAN J.  
 PA (PAONI/) PAONI N F.  
 PA (STEP/) STEPHAN J F.  
 PA (WATA/) WATANABE C K.  
 PA (WILL/) WILLIAMS P M.  
 PA (WOOD/) WOOD W I.  
 XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF, Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
 XX WPI: 2002-171999/22.  
 DR N-PSDB; ABL95740.  
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal -  
 XX Claim 11; Fig 360; 567pp; English.  
 XX The present invention provides the protein and coding sequences of human

CC PRO proteins. These are useful for treating or diagnosing a  
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac  
 CC hypertrophy, trauma, cancer, age-related macular degeneration, rheumatoid arthritis,  
 CC atherosclerosis, hypertension, arterial restenosis, lymphangitis, tumour  
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
 CC healing. The present sequence is a PRO protein of the invention.  
 XX Sequence 128 AA;  
 SQ Query Match 100.0%; Score 676; DB 23; Length 128;  
 Best Local Similarity 100.0%; Pred. No. 7.9e-80;  
 Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MARILLFLPLVAVCAVHGIFMDRLASKKLCADDECVTYISLASAQEDYNAPDCRINV 60  
 DB 1 MARILLFLPLVAVCAVHGIFMDRLASKKLCADDECVTYISLASAQEDYNAPDCRINV 60  
 QY 61 KKGQIYVYVKLVKENGAGFVAGSVVGDQEMGVVGVYPRNLVKEQRYQEAKEVPT 120  
 DB 61 KKGQIYVYVKLVKENGAGFVAGSVVGDQEMGVVGVYPRNLVKEQRYQEAKEVPT 120  
 QY 121 TDIDFFCE 128  
 DB 121 TDIDFFCE 128  
 RESULT 4  
 ABB84996  
 ID ABB84996 standard; Protein; 128 AA.  
 XX AC ABB84996;  
 XX DT 16-MAY-2002 (first entry)  
 XX DE Human PRO9873 protein sequence SEQ ID NO:360.  
 XX KW Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;  
 KW vulnary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
 KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
 KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
 KW age-related macular degeneration; arterial restenosis; angina;  
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
 KW wound healing; chromosome mapping; gene mapping.  
 XX OS Homo sapiens.  
 XX WO200200690-A2.  
 XX 03-JAN-2002.  
 XX 20-JUN-2001; 2001WO-US19692.  
 XX 23-JUN-2000; 2000US-213637P.  
 PR 20-JUL-2000; 2000US-219556P.  
 PR 25-JUL-2000; 2000US-220624P.  
 PR 25-JUL-2000; 2000US-220624P.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 02-AUG-2000; 2000US-222695P.  
 PR 17-AUG-2000; 2000US-0643657.  
 PR 23-AUG-2000; 2000WO-US23328.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 07-SEP-2000; 2000US-230978P.  
 PR 18-SEP-2000; 2000US-0664610.  
 PR 18-SEP-2000; 2000US-0665350.  
 PR 24-OCT-2000; 2000US-242922P.  
 PR 08-NOV-2000; 2000US-0709238.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 10-NOV-2000; 2000WO-US30873.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000US-0747259.  
 PR 20-DEC-2000; 2000WO-US34956.





[illegible]

Best Local Similarity 86.7%; Pred. No. 3.6e-70;  
Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECYVTTISLASAQEDYNAPDCRFINV 60  
DB 1 MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECYVTTISLASAQEDYNAPDCRFIDV 60

QY 61 KKGQIYVYVKLVKENGAGFAGFAGSVYGDQDMGVGVYFPRNLVKQRYQVQATKEVPT 120  
DB 61 KKGQIYVYVKLVKENGAGFAGFAGSVYGDQDMGVGVYFPRNLVKQRYQVQATKEIPT 120

QY 121 TDIDFFCE 128  
DB 121 TDIDFFCE 128

RESULT 8  
AAB69130  
ID AAB69130 standard; Protein; 128 AA.  
XX  
AC AAB69130;  
XX  
DT 23-APR-2001 (first entry)  
XX  
DE Rat MLP protein sequence SEQ ID NO:47.  
XX  
KW MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
KW cardiant; gene therapy; secretory cell function regulator; promoter;  
KW inhibitor.  
XX  
OS Rattus sp.  
XX  
PN WO200102564-A1.  
XX  
PD 11-JAN-2001.  
XX  
PF 29-JUN-2000; 2000WO-JP04278.  
XX  
PR 30-JUN-1999; 99JP-0186718.  
XX  
PA (TAKE ) TAKEDA CHEM IND LTD.  
XX  
PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
PI Tanaka H;  
XX  
DR WPI; 2001-159271/16.  
DR N-PSDB; AAF59098.  
XX  
PT Safe, low-toxicity secretory cell function-regulatory protein and  
PT encoded DNA, applicable as drugs, in diagnosis and development of  
PT promoters and inhibitors for preventing or treating e.g. bone and joint  
PT diseases -  
XX  
PS Claim 6; Page 106; 11lpp; Japanese.  
XX  
CC The present invention describes novel MLP proteins and their encoding  
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
CC activities, and can be used in gene therapy and as secretory cell  
CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
CC the diagnosis and development of promoters and inhibitors for preventing  
CC or treating bone and joint diseases as well as pathologic angiogenesis.  
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
CC in the exemplification of the present invention.  
XX  
SQ Sequence 128 AA;

Query Match 88.8%; Score 600; DB 22; Length 128;  
Best Local Similarity 86.7%; Pred. No. 6.6e-70;  
Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECYVTTISLASAQEDYNAPDCRFINV 60  
DB 1 MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECYVTTISLASAQEDYNAPDCRFIDV 60

Db 1 MARILLLLGGIVALCAGHGMFMDKLSKKLCADEECYVTTISLARAQEDYNAPDCRFINV 60

QY 61 KKGQIYVYVKLVKENGAGFAGFAGSVYGDQDMGVGVYFPRNLVKQRYQVQATKEVPT 120  
DB 61 KKGQIYVYVKLVKENGAGFAGFAGSVYGDQDMGVGVYFPRNLVKQRYQVQATKEIPT 120

QY 121 TDIDFFCE 128  
DB 121 TDIDFFCE 128

RESULT 9  
AAB69126  
ID AAB69126 standard; Protein; 110 AA.  
XX  
AC AAB69126;  
XX  
DT 23-APR-2001 (first entry)  
XX  
DE Human MLP protein sequence SEQ ID NO:24.  
XX  
KW MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
KW cardiant; gene therapy; secretory cell function regulator; promoter;  
KW inhibitor.  
XX  
OS Homo sapiens.  
XX  
PN WO200102564-A1.  
XX  
PD 11-JAN-2001.  
XX  
PF 29-JUN-2000; 2000WO-JP04278.  
XX  
PR 30-JUN-1999; 99JP-0186718.  
XX  
PA (TAKE ) TAKEDA CHEM IND LTD.  
XX  
PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
PI Tanaka H;  
XX  
DR WPI; 2001-159271/16.  
DR N-PSDB; AAF59079.  
XX  
PT Safe, low-toxicity secretory cell function-regulatory protein and  
PT encoded DNA, applicable as drugs, in diagnosis and development of  
PT promoters and inhibitors for preventing or treating e.g. bone and joint  
PT diseases -  
XX  
PS Claim 1; Page 97-98; 11lpp; Japanese.  
XX  
CC The present invention describes novel MLP proteins and their encoding  
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
CC activities, and can be used in gene therapy and as secretory cell  
CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
CC the diagnosis and development of promoters and inhibitors for preventing  
CC or treating bone and joint diseases as well as pathologic angiogenesis.  
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
CC in the exemplification of the present invention.  
XX  
SQ Sequence 110 AA;

Query Match 87.3%; Score 590; DB 22; Length 110;  
Best Local Similarity 100.0%; Pred. No. 1.1e-68;  
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 HGIFMDRLASKKLCADDECYVTTISLASAQEDYNAPDCRFINVKKGQIYVYVKLVKENG 78  
DB 1 HGIFMDRLASKKLCADDECYVTTISLASAQEDYNAPDCRFINVKKGQIYVYVKLVKENG 60

QY 79 GEFWAGSVYGDQDMGVGVYFPRNLVKQRYQVQATKEVPTTIDFFCE 128  
DB 61 GEFWAGSVYGDQDMGVGVYFPRNLVKQRYQVQATKEVPTTIDFFCE 110



## RESULT 12

AAB69131 ID AAB69131 standard; Protein; 110 AA.  
 XX AC AAB69131;  
 XX DT 23-APR-2001 (first entry)  
 XX DE Rat MLP protein sequence SEQ ID NO:49.  
 XX XX  
 XX MLF; MIA; melanoma inhibitory activity; cancer; bone disease;  
 KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
 KW cardiant; gene therapy; secretory cell function regulator; promoter;  
 KW inhibitor.  
 XX OS Rattus sp.  
 XX XX  
 XX WO200102564-A1.  
 XX PD 11-JAN-2001.  
 XX PF 29-JUN-2000; 2000WO-JP04278.  
 XX PR 30-JUN-1999; 99JP-0186718.  
 XX PA (TAKE ) TAKEDA CHEM IND LTD.  
 XX PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
 PI Tanaka H;  
 XX WPI; 2001-159271/16.  
 XX DR N-PSDB; AAF59099.  
 XX PT Safe, low-toxicity secretory cell function-regulatory protein and  
 PT encoded DNA, applicable as drugs, in diagnosis and development of  
 PT promoters and inhibitors for preventing or treating e.g. bone and joint  
 PT diseases -  
 XX Claim 5; Page 107; 111pp; Japanese.  
 XX PS  
 XX CC The present invention describes novel MLP proteins and their encoding  
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
 CC activities, and can be used in gene therapy and as secretory cell  
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
 CC the diagnosis and development of promoters and inhibitors for preventing  
 CC or treating bone and joint diseases as well as pathologic angiogenesis.  
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
 CC in the exemplification of the present invention.  
 XX SQ Sequence 110 AA;  
 XX Query Match 80.0%; Score 541; DB 22; Length 110;  
 XX Best Local Similarity 89.1%; Pred. No. 2.7e-62;  
 XX Matches 98; Conservative 7; Mismatches 5; Indels 0; Gaps 0;  
 Qy 19 HGIFMDRLSKKLCADCECVYTTISLAAQEDYNAPDCRFINVKKGQIYVYKLVKXNGA 78  
 Db 1 HGMFMDKLSKKLCADCECVYTTISLAAQEDYNAPDCRFINVKKGQIYVYKLVKXNGA 60  
 Qy 79 GEFWAGSVYGDGDEMVGVPFPRNLVKEQRYQVQATKEVPTTIDIDFCE 128  
 Db 61 GAFWAGSVYGDHDEMVGVPFPRNLVREQRVYQVQATKEIPTTIDIDFCE 110  
 RESULT 13  
 AAB69129 ID AAB69129 standard; Protein; 87 AA.  
 XX AC AAB69129;  
 XX DT 23-APR-2001 (first entry)  
 XX DE Rat MLP protein sequence SEQ ID NO:39.

XX MLF; MIA; melanoma inhibitory activity; cancer; bone disease;  
 KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
 KW cardiant; gene therapy; secretory cell function regulator; promoter;  
 KW inhibitor.  
 XX OS Rattus sp.  
 XX XX  
 XX WO200102564-A1.  
 XX PD 11-JAN-2001.  
 XX PF 29-JUN-2000; 2000WO-JP04278.  
 XX PR 30-JUN-1999; 99JP-0186718.  
 XX PA (TAKE ) TAKEDA CHEM IND LTD.  
 XX PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
 PI Tanaka H;  
 XX WPI; 2001-159271/16.  
 XX DR N-PSDB; AAF59099.  
 XX PT Safe, low-toxicity secretory cell function-regulatory protein and  
 PT encoded DNA, applicable as drugs, in diagnosis and development of  
 PT promoters and inhibitors for preventing or treating e.g. bone and joint  
 PT diseases -  
 XX Example 9; Page 103; 111pp; Japanese.  
 XX PS  
 XX CC The present invention describes novel MLP proteins and their encoding  
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
 CC activities, and can be used in gene therapy and as secretory cell  
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
 CC the diagnosis and development of promoters and inhibitors for preventing  
 CC or treating bone and joint diseases as well as pathologic angiogenesis.  
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
 CC in the exemplification of the present invention.  
 XX SQ Sequence 87 AA;  
 XX Query Match 61.7%; Score 417; DB 22; Length 87;  
 XX Best Local Similarity 88.5%; Pred. No. 3e-46;  
 XX Matches 77; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
 Qy 24 DRLASKKLCADCECVYTTISLAAQEDYNAPDCRFINVKKGQIYVYKLVKXNGAFWA 83  
 Db 1 DLSSKKLCADCECVYTTISLAAQEDYNAPDCRFINVKKGQIYVYKLVKXNGAFWA 60  
 Qy 84 GSVYGDGDEMVGVPFPRNLVKEQRY 110  
 Db 61 GSVYGDHDEMVGVPFPRNLVREQRV 87  
 RESULT 14  
 AAB69811 ID AAB69811 standard; Protein; 131 AA.  
 XX AC AAB69811;  
 XX DT 25-MAR-2003 (updated)  
 XX DT 26-OCT-1995 (first entry)  
 XX DE Melanoma inhibiting protein (human).  
 XX Melanoma; inhibition; cancer; melanoma; glioblastoma; neuroblastoma;  
 KW small cell lung cancer; neuroectodermal tumours; immunosuppressant;  
 KW phytohaemagglutinin; lymphocyte; interleukin 2; IL-2; detection;  
 KW probe; fusion protein.  
 XX OS Homo sapiens.  
 XX XX  
 XX WO9503328-A2.

XX 02-FEB-1995.  
XX 19-JUL-1994; 94WO-EP02369.  
XX 20-JUL-1993; 93DE-4324247.  
XX (BOEF ) BOEHRINGER MANNHEIM GMBH.  
XX Bogdahn U, Buettner R, Kaluza B;  
XX WPI; 1995-075191/10.  
XX N-PSDB; AAQ84050, AAQ84051.  
XX New melanoma inhibiting protein and related nucleic acid -  
XX vectors, transformed cells, antibodies etc., useful for treating  
XX tumours and as immunosuppressant e.g. by gene therapy  
XX Claim 1; Page 54; 85pp; German.  
XX This protein has melanoma-inhibiting activity and can be used to  
XX treat cancer (melanoma, glioblastoma, neuroblastoma, small cell  
XX lung cancer, neuroectodermal tumours) or as an immunosuppressant  
XX (it inhibits IL-2 or phytohaemagglutinin induced proliferation of  
XX peripheral blood lymphocytes). Antibodies raised against the  
XX protein can be used to detect cell producing the protein and also  
XX for protein purification. Probes derived from DNA encoding the  
XX protein (AAQ84050, AAQ84051) can be used to detect sequences encoding  
XX the protein or related proteins. The protein may be expressed as  
XX a fusion protein (conjugated with dihydrofolate reductase (DHFR)).  
XX (Updated on 25-MAR-2003 to correct PN field.)  
XX Sequence 131 AA;  
Query Match 38.1%; Score 257.5; DB 16; Length 131;  
Best Local Similarity 41.2%; Pred. No. 3.6e-25;  
Matches 56; Conservative 26; Mismatches 41; Indels 13; Gaps 5;  
Qy 1 MARILLFLPGLVAVCA-----VHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPD 54  
Db 1 MARSLVCL--GVIIILSAFSGVGRGPMPLADRLKLCADQECSPISMAVALQDYMAPD 58  
Qy 55 CRFINVKGGQIYYVYKLVKENGAGE-FWAGSVYGDGDENG-V-VGYFPRNLVKEQRYVQ 112  
Db 59 CRFLTIRHGQVYVYVFSKL---KGRGLFWGGSVQDYYGDLAARLGYFPSSIVREDQTLK 115  
Qy 113 EATKEVPTTIDFFCE 128  
Db 116 PGKVDVKTDRKWFYCY 131  
RESULT 15  
ID AAG65614  
XX AAG65614 standard; Protein; 131 AA.  
XX AC AAG65614;  
XX 07-JAN-2002 (first entry)  
XX Human MIA protein sequence.  
XX MIA; melanoma inhibiting activity protein; antiinflammatory; human;  
XX antiarthritic; antirheumatic; antithyroid; osteopathic; nephrotropic;  
XX immunosuppressive; ophthalmological; dermatological; antidiabetic;  
XX neuroprotective; immune tolerance; T-cell tolerance.  
XX Homo sapiens.  
XX WO200170253-A1.  
XX 27-SEP-2001.  
XX 15-MAR-2001; 2001WO-EP02991.

XX 23-MAR-2000; 2000EP-0201063.  
XX (ALKU ) AKZO NOBEL NV.  
XX Nelissen RLH, Verheijden GFM;  
XX WPI; 2001-611446/70.  
XX N-PSDB; AAH47783.  
XX Use of melanoma inhibiting activity protein or its derivatives as  
XX immune modulatory agents for the treatment of inflammatory diseases,  
XX specifically rheumatoid arthritis -  
XX Example 4; Page 34; 41pp; English.  
XX The invention relates to the use of melanoma inhibiting activity (MIA)  
XX protein and/or its fragments that have anti-inflammatory effects and  
XX induce systemic immune tolerance or specific T-cell tolerance to MIA  
XX antigen, for manufacturing a preparation against inflammatory diseases  
XX and for induction of systemic immune tolerance or specific T-cell  
XX tolerance in patients suffering from or susceptible to inflammatory  
XX diseases. A fragment of MIA is useful as a therapeutic substance and is  
XX useful for manufacture of pharmaceutical preparations against  
XX inflammatory diseases such as an immune-cell mediated cartilage  
XX destruction disease, specifically rheumatoid arthritis, autoimmune  
XX diseases like Graves' disease, juvenile arthritis, primary  
XX glomerulonephritis, polyarthritis, osteoarthritis, Sjogren's syndrome,  
XX myasthenia gravis, Addison's disease, primary biliary sclerosis,  
XX uveitis, systemic lupus erythematosus, inflammatory bowel disease,  
XX multiple sclerosis or diabetes. The MIA polypeptides have specific  
XX effect on the autoreactive T-cells thus leaving the other components of  
XX the immune system intact as compared to the non-specific suppressive  
XX effect of immunosuppressive drugs. The present sequence represents a  
XX human MIA protein.  
XX Sequence 131 AA;  
Query Match 38.1%; Score 257.5; DB 22; Length 131;  
Best Local Similarity 41.2%; Pred. No. 3.6e-25;  
Matches 56; Conservative 26; Mismatches 41; Indels 13; Gaps 5;  
Qy 1 MARILLFLPGLVAVCA-----VHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPD 54  
Db 1 MARSLVCL--GVIIILSAFSGVGRGPMPLADRLKLCADQECSPISMAVALQDYMAPD 58  
Qy 55 CRFINVKGGQIYYVYKLVKENGAGE-FWAGSVYGDGDENG-V-VGYFPRNLVKEQRYVQ 112  
Db 59 CRFLTIRHGQVYVYVFSKL---KGRGLFWGGSVQDYYGDLAARLGYFPSSIVREDQTLK 115  
Qy 113 EATKEVPTTIDFFCE 128  
Db 116 PGKVDVKTDRKWFYCY 131

Search completed: December 29, 2003, 16:09:02  
Job time : 27.098 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2003, 16:09:08 ; Search time 17.5686 Seconds  
(without alignments)  
1449,984 Million cell updates/sec

Title: US-10-019-455A-6

Perfect score: 676

Sequence: 1 MARILLFLFGLVAVCAVHG.....RVYQKATKEVPTDIDFFCE 128

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 724715 seqs, 199017464 residues

Total number of hits satisfying chosen parameters: 724715

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pcp.\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pcp.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pcp.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pcp.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pcp.\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pcp.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pcp.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pcp.\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pcp.\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pcp.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pcp.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pcp.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pcp.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pcp.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pcp.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pcp.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pcp.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	676	100.0	128	12	US-10-216-163-72
2	676	100.0	128	12	US-10-218-765-72
3	676	100.0	128	12	US-10-219-063-72
4	676	100.0	128	12	US-10-219-066-72
5	676	100.0	128	12	US-10-219-067-72
6	676	100.0	128	12	US-10-219-068-72
7	676	100.0	128	12	US-10-219-069-72
8	676	100.0	128	12	US-10-219-073-72
9	676	100.0	128	12	US-10-219-475-72
10	676	100.0	128	12	US-10-219-480-72
11	676	100.0	128	12	US-10-219-483-72
12	676	100.0	128	12	US-10-219-525-72
13	676	100.0	128	12	US-10-219-526-72
14	676	100.0	128	12	US-10-219-530-72
15	676	100.0	128	12	US-10-219-531-72

16	676	100.0	128	12	US-10-219-532-72	Sequence 72, Appl
17	676	100.0	128	12	US-10-219-533-72	Sequence 72, Appl
18	676	100.0	128	12	US-10-223-081-360	Sequence 360, App
19	676	100.0	128	12	US-10-230-437-72	Sequence 72, Appl
20	676	100.0	128	12	US-10-232-228-72	Sequence 72, Appl
21	676	100.0	128	12	US-10-223-082-360	Sequence 360, App
22	676	100.0	128	15	US-10-227-884-72	Sequence 72, Appl
23	676	100.0	128	15	US-10-230-163-72	Sequence 72, Appl
24	676	100.0	128	15	US-10-230-338-72	Sequence 72, Appl
25	676	100.0	128	15	US-10-218-631-72	Sequence 72, Appl
26	676	100.0	128	15	US-10-230-414-72	Sequence 72, Appl
27	676	100.0	128	15	US-10-216-1598-72	Sequence 72, Appl
28	676	100.0	128	15	US-10-218-849-72	Sequence 72, Appl
29	676	100.0	128	15	US-10-227-883-72	Sequence 72, Appl
30	676	100.0	128	15	US-10-227-883-72	Sequence 72, Appl
31	676	100.0	128	15	US-10-219-076-72	Sequence 72, Appl
32	676	100.0	128	15	US-10-230-434-72	Sequence 72, Appl
33	676	100.0	128	15	US-10-219-003-72	Sequence 72, Appl
34	676	100.0	128	15	US-10-219-075-72	Sequence 72, Appl
35	676	100.0	128	15	US-10-219-464-72	Sequence 72, Appl
36	676	100.0	128	15	US-10-219-466-72	Sequence 72, Appl
37	676	100.0	128	15	US-10-219-479-72	Sequence 72, Appl
38	676	100.0	128	15	US-10-219-481-72	Sequence 72, Appl
39	676	100.0	128	15	US-10-230-260-72	Sequence 72, Appl
40	676	100.0	128	15	US-10-232-231-72	Sequence 72, Appl
41	676	100.0	128	15	US-10-232-233-72	Sequence 72, Appl
42	676	100.0	128	15	US-10-216-165-72	Sequence 72, Appl
43	676	100.0	128	15	US-10-218-956-72	Sequence 72, Appl
44	676	100.0	128	15	US-10-219-468-72	Sequence 72, Appl
45	676	100.0	128	15	US-10-219-478-72	Sequence 72, Appl

#### ALIGNMENTS

#### RESULT 1

US-10-216-163-72  
; Sequence 72, Application US/10216163  
; Publication No. US20030149239A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin I.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3530P1C3  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; CURRENT APPLICATION NUMBER: US/10/216,163  
; CURRENT FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: 10/119,480  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/069873  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656

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; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-163-72

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Best Local Similarity 100.0%; Pred. No. 7.8e-74;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MARILLFLPLGVAVCAVHGIFMDRLASKKLCADDECVTITSLASQEDYNAPDCRFINV 60

Qy 61 KKGQIIVYVKLVKENGAGFWAGSVYGDQDENGWVGVYFPRNLVKEQRVYQATKEVPT 120
Db 61 KKGQIIVYVKLVKENGAGFWAGSVYGDQDENGWVGVYFPRNLVKEQRVYQATKEVPT 120

Qy 121 TDIDFFCE 128
Db 121 TDIDFFCE 128

RESULT 2
US-10-218-765-72
; Sequence 72, Application US/10218765
; Publication No. US20030187201A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530F1C19
; CURRENT APPLICATION NUMBER: US/10/218,765
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/064103
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; PRIOR FILING DATE: 1998-03-20
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; PRIOR APPLICATION NUMBER: 60/082804
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; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/097986
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: 60/098544
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/099596
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; PRIOR APPLICATION NUMBER: 60/099812
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; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101786
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: 60/101916
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QY 121 TDIDFFCE 128  
Db 121 TDIDFFCE 128

## RESULT 6

US-10-219-068-72  
; Sequence 72, Application US/10219068  
; Publication No. US20030187205A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3530PIC31  
; CURRENT APPLICATION NUMBER: US/10/219,068  
; CURRENT FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: 10/119,480  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/069873  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 246  
; SEQ ID NO 72  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Homo Sapien

US-10-219-068-72  
Query Match 100.0%; Score 676; DB 12; Length 128;  
Best Local Similarity 100.0%; Pred. No. 7.8e-74;  
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFV 60  
Db 1 MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFV 60  
QY 61 KKGQIYVYVKLVKENGAGFVAGSVYGDQDMGVGFPPNVLKQRYVQATKEVPT 120  
Db 61 KKGQIYVYVKLVKENGAGFVAGSVYGDQDMGVGFPPNVLKQRYVQATKEVPT 120  
QY 121 TDIDFFCE 128  
Db 121 TDIDFFCE 128

US-10-219-068-72  
Query Match 100.0%; Score 676; DB 12; Length 128;  
Best Local Similarity 100.0%; Pred. No. 7.8e-74;  
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFV 60  
Db 1 MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFV 60  
QY 61 KKGQIYVYVKLVKENGAGFVAGSVYGDQDMGVGFPPNVLKQRYVQATKEVPT 120  
Db 61 KKGQIYVYVKLVKENGAGFVAGSVYGDQDMGVGFPPNVLKQRYVQATKEVPT 120  
QY 121 TDIDFFCE 128  
Db 121 TDIDFFCE 128

## RESULT 7

US-10-219-069-72  
; Sequence 72, Application US/10219069  
; Publication No. US20030187206A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3530PIC40  
; CURRENT APPLICATION NUMBER: US/10/219,069  
; CURRENT FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: 10/119,480  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/069873  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 246  
; SEQ ID NO 72  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Homo Sapien

US-10-219-069-72  
Query Match 100.0%; Score 676; DB 12; Length 128;  
Best Local Similarity 100.0%; Pred. No. 7.8e-74;  
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFV 60  
Db 1 MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFV 60  
QY 61 KKGQIYVYVKLVKENGAGFVAGSVYGDQDMGVGFPPNVLKQRYVQATKEVPT 120  
Db 61 KKGQIYVYVKLVKENGAGFVAGSVYGDQDMGVGFPPNVLKQRYVQATKEVPT 120  
QY 121 TDIDFFCE 128  
Db 121 TDIDFFCE 128

US-10-219-069-72  
Query Match 100.0%; Score 676; DB 12; Length 128;  
Best Local Similarity 100.0%; Pred. No. 7.8e-74;  
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFV 60  
Db 1 MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFV 60  
QY 61 KKGQIYVYVKLVKENGAGFVAGSVYGDQDMGVGFPPNVLKQRYVQATKEVPT 120  
Db 61 KKGQIYVYVKLVKENGAGFVAGSVYGDQDMGVGFPPNVLKQRYVQATKEVPT 120  
QY 121 TDIDFFCE 128  
Db 121 TDIDFFCE 128

RESULT 8  
US-10-219-073-72  
; Sequence 72, Application US/10219073  
; Publication No. US20030187207A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.

RESULT 9  
US-10-219-475-72  
; Sequence 72, Application US/10219475  
; Publication No. US20030187208A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria

```

RESULT 10
US-10-219-480-72
/ Sequence 72, Application US/10219480
/ Publication NO. US20030187209A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Gerritsen, Mary
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe F.
/ APPLICANT: Watanabe, Colin L.
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: SECRETED AND TRAN
/ TITLE OF INVENTION: ACIDS ENCODING T
/ FILE REFERENCE: P3530PIC38
/ CURRENT APPLICATION NUMBER: US/10/219

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; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-480-72

Query Match      100.0%; Score 676; DB 12; Length 128;
Best Local Similarity 100.0%; Pred. No. 7.8e-74;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARILLFLGLVAVCAVHGIFMDRLASKKLCADDECVYTIISLASAQEDYNAPDCRFINV 60
DB 1 MARILLFLGLVAVCAVHGIFMDRLASKKLCADDECVYTIISLASAQEDYNAPDCRFINV 60

QY 61 KKGQIIVYVKLVKENGAGFWAGSVYGDQDGMGVYGFPRNLVKEQRYQVQATKEVPT 120
DB 61 KKGQIIVYVKLVKENGAGFWAGSVYGDQDGMGVYGFPRNLVKEQRYQVQATKEVPT 120

QY 121 TDIDFFCE 128
DB 121 TDIDFFCE 128

RESULT 11
US-10-219-483-72
; Sequence 72, Application US/10219483
; Publication No. US20030187210A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC43
; CURRENT APPLICATION NUMBER: US/10/219,483
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
```

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; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-483-72

Query Match      100.0%; Score 676; DB 12; Length 128;
Best Local Similarity 100.0%; Pred. No. 7.8e-74;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARILLFLGLVAVCAVHGIFMDRLASKKLCADDECVYTIISLASAQEDYNAPDCRFINV 60
DB 1 MARILLFLGLVAVCAVHGIFMDRLASKKLCADDECVYTIISLASAQEDYNAPDCRFINV 60

QY 61 KKGQIIVYVKLVKENGAGFWAGSVYGDQDGMGVYGFPRNLVKEQRYQVQATKEVPT 120
DB 61 KKGQIIVYVKLVKENGAGFWAGSVYGDQDGMGVYGFPRNLVKEQRYQVQATKEVPT 120

QY 121 TDIDFFCE 128
DB 121 TDIDFFCE 128

RESULT 12
US-10-219-525-72
; Sequence 72, Application US/10219525
; Publication No. US20030187211A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC29
; CURRENT APPLICATION NUMBER: US/10/219,525
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
```

```
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-526-72

Query Match      100.0%; Score 676; DB 12; Length 128;
Best Local Similarity 100.0%; Pred. No. 7.8e-74;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECVTYISLASAQEDYNAPDCRFINV 60
      |||||||
Db      1  MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECVTYISLASAQEDYNAPDCRFINV 60
      |||||||

QY      61  KKGQIYVYKLVKENGAGFWAGSVYGDGQDENGWVGYPFRLNVKEQRYQVQATKEVPT 120
      |||||||
Db      61  KKGQIYVYKLVKENGAGFWAGSVYGDGQDENGWVGYPFRLNVKEQRYQVQATKEVPT 120
      |||||||

QY      121  TDIDFFCE 128
      |||||||
Db      121  TDIDFFCE 128
      |||||||

RESULT 13
US-10-219-526-72
; Sequence 72, Application US/10219526
; Publication No. US20030187212A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC41
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-526-72

Query Match      100.0%; Score 676; DB 12; Length 128;
Best Local Similarity 100.0%; Pred. No. 7.8e-74;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECVTYISLASAQEDYNAPDCRFINV 60
      |||||||
Db      1  MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECVTYISLASAQEDYNAPDCRFINV 60
      |||||||

QY      61  KKGQIYVYKLVKENGAGFWAGSVYGDGQDENGWVGYPFRLNVKEQRYQVQATKEVPT 120
      |||||||
Db      61  KKGQIYVYKLVKENGAGFWAGSVYGDGQDENGWVGYPFRLNVKEQRYQVQATKEVPT 120
      |||||||

QY      121  TDIDFFCE 128
      |||||||
Db      121  TDIDFFCE 128
      |||||||

RESULT 14
US-10-219-530-72
; Sequence 72, Application US/10219530
; Publication No. US20030187213A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC54
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-530-72
```

Query Match	100.0%;	Score 676;	DB 12;	Length 128;
Best Local Similarity	100.0%;	Pred. No. 7.8e-74;		
Matches 128;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MARIILLFLPGLVAVCAVHGIFMDRLASKKLCADDECVTYISLASAQEDYNAPDCRFNV	60	
Db	1	MARIILLFLPGLVAVCAVHGIFMDRLASKKLCADDECVTYISLASAQEDYNAPDCRFNV	60	
QY	61	KKGQIQIYVYSKLVKENGAGEFWAGSVYGDQDQDGVVGFPPRLNVKEQVYQEAKEVPT	120	
Db	61	KKGQIQIYVYSKLVKENGAGEFWAGSVYGDQDQDGVVGFPPRLNVKEQVYQEAKEVPT	120	
QY	121	TDIDFFCE	128	
Db	121	TDIDFFCE	128	

```

RESULT 15
US-10-219-531-72
  Sequence 72, Application US/10219531
  Publication No. US20030187214A1
  GENERAL INFORMATION:
    APPLICANT: Baker, Kevin P.
    APPLICANT: Desnoyers, Luc
    APPLICANT: Gerritsen, Mary
    APPLICANT: Goddard, Audrey
    APPLICANT: Godowski, Paul J.
    APPLICANT: Grimaldi, J. Christopher
    APPLICANT: Gurney, Austin L.
    APPLICANT: Smith, Victoria
    APPLICANT: Stephan, Jean-Philippe F.
    APPLICANT: Watanabe, Colin L.
    APPLICANT: Wood, William I.
  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
  FILE OF INVENTION: ACIDS ENCODING THE SAME
  FILE REFERENCE: P3530PIC66
  CURRENT APPLICATION NUMBER: US/10/219,531
  CURRENT FILING DATE: 2002-08-14
  PRIOR APPLICATION NUMBER: 10/119,480
  PRIOR FILING DATE: 2002-04-09
  PRIOR APPLICATION NUMBER: 60/059113
  PRIOR FILING DATE: 1997-09-17
  PRIOR APPLICATION NUMBER: 60/062287
  PRIOR FILING DATE: 1997-10-17
  PRIOR APPLICATION NUMBER: 60/063549
  PRIOR FILING DATE: 1997-10-28
  PRIOR APPLICATION NUMBER: 60/064103
  PRIOR FILING DATE: 1997-10-31
  PRIOR APPLICATION NUMBER: 60/069873
  PRIOR FILING DATE: 1997-12-17
  PRIOR APPLICATION NUMBER: 60/078910
  PRIOR FILING DATE: 1998-03-20
  PRIOR APPLICATION NUMBER: 60/079294
  PRIOR FILING DATE: 1998-03-25
  PRIOR APPLICATION NUMBER: 60/079656
  PRIOR FILING DATE: 1998-03-26
  PRIOR APPLICATION NUMBER: 60/079728
  PRIOR FILING DATE: 1998-03-27
  Remaining Prior Application data removed - See File Wrapper or PALM.
  NUMBER OF SEQ ID NOS: 246
  SEQ ID NO 72
  LENGTH: 128
  TYPE: PRT
  ORGANISM: Homo Sapien
US-10-219-531-72

```

```

Query Match      100.0%; Score 676; DB 12; Length 128;
Best Local Similarity 100.0%; Pred. No. 7.8e-74;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MARILLFLPGLVAVCAVHGTFMDRLASKKLCADDECVTTISLASAQEDYNAPDCRFINV 60

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Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	257.5	38.1	131	1	US-08-578-649-2	Sequence 2, Appli
2	231.5	34.2	130	1	US-08-578-649-5	Sequence 5, Appli
3	85.5	12.6	844	1	US-07-646-537B-2	Sequence 2, Appli
4	81.5	12.1	54	3	US-09-346-510B-21	Sequence 21, Appli
5	78.5	11.6	1589	3	US-09-356-953-4	Sequence 4, Appli
6	78	11.5	625	3	US-08-996-139-15	Sequence 15, Appli
7	78	11.5	625	3	US-08-995-659-15	Sequence 15, Appli
8	78	11.5	625	3	US-09-215-649A-15	Sequence 15, Appli
9	78	11.5	625	4	US-09-577-780-15	Sequence 15, Appli
10	78	11.5	625	4	US-09-577-800-15	Sequence 15, Appli
11	78	11.5	625	4	US-09-466-496-15	Sequence 15, Appli
12	78	11.5	625	4	US-09-871-856-15	Sequence 15, Appli
13	78	11.5	625	4	US-09-871-291-15	Sequence 15, Appli
14	76	11.2	526	4	US-09-071-035-84	Sequence 84, Appli
15	76	11.2	546	4	US-09-071-035-82	Sequence 82, Appli
16	75	11.1	462	4	US-08-630-915A-38	Sequence 38, Appli
17	72.5	10.7	48	3	US-09-346-510B-24	Sequence 24, Appli
18	70.5	10.4	663	4	US-09-134-078-61	Sequence 61, Appli
19	70.5	10.4	680	4	US-09-134-078-25	Sequence 25, Appli
20	66.5	9.8	62	4	US-08-630-915A-135	Sequence 135, App
21	66.5	9.8	642	2	US-08-345-511-48	Sequence 48, Appli
22	66.5	9.8	642	2	US-08-600-993A-48	Sequence 48, Appli
23	66.5	9.8	1326	4	US-09-328-353-4886	Sequence 4886, Ap
24	66	9.8	248	4	US-08-630-915A-40	Sequence 40, Appli
25	66	9.8	280	1	US-08-434-255-8	Sequence 8, Appli
26	66	9.8	280	1	US-08-459-967-8	Sequence 8, Appli
27	66	9.8	280	1	US-08-460-327-8	Sequence 8, Appli

Db 1 MARSLVCL--GVILLSAFSGVGRGMPKLRKLCADQECSPISMVAVALQDYMAPD 58  
 QY 55 CRINVKKGQIYVYVKLVKENGAGE-FWAGSVYGDQDQEMGV-VGYFPRNLVKEQRYQ 112  
 Db 59 CRFLTHRGQGVVVFVSKL---KRGRLFWGGSVQSDYVYGDLAARLGYPFSSIVREDQTLK 115  
 QY 113 EATKEVPTTDDPFCE 128  
 Db 116 PGKVDVKTCKWDFYCQ 131

## RESULT 2

US-08-578-649-5  
 ; Sequence 5, Application US/08578649  
 ; Patent No. 5770366  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ulrich Bogdan  
 ; APPLICANT: Reinhard Buttner  
 ; APPLICANT: Brigitte Kaluza  
 ; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN  
 ; NUMBER OF SEQUENCES: 24  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Felfe & Lynch  
 ; STREET: 805 Third Avenue  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10022  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette  
 ; COMPUTER: IBM PS/2  
 ; OPERATING SYSTEM: PC-DOS  
 ; SOFTWARE: Wordperfect  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/578,649  
 ; FILING DATE: 29-July-1994  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: DE P 43 24 247.2  
 ; FILING DATE: 20-July-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Andrew L. Tiajolloff  
 ; REGISTRATION NUMBER: 31,575  
 ; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 688-9200  
 ; TELEFAX: (212) 838-3884  
 ; INFORMATION FOR SEQ ID NO: 5:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 130 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-578-649-5

Query Match 34.2%; Score 231.5; DB 1; Length 130;  
 Best Local Similarity 43.5%; Pred. No. 1.7e-22;  
 Matches 47; Conservative 21; Mismatches 35; Indels 5; Gaps 3;  
 QY 23 MDRLSKLCADDECVVTTISASAQEDYNAPDCRFINVKKGQIYVYVKLVKENGAGE-F 81  
 Db 26 MPKLADWKLCADESCSPISMVAVALQDYVAPDCRFITRYRGQVYVFSKL---KGRGLRF 82  
 QY 82 WAGSVYGDQDQEMGV-VGYFPRNLVKEQRYQVQATKEVPTTDDPFCE 128  
 Db 83 WGGSVQGGYGYDLAARLGYPFSSIVREDLNSKPKIDMKTDQWDFYCQ 130

## RESULT 3

US-07-646-537B-2  
 ; Sequence 2, Application US/07646537B  
 ; Patent No. 5348864  
 ; GENERAL INFORMATION:

; APPLICANT: Barbacid, Mariano  
 ; TITLE OF INVENTION: Vav Proto-Oncogene Protein  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Bristol-Myers Squibb Company  
 ; STREET: P.O. Box 4000  
 ; CITY: Princeton  
 ; STATE: New Jersey  
 ; COUNTRY: U.S.A.  
 ; ZIP: 08543-4000  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/646,537B  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Gaul, Timothy J.  
 ; REGISTRATION NUMBER: 33,111  
 ; REFERENCE/DOCKET NUMBER: DC10  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (609) 921-5901  
 ; TELEFAX: (609) 921-4526  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 844 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-07-646-537B-2

Query Match 12.6%; Score 85.5; DB 1; Length 844;  
 Best Local Similarity 31.4%; Pred. No. 0.039;  
 Matches 22; Conservative 14; Mismatches 21; Indels 13; Gaps 3;  
 QY 44 ASAQEDYNAPDCRFINVKKGQIYVYVKLVKENGAGEFWAGSVYGDQDQEMGVYGFPRN 103  
 Db 786 AKARYDFCARDSELSLKEGDI---KILNKKGGQGWVRGEIYGR-----IGMFFSN 834  
 QY 104 LVKEQRYVQE 113  
 Db 835 YVEED--YSE 842

## RESULT 4

US-09-346-510B-21  
 ; Sequence 21, Application US/09346510B  
 ; Patent No. 6281014  
 ; GENERAL INFORMATION:  
 ; APPLICANT: O'Brien, Timothy J.  
 ; APPLICANT: Wang, Yinxiang  
 ; TITLE OF INVENTION: SH3-Containing Protein, DNA and Uses Thereof  
 ; FILE REFERENCE: D6221CIP  
 ; CURRENT APPLICATION NUMBER: US/09/346,510B  
 ; CURRENT FILING DATE: 1999-07-01  
 ; PRIOR APPLICATION NUMBER: 08/871,732  
 ; PRIOR FILING DATE: 1997-06-09  
 ; NUMBER OF SEQ ID NOS: 32  
 ; SEQ ID NO 21  
 ; LENGTH: 54  
 ; TYPE: PRT  
 ; ORGANISM: unknown  
 ; FEATURE:  
 ; NAME/KEY: Domain  
 ; OTHER INFORMATION: amino acid sequence of Vav SH3 domain  
 ; US-09-346-510B-21

Query Match 12.1%; Score 81.5; DB 3; Length 54;  
 Best Local Similarity 32.3%; Pred. No. 0.0024;  
 Matches 20; Conservative 13; Mismatches 18; Indels 11; Gaps 2;



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; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2852-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 625 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-08-995-659-15

Query Match 11.5%; Score 78; DB 3; Length 625;
Best Local Similarity 21.1%; Pred. No. 0.24;
Matches 30; Conservative 26; Mismatches 48; Indels 38; Gaps 5;

QY 4 ILLFLPLGLVAVCAVHGIFMDR-----LASKKLCADDECYYTISLA 44
Db 217 VLLLFISVVAALIFGVYRKGGKALTANLWNVNDACSSLGNKSSGDRCAHSAT 276
QY 45 SAQEDYNAPDCRFNVKKGQIYYVSKLVKENGAGEFW----AGSVYGDGDEMVGWGYF 100
Db 277 SSQDEV---CEGILLMTREE-----KWPEDGAGVCGPVCAGGPAEVRDSRTF 323
QY 101 PRNLVKEQRYVQEATKEVPTTD 122
Db 324 --TLVSEVETQGLSRKIPTED 343

RESULT 8
US-09-215-649A-15
; Sequence 15, Application US/09215649A
; Patent No. 6271349
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/215,649A
; FILING DATE: 17-Dec-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/996,139
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2852-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-577-780-15

Query Match 11.5%; Score 78; DB 3; Length 625;
Best Local Similarity 21.1%; Pred. No. 0.24;
Matches 30; Conservative 26; Mismatches 48; Indels 38; Gaps 5;

QY 4 ILLFLPLGLVAVCAVHGIFMDR-----LASKKLCADDECYYTISLA 44
Db 217 VLLLFISVVAALIFGVYRKGGKALTANLWNVNDACSSLGNKSSGDRCAHSAT 276
QY 45 SAQEDYNAPDCRFNVKKGQIYYVSKLVKENGAGEFW----AGSVYGDGDEMVGWGYF 100
Db 277 SSQDEV---CEGILLMTREE-----KWPEDGAGVCGPVCAGGPAEVRDSRTF 323
QY 101 PRNLVKEQRYVQEATKEVPTTD 122
Db 324 --TLVSEVETQGLSRKIPTED 343

RESULT 9
US-09-577-780-15
; Sequence 15, Application US/09577780
; Patent No. 6419929
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/577,780
; FILING DATE: 24-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/995,659
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2852-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-215-649A-15

Query Match 11.5%; Score 78; DB 3; Length 625;
Best Local Similarity 21.1%; Pred. No. 0.24;
Matches 30; Conservative 26; Mismatches 48; Indels 38; Gaps 5;

QY 4 ILLFLPLGLVAVCAVHGIFMDR-----LASKKLCADDECYYTISLA 44
Db 217 VLLLFISVVAALIFGVYRKGGKALTANLWNVNDACSSLGNKSSGDRCAHSAT 276
QY 45 SAQEDYNAPDCRFNVKKGQIYYVSKLVKENGAGEFW----AGSVYGDGDEMVGWGYF 100
Db 277 SSQDEV---CEGILLMTREE-----KWPEDGAGVCGPVCAGGPAEVRDSRTF 323
QY 101 PRNLVKEQRYVQEATKEVPTTD 122
Db 324 --TLVSEVETQGLSRKIPTED 343

RESULT 9
US-09-577-780-15
; Sequence 15, Application US/09577780
; Patent No. 6419929
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/577,780
; FILING DATE: 24-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/995,659
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2852-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-215-649A-15

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;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 625 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-577-780-15

Query Match 11.5%; Score 78; DB 4; Length 625;
Best Local Similarity 21.1%; Pred. No. 0.24;
Matches 30; Conservative 26; Mismatches 48; Indels 38; Gaps 5;

QY 4 ILLFLPGLVAVCAVGHIFMDR-----LASKKLCADDECVTYISLA 44
Db 217 VLLLFISVVVAALIFGVYRKGGKALTANLWNVNDACSSLSGNKSSGDRCAAGSHSAT 276
QY 45 SAQEDYNADCRFINVKKQOIYVYKLVKENGAGEFW-----AGSVYGDGODEMGVVGYF 100
Db 277 SSQGEV-----CEGILLMTREE-----KMPEDGAGVCGPVCAAGGPWAEVRDSRTF 323
QY 101 PRNLVKEQRYQEAATKEVPTTD 122
Db 324 --TLVSEVETQGLSRKIPTED 343

RESULT 10
US-09-577-800-15
; Sequence 15, Application US/09577800
; Patent No. 6479635
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION NUMBER: US/09/577,800
; FILING DATE: 24-MAY-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/996,139
; FILING DATE: 22 DECEMBER 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELEPHONE: (206)587-0430
; TELEFAX: (206)587-0644
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 625 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-466-496-15

;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 625 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-577-800-15

Query Match 11.5%; Score 78; DB 4; Length 625;
Best Local Similarity 21.1%; Pred. No. 0.24;
Matches 30; Conservative 26; Mismatches 48; Indels 38; Gaps 5;

QY 4 ILLFLPGLVAVCAVGHIFMDR-----LASKKLCADDECVTYISLA 44
Db 217 VLLLFISVVVAALIFGVYRKGGKALTANLWNVNDACSSLSGNKSSGDRCAAGSHSAT 276
QY 45 SAQEDYNADCRFINVKKQOIYVYKLVKENGAGEFW-----AGSVYGDGODEMGVVGYF 100
Db 277 SSQGEV-----CEGILLMTREE-----KMPEDGAGVCGPVCAAGGPWAEVRDSRTF 323
QY 101 PRNLVKEQRYQEAATKEVPTTD 122
Db 324 --TLVSEVETQGLSRKIPTED 343

RESULT 11
US-09-466-496-15
; Sequence 15, Application US/09466496
; Patent No. 6528482
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION NUMBER: US/09/466,496
; FILING DATE: 17-DEC-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,139
; FILING DATE: 22 DECEMBER 1997
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 625 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-466-496-15
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Query Match      11.5%; Score 78; DB 4; Length 625;
Best Local Similarity 21.1%; Pred. No. 0.24;
Matches 30; Conservative 26; Mismatches 48; Indels 38; Gaps 5;

QY 4 ILLFLPLGLVAVCAVHGIFMDR-----LASKKLCADCECVYTISLA 44
DB 217 VLLLFISVVVAAIIFGVYRKGGKALTANLWNVDACSSLSGNKSSGDRCAHSAT 276

QY 45 SAQEDYNAPDCRFINVKKGQIYVYKLVKENGAGEFW-----AGSVYGDQDGMGVGYF 100
DB 277 SSQQEV---CEGILLMTREE-----KMWPDGAGVCGPVCAGGPPWAEVRDSRTF--- 323

QY 101 PRNLVKEQRVYQEAATKEVPTTD 122
DB 324 --TLVSEVETQGLSRKIPTD 343

RESULT 13
US-09-871-856-15
; Sequence 15, Application US/09871856
; Patent No. 6537763
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/871,856
; FILING DATE: 31-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/996,139
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)233-0644
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 625 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-871-856-15

Query Match      11.5%; Score 78; DB 4; Length 625;
Best Local Similarity 21.1%; Pred. No. 0.24;
Matches 30; Conservative 26; Mismatches 48; Indels 38; Gaps 5;

QY 4 ILLFLPLGLVAVCAVHGIFMDR-----LASKKLCADCECVYTISLA 44
DB 217 VLLLFISVVVAAIIFGVYRKGGKALTANLWNVDACSSLSGNKSSGDRCAHSAT 276

QY 45 SAQEDYNAPDCRFINVKKGQIYVYKLVKENGAGEFW-----AGSVYGDQDGMGVGYF 100
DB 277 SSQQEV---CEGILLMTREE-----KMWPDGAGVCGPVCAGGPPWAEVRDSRTF--- 323

QY 101 PRNLVKEQRVYQEAATKEVPTTD 122
DB 324 --TLVSEVETQGLSRKIPTD 343

RESULT 12
US-09-871-856-15
; Sequence 15, Application US/09871856
; Patent No. 6537763
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/871,856
; FILING DATE: 31-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/996,139
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)233-0644
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 625 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-871-856-15

Query Match      11.5%; Score 78; DB 4; Length 625;
Best Local Similarity 21.1%; Pred. No. 0.24;
Matches 30; Conservative 26; Mismatches 48; Indels 38; Gaps 5;

QY 4 ILLFLPLGLVAVCAVHGIFMDR-----LASKKLCADCECVYTISLA 44
DB 217 VLLLFISVVVAAIIFGVYRKGGKALTANLWNVDACSSLSGNKSSGDRCAHSAT 276

QY 45 SAQEDYNAPDCRFINVKKGQIYVYKLVKENGAGEFW-----AGSVYGDQDGMGVGYF 100
DB 277 SSQQEV---CEGILLMTREE-----KMWPDGAGVCGPVCAGGPPWAEVRDSRTF--- 323

QY 101 PRNLVKEQRVYQEAATKEVPTTD 122
DB 324 --TLVSEVETQGLSRKIPTD 122

Query Match      11.5%; Score 78; DB 4; Length 625;
Best Local Similarity 21.1%; Pred. No. 0.24;
Matches 30; Conservative 26; Mismatches 48; Indels 38; Gaps 5;

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QY 45 SAQEDYNAPDCRFINVKKGQIYVYKLVKENGAGEFW-----AGSVYGDQDGMGVGYF 100
DB 277 SSQQEV---CEGILLMTREE-----KMWPDGAGVCGPVCAGGPPWAEVRDSRTF--- 323

QY 101 PRNLVKEQRVYQEAATKEVPTTD 122
DB 324 --TLVSEVETQGLSRKIPTD 343

RESULT 13
US-09-871-291-15
; Sequence 15, Application US/09871291
; Patent No. 6562948
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/871,291
; FILING DATE: 30-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/996,139
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 625 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-871-291-15

Query Match      11.5%; Score 78; DB 4; Length 625;
Best Local Similarity 21.1%; Pred. No. 0.24;
Matches 30; Conservative 26; Mismatches 48; Indels 38; Gaps 5;

QY 4 ILLFLPLGLVAVCAVHGIFMDR-----LASKKLCADCECVYTISLA 44
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QY 45 SAQEDYNAPDCRFINVKKGQIYVYKLVKENGAGEFW-----AGSVYGDQDGMGVGYF 100
DB 277 SSQQEV---CEGILLMTREE-----KMWPDGAGVCGPVCAGGPPWAEVRDSRTF--- 323

QY 101 PRNLVKEQRVYQEAATKEVPTTD 122
DB 324 --TLVSEVETQGLSRKIPTD 122
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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model  
Run on: December 29, 2003, 16:11:59 ; Search time 2106.98 Seconds  
(without alignments)  
2485.278 Million cell updates/sec

Title: US-10-019-455A-6  
Perfect score: 676  
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Xgapop 10.0 , Xgapext 0.5  
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Searched: 2888711 seqs, 2045481386 residues  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	676	100.0	384	6	BD010802 Novel pol
2	676	100.0	384	6	BD093103 Novel pol
3	676	100.0	521	6	AX358818 Sequence
4	676	100.0	521	6	AX362311 Sequence
5	676	100.0	521	6	AX454774 Sequence
6	676	100.0	521	6	AX491252 Sequence
7	676	100.0	846	9	AF233261 Homo sapi
8	676	100.0	865	9	AF243505 Homo sapi
9	676	100.0	923	6	BD010820 Novel pol
10	676	100.0	923	6	BD093121 Novel pol
11	676	100.0	1422	9	AJ742552 Homo sapi
12	602	89.1	384	6	BD010805 Novel pol
13	602	89.1	384	6	BD093106 Novel pol
14	602	89.1	929	10	AF243504 Mus muscu
15	602	89.1	947	6	BD010821 Novel pol
16	602	89.1	947	6	BD093122 Novel pol
17	602	89.1	958	10	MMU243939 Mus muscu
18	602	89.1	1054	10	AF233333 Mus muscu
19	600	88.8	384	6	BD010835 Novel pol
20	600	88.8	384	6	BD093136 Novel pol
21	590	87.3	330	6	BD010816 Novel pol
22	590	87.3	330	6	BD093117 Novel pol
23	547	80.9	330	6	BD010817 Novel pol
24	547	80.9	330	6	BD093118 Novel pol
25	541	80.0	330	6	BD010836 Novel pol
26	541	80.0	330	6	BD093137 Novel pol
27	480	71.0	484	5	AF233518 Gallus ga
28	472	69.8	307	6	BD010830 Novel pol
29	472	69.8	307	6	BD093131 Novel pol
30	413	61.1	261	6	BD010829 Novel pol
31	413	61.1	261	6	BD093130 Novel pol
32	391	57.8	466	5	AF233519 Rana cate
33	355	52.5	121151	9	HS705D16 Human DNA
34	324.5	48.0	215581	2	AC106161 Rattus no
35	321.5	47.6	144765	2	BX510362 Mus muscu
36	257.5	38.1	396	9	BT007044 Homo sapi
37	257.5	38.1	396	12	BT007775 Synthetic
38	257.5	38.1	459	6	A42942 Sequence 1
39	257.5	38.1	459	6	AX016785 Sequence
40	257.5	38.1	459	6	AX252508 Sequence
41	257.5	38.1	459	6	AX287209 Sequence
42	257.5	38.1	459	9	HSNGRPM
43	257.5	38.1	518	9	BC005910 Homo sapi
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ALIGNMENTS

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QY 81 PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100  
 DB 241 TTTTGGGCTGGCAGTGTATGATGGCCAGGACGAGATGGAGTGTGGGTATTTC 300

QY 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120  
 DB 301 CCNAGAACTTGGTCAAGGACAGCGTGTGTACCAGGAGCTTACCAAGGAAGTTCACCACC 360

QY 121 ThrAspIleAspPheCysGlu 128  
 DB 361 ACGGATATTGACTTCTTCTCGGAG 384

RESULT 3  
 LOCUS AX358818 521 bp DNA linear PAT 13-FEB-2002  
 DEFINITION Sequence 71 from Patent WO0193983.  
 ACCESSION AX358818  
 VERSION AX358818.1 GI:18675310  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
 AUTHORS Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,  
 Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,  
 Watanabe, C.K. and Wood, W.I.  
 TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
 the same  
 JOURNAL Patent: WO 0193983-A 71 13-DEC-2001;  
 Genentech Inc. (US)  
 FEATURES  
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 Location/Qualifiers  
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 Pred. No.: 1.4e-76 Length: 521  
 Score: 676.00 Matches: 128  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-10-019-455A-6 (1-128) x AX358818 (1-521)

QY 1 MetAlaArgIleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20  
 DB 38 ATGGCAAGATATTGTACTTTCTCCCGGGTCTTGTGGCTGTATGTGTGATGGA 97

QY 21 IlePheMetAspArgLeuAlaSerLysLysLeuValCysAlaAspGluCysValThr 40  
 DB 98 ATATTTATGACGCTAGCTTCCAGAGCTCTGTGCAGATGATGATGTGTCTATCT 157

QY 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60  
 DB 158 ATTTCTGTGGCTAGTGTCTCAAGAGATTATTAATGCCCGGACTGTAGATTCAATTAAGTT 217

QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80  
 DB 218 AAAAAAGGCGCAGATCTATGTACTCAAGCTGTGTAAGCTGTAAGAAATGGAGCTGGAGAA 277

QY 81 PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100  
 DB 278 TTTTGGGCTGGCAGTGTATGATGGCCAGGACGAGATGGAGTGTGGGTATTTC 337

QY 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120  
 DB 338 CCCAGGAATTTGGTCAAGGAACAGCGTGTGTACCAGGAGCTACCAAGGAAGTTCACCACC 397

QY 121 ThrAspIleAspPheCysGlu 128  
 DB 398 ACGGATATTGACTTCTTCTCGGAG 421

RESULT 4  
 LOCUS AX362311 521 bp DNA linear PAT 15-FEB-2002  
 DEFINITION Sequence 71 from Patent WO0208288.  
 ACCESSION AX362311  
 VERSION AX362311.1 GI:18694613  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
 AUTHORS Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,  
 Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,  
 Watanabe, C.K. and Wood, W.I.  
 TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
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 JOURNAL Patent: WO 0208288-A 71 31-JAN-2002;  
 Genentech, Inc. (US)  
 FEATURES  
 source 1..521  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 BASE COUNT 167 a 86 c 131 g 137 t  
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 Pred. No.: 1.4e-76 Length: 521  
 Score: 676.00 Matches: 128  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-10-019-455A-6 (1-128) x AX362311 (1-521)

QY 1 MetAlaArgIleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20  
 DB 38 ATGGCAAGATATTGTACTTTCTCCCGGGTCTTGTGGCTGTATGTGTGATGGA 97

QY 21 IlePheMetAspArgLeuAlaSerLysLysLeuValCysAlaAspGluCysValThr 40  
 DB 98 ATATTTATGACGCTAGCTTCCAGAGCTCTGTGCAGATGATGATGTGTCTATCT 157

QY 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60  
 DB 158 ATTTCTGTGGCTAGTGTCTCAAGAGATTATTAATGCCCGGACTGTAGATTCAATTAAGTT 217

QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80  
 DB 218 AAAAAAGGCGCAGATCTATGTACTCAAGCTGTGTAAGCTGTAAGAAATGGAGCTGGAGAA 277

QY 81 PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100  
 DB 278 TTTTGGGCTGGCAGTGTATGATGGCCAGGACGAGATGGAGTGTGGGTATTTC 337

QY 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120  
 DB 398 CCCAGGAATTTGGTCAAGGAACAGCGTGTGTACCAGGAGCTACCAAGGAAGTTCACCACC 397

QY 121 ThrAspIleAspPheCysGlu 128  
 DB 398 ACGGATATTGACTTCTTCTCGGAG 421

RESULT 5  
 LOCUS AX454774 521 bp DNA linear PAT 06-JUL-2002

DEFINITION	Sequence 359 from Patent WO0208284.
ACCESSION	AX454774
VERSION	AX454774.1 GI:21714011
KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens (human)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J., Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I. and Ye,W. Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis Patent: WO 0208284-A 359 31-JAN-2002;
JOURNAL	Genentech, Inc. (US)  
TITLE	Location/Qualifiers source 1..521 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"
BASE COUNT	167 a _86 c 131 g 137 t
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Dc	38 ATGGCAAGATATTGTACTTTCTCCCGGCCTTGTCGTATGCTGTGCATGGA 97
Qy	21 IlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspGluCysValThr 40
Dc	98 ATAATTATGACCCTTAGTCTCCAAGAAGCTCTGCCAGATCATGATGCTATACT 157
Qy	41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
Dc	158 ATTCTCTGGCTAGTGCTCAAGAAGATTATAATGCCCGGACTGTAGATTAACGTT 217
Qy	61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80
Dc	218 AAAAAAGGCAGCAGATCTATGTACTCAAAGCTGTTAAAGAAAATGAGCTGGAGAA 277
Qy	81 PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100
Dc	278 TTTTGGGCTGGCAGTGTATTATGTGTGATGGCAGCACGATGGAGTCTGGTTATTC 337
Qy	101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120
Dc	338 CCCAGGAACCTTGTTCACGAGAACAGCGTGTTACAGGAAGTACCAGGAAGTCCCACC 397
Qy	121 ThrAspileaspPhePheCysGlu 128
Dc	398 ACCGATATTGACTTCTTCGCGAG 421
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AF233261	
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DEFINITION	Homo sapiens otoraplin (OTOR) mRNA, complete cds.
ACCESSION	AF233261
VERSION	AF233261.1 GI:8927427
KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[illegible]

REFERENCE 1 (bases 1 to 846)  
AUTHORS Roberton,N.G., Heller,S., Lin,J.S., Resendes,B.L., Weremowicz,S., Denis,C.S., Bell,A.M., Hudspeth,A.J. and Morton,C.C.  
TITLE A novel conserved cochlear gene, OTOR: identification, expression analysis, and chromosomal mapping  
JOURNAL Genomics 66 (3), 242-248 (2000)  
MEDLINE 20334619  
PUBMED 10873378  
REFERENCE 2 (bases 1 to 846)  
AUTHORS Roberton,N.G., Heller,S., Lin,J.S., Resendes,B.L., Weremowicz,S., Denis,C.S., Bell,A.M., Hudspeth,A.J. and Morton,C.C.  
TITLE Direct Submission  
JOURNAL Submitted (09-FEB-2000) Pathology, Brigham and Women's Hospital, 75 Francis Street, Boston, MA 02115, USA  
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Score: 676.00 Matches: 128  
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Best Local Similarity: 100.00% Mismatches: 0  
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Qy 21 IlePheMetAspArgLeuAlaSerLysLeuCysAlaAspGluCysValTyrThr 40  
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Qy 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60  
Db 165 ATTCTCTGGCTAGTGTCTCAAGAAGATTATAATGCCCGGAGCTGTAGATTCATTAAAGTT 224  
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Db 225 AAAAAAGGGCAGCAGATCTATGTGTACTCAAGCTGTGTAAGAAATAATGGAGCTGGAGAA 284  
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Qy 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120  
Db 345 CCCAGGAACCTTGTCAAGGAACAGCGTGTGTACAGGAAGCTACCAAGGAAGTTCCACC 404  
Qy 121 ThrAspIleAspPhePheCysGlu 128

Db 405 ACCGATATTGACTTCTTCTGGAG 428  
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DEFINITION AF243505  
ACCESSION AF243505  
VERSION AF243505.1 GI:11991843  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 865)  
REFERENCE Cohen-Salmon,M., Frenz,D., Liu,W., Verpy,E., Voegeling,S. and Petit,C.  
AUTHORS Fdp, a new fibrocyte-derived protein related to MIA/CD-RAP, has an in vitro effect on the early differentiation of the inner ear mesenchyme  
JOURNAL J. Biol. Chem. 275 (51), 40036-40041 (2000)  
MEDLINE 20568254  
PUBMED 10998416  
REFERENCE 2 (bases 1 to 865)  
AUTHORS Cohen-Salmon,M., Frenz,D., Verpy,E., Voegeling,S. and Petit,C.  
TITLE Direct Submission  
JOURNAL Submitted (09-MAR-2000) Biotechnologies, Institut Pasteur, 25 rue du Dr. Roux, Paris 75015, France  
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Query Match: 100.00% Indels: 0  
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Db      188 AAAAAAGGCGCAGCATCTATCTGTACTCAAGAGCTGTAAAAAGAAAAATGGAGCTGGAGAA 247
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Qy      101 ProArgAsnLeuVallyGlnArgValTyrGlnGluAlaThrllysGluValProThr 120
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Qy      121 ThrAspIleAspPheCysGlu 128
Db      368 ACGGATATTGACTTCTCTGCGGAG 391

RESULT 9
LOCUS   BD010820
DEFINITION Novel polypeptide and DNA thereof.
ACCESSION BD010820
VERSION   BD010820.1 GI:18639193
KEYWORDS JP 2001069994-A/21.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 923)
AUTHORS Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y.,
Yoshimura,K. and Tanaka,H.
TITLE Novel polypeptide and DNA thereof
JOURNAL Patent: JP 2001069994-A 21 21-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD
COMMENT OS Homo sapiens (human)
PN JP 2001069994-A/21
PD 21-MAR-2001
PF 29-JUN-2000 JP 2000195911
PR YASUAKI ITO,KAZUNORI NISHI,KAZUHIRO OGI,SHOICHI OKUBO, PI
SHINICHI MOGI,
PI YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA
PC C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P9/00,A61P19/02, PC
A61P19/08,
PC C07K14/47,C07K16/18,C12N1/21,C12N5/10,G01N33/15,G01N33/50, PC
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Pred. No.: 2.82e-76 Length: 923
Score: 676.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-10-019-455A-6 (1-128) x BD010820 (1-923)

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Qy      81 PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100
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Qy      101 ProArgAsnLeuVallyGlnArgValTyrGlnGluAlaThrllysGluValProThr 120
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Db      394 ACGGATATTGACTTCTCTGCGGAG 417

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LOCUS   BD093121
DEFINITION Novel polypeptide and its DNA.
ACCESSION BD093121
VERSION   BD093121.1 GI:22638709
KEYWORDS WO 0102564-A/21.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 923)
AUTHORS Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y.,
Yoshimura,K. and Tanaka,H.
TITLE Novel polypeptide and its DNA
JOURNAL Patent: WO 0102564-A 21 11-JAN-2001;
TAKEDA CHEMICAL INDUSTRIES LTD,YASUAKI ITO,KAZUNORI NISHI, KAZUHIRO
OGI, SHOICHI OKUBO,SHINICHI MOGI,YUKO NOGUCHI,KOJI YOSHIMURA,
HIDEYUKI TANAKA
COMMENT OS Homo sapiens (human)
PN WO 0102564-A/21
PD 11-JAN-2001
PF 29-JUN-2000 WO 2000JP004278
PR 30-JUN-1999 JP 99P 186718
PI YASUAKI ITO,KAZUNORI NISHI,KAZUHIRO OGI,SHOICHI OKUBO,SHINICHI
MOGI,
PI YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA
PC C12N15/12,C12N5/10,C12P21/02,C07K14/47,C07K16/18,A61K45/00, PC
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PC A61K39/395,A61K49/16,A61P19/02,A61P19/08,A61K31/7088//(C12P21/
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Score: 676.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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DB: 6 Gaps: 0

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RESULT 11
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LOCUS
DEFINITION HSA242552 1422 bp mRNA linear PRI 29-JAN-2001
melanoma inhibitory activity like protein; Mial gene.
ACCESSION AJ242552
VERSION AJ242552.1 GI:12619172
KEYWORDS melanoma inhibitory activity like protein; Mial gene.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Rendtorff,N.D., Frodin,M., Attie-Bitach,T., Vekemans,M. and
Tommerup,N.
TITLE Identification and characterization of an inner ear-expressed human
melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent
polymorphism that abolishes translation
JOURNAL Genomics 71 (1), 40-52 (2001)
MEDLINE 21100875
PubMed 11161796
REFERENCE 2 (bases 1 to 1422)
AUTHORS Rendtorff,N.D.
TITLE Direct Submission
JOURNAL Submitted (21-MAY-1999) Rendtorff N.D., Department of Medical
Genetics, Institute of Medical Biochemistry and Genetics,
Blegdamsvej 3, 2200 Copenhagen N, DENMARK
REMARK Revised by author 03-AUG-1999
COMMENT Related sequence: AJ243939 (Mus musculus mRNA)
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ORIGIN
Alignment Scores:
Pred. No.: 4,77e-76 Length: 1422
Score: 676.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-019-455A-6 (1-128) x HSA242552 (1-1422)
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Db 301 CCCAGGAACCTTGGTCAAGGAACAGCGTGTGTACCAAGGAAGCTACCAAGGAAGTTCCACC 360
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QY 121 ThrAspIleAspPheCysGlu 128
Db 361 ACCGATATTGACTTCTCTCGGAG 384

RESULT 12
LOCUS BD010805 384 bp DNA linear PAT 31-JAN-2002
DEFINITION Novel polypeptide and DNA thereof.
ACCESSION BD010805
VERSION BD010805.1 GI:18639178
KEYWORDS JP 2001069994-A/6.
SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 384)
Yoshimura, K. and Tanaka, H.
TITLE Novel polypeptide and DNA thereof
JOURNAL Patent: JP 2001069994-A 6 21-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD
COMMENT OS Mus sp. (mouse)
PN JP 2001069994-A/6
PD 21-MAR-2001
PF 29-JUN-2000 JP 2000195911
PR
PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI
SHINICHI MOGI,
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC
A61P19/08,
PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC
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Best Local Similarity: 86.72% Mismatches: 8
Query Match: 89.05% Indels: 0
DB: 6 Gaps: 0

US-10-019-455A-6 (1-128) x BD010805 (1-384)

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Qy      121 ThrAspIleAspPheCysGlu 128
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DEFINITION Mus musculus fibrocyte-derived protein (Fdp) mRNA, complete cds.
ACCESSION AF243504
VERSION AF243504.1 GI:11991841
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Cohen-Salmon,M., Frenz,D., Liu,W., Verpy,E., Voegelings,S. and
AUTHORS Petit,C.
TITLE Fdp, a new fibrocyte-derived protein related to MIA/CD-3AP, has an
in vitro effect on the early differentiation of the inner ear
mesenchyme
JOURNAL J. Biol. Chem. 275 (51), 40036-40041 (2000)
MEDLINE 20568254
PUBMED 10998416
REFERENCE Cohen-Salmon,M., Frenz,D., Verpy,E., Voegelings,S. and Petit,C.
AUTHORS Direct Submission
TITLE Submitted (09-MAR-2000) Biotechnologies, Institut Pasteur, 25 rue
JOURNAL du Dr. Roux, Paris 75015, France
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Alignment Scores:
Pred. No.: 7,29e-67 Length: 929
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Percent Similarity: 93.75% Conservative: 9
Best Local Similarity: 86.72% Mismatches: 8
Query Match: 89.05% Indels: 0
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US-10-019-455A-6 (1-128) x AF243504 (1-929)

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RESULT 15
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LOCUS      947 bp DNA linear PAT 31-JAN-2002
DEFINITION Novel polypeptide and DNA thereof.
ACCESSION BD010821
VERSION BD010821.1 GI:18639194
KEYWORDS JP 2001069994-A/22.
SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y.,
Yoshimura,K. and Tanaka,H.
TITLE Novel polypeptide and DNA thereof
JOURNAL Patent: JP 2001069994-A 22 21-MAR-2001;
COMMENT TAKEDA CHEMICAL INDUSTRIES LTD
OS Mus sp. (mouse)
PN JP 2001069994-A/22
PD 21-MAR-2001
PF 29-JUN-2000 JP 2000195911
PR PI YASUAKI ITO,KAZUNORI NISHI,KAZUHIRO OGI,SHOICHI OKUBO, PI
SHINICHI MOGI,
PI YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA
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Alignment Scores:
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Job time : 2110.98 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 29, 2003, 16:23:14 : Search time 1324.28 Seconds  
(without alignments)  
2349.180 Million cell updates/sec

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Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_eston:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vri:\*  
28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	602	89.1	398	13	BQ570035	BQ570035 gi143b10.
2	602	89.1	488	13	BQ564607	BQ564607 gi19h02.y
3	602	89.1	514	13	BQ568498	BQ568498 gi109c02.y
4	602	89.1	534	13	BQ564134	BQ564134 gi11d01.y
5	602	89.1	560	13	BQ569741	BQ569741 gi135f01.y
6	602	89.1	620	13	BQ564944	BQ564944 gi127g09.y
7	602	89.1	630	13	BQ568471	BQ568471 gi108g04.y
8	602	89.1	696	10	BB611549	BB611549 BB611549
9	597	88.3	474	13	BQ565637	BQ565637 gi42g03.y
10	595	88.0	684	13	BQ563768	BQ563768 gi06c09.y
11	572	84.6	409	13	BQ566932	BQ566932 gi73g09.y
12	541	80.0	490	13	BQ565411	BQ565411 gi37b12.y
13	522	77.2	527	10	BE236443	BE236443 144645 MA
14	512	75.7	365	13	BY232622	BY232622 BY232622
15	502	74.3	604	13	BQ567343	BQ567343 gi88d08.y
16	413	61.1	485	13	BQ565179	BQ565179 gi32a07.y
17	410.5	60.7	795	13	BU748241	BU748241 CH3#018.G
18	390	57.7	280	13	BQ568785	BQ568785 gi114f04.y
19	377.5	55.8	533	9	AL925854	AL925854 AL925854
20	343	50.7	588	13	BQ566776	BQ566776 gi69b07.y
21	321.5	47.6	677	13	BQ563227	BQ563227 gi01a05.y
22	321.5	47.6	3240	11	AK047965	AK047965 Mus muscu
23	302.5	44.7	678	10	BB647928	BB647928 BB647928
24	285	42.2	349	9	AW023324	AW023324 df53d01.y
25	279	41.3	633	14	CD360404	CD360404 AGENCOURT
26	258.5	38.2	929	13	BU195892	BU195892 AGENCOURT
27	257.5	38.1	480	12	BM715936	BM715936 UI-E-EJ0-
28	257.5	38.1	492	12	EM856478	EM856478 K-EST0140
c 29	257.5	38.1	507	12	BM674250	BM674250 UI-E-EJ0-
30	257.5	38.1	515	13	BQ892734	BQ892734 AGENCOURT
31	257.5	38.1	522	13	BQ681978	BQ681978 AGENCOURT
32	257.5	38.1	522	13	BU157778	BU157778 AGENCOURT
33	257.5	38.1	529	13	BU194561	BU194561 AGENCOURT
34	257.5	38.1	609	12	BM791767	BM791767 K-EST0071
35	257.5	38.1	890	12	EG766328	EG766328 602739014
36	257.5	38.1	1140	12	BG765502	BG765502 602739414
c 37	256.5	37.9	437	9	AV592759	AV592759 AV592759
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c 39	256.5	37.9	517	10	BE665724	BE665724 154861 MA
c 40	255.5	37.8	473	14	CA433401	CA433401 UI-H-COO-
c 41	254	37.6	594	14	CA509768	CA509768 UI-R-F50-
c 42	252.5	37.4	453	9	AA627297	AA627297 nq68g01.s
c 43	251.5	37.2	430	10	BF439750	BF439750 nad13c10.
c 44	251	37.1	544	13	BQ208982	BQ208982 UI-R-DY1-
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# ALIGNMENTS

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DEFINITION gi143b10.y1 Mouse Organ of Corti cDNA pbluescript Mus musculus cDNA  
clone gi143b10 5', mRNA sequence.  
ACCESSION BQ570035  
VERSION BQ570035.1 GI:21473352  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Rukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 398)

# AUTHORS TITLE JOURNAL COMMENT

Kachar,B.  
EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing  
Unpublished  
Contact: Kachar,B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kachar@nidcd.nih.gov  
Plate: 143 row: b column: 10  
Seq primer: M13RPI reverse primer (ABI).  
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/clone\_lib="Mouse Organ of Corti cDNA pBluescript"  
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## FEATURES source

City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 105 a 69 c 116 g 108 t  
ORIGIN

Alignment Scores:  
Pred. No.: 3-21e-70 Length: 398  
Score: 602.00 Matches: 111  
Percent Similarity: 93.75% Conservative: 9  
Best Local Similarity: 86.72% Mismatches: 8  
Query Match: 89.05% Indels: 0  
DB: 13 Gaps: 0

US-10-019-455A-6 (1-128) x BQ570035 (1-398)

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Db 193 AAGAAAGGGCAGCAGATCTATGTTTACTCCAACTGGTAACAGAAAAACGAGCTGGAGAG 252  
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Db 313 CCCAGCACTTGGTAGGAGGAGGAGGCTGTATACCGAGGAGGCCACCAAGGAGATCCCAACC 372  
QY 121 ThrAspIleAspPhePheCysGlu 128  
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RESULT 2  
BQ564607  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BQ564607 488 bp mRNA linear EST 19-JUN-2002  
g119h02.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA  
clone g119h02 5', mRNA sequence.  
BQ564607  
BQ564607.1 GI:21467924  
EST.  
Mus musculus (house mouse)  
Mus musculus  
Mus musculus  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 488)  
Kachar,B.  
EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing  
Unpublished  
Contact: Kachar,B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kachar@nidcd.nih.gov  
Plate: 19 row: h column: 02  
Seq primer: M13RPI reverse primer (ABI).

**FEATURES**  
**SOURCE**

Location/Qualifiers

1. .486

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/sex="male and female"

/dev\_stage="Post natal day 5 to 13"

/clone\_libs="Mouse Organ of Corti cDNA pBluescript"

/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fastrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp , respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on XLI Blue MRF<sup>+</sup> cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTATGACC) and 25x strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster city, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

143 a 83 c 135 g 127 t

4.3e-70 Length: 488

602.00 Matches: 111

93.75% Conservative: 9

BASE COUNT	143 a	83 c	135 g	127 t
ORIGIN				
Alignment Scores:				
Pred. No.:	4.3e-70	Length:	488	
Score:	602.00	Matches:	111	
Percent Similarity:	93.75%	Conservative:	9	

Best Local Similarity:	86.72%	Mismatches:	8
Query Match:	89.05%	Indels:	0
DB:	13	Gaps:	0

US-10-019-455A-6 (1-128) x BQ564607 (1-488)

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Qy	21	IlePheMetAspArgLeuAlaSerIlysIysLeuCysAlaAspAspGluCysValTyrThr	40
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Qy	41	IleSerIleuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal	60
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Qy	61	LysLysGlyGlnGlnIleTyrValTyrSerIysLeuValLysGluAsnGlyAlaGlyGlu	80
Db	187	AAGAAAGGGCAGCAGATCTATGTTTACTCCAAAGCTGGGTAAACAGAAAAACGGAGCTGGAGAG	246
Qy	81	PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe	100
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Qy	101	ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr	120
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RESULT 3  
B0568498

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DEFINITION	gi190c02.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone Q109c02 5', mRNA sequence.				
ACCESSION	BQ568498				
VERSION	BQ568498.1	GI:21471815			
KEYWORDS	EST.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 514)				
TITLE	Kachar,B.				
JOURNAL	EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing				
COMMENT	Unpublished				
	Contact: Kachar, B.				
	Structural Cell Biology				
	National Institute of Deafness and other Communication Disorders				
	50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA				
	Tel: 301-402-1599				
	Fax: 301-402-1765				
	Email: kacharb@nidcd.nih.gov				
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	Seq primer: M13Rpl reverse primer (ABI).				

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/db_xref="taxon:10090"
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/note="Organ: Organ of Corti; Vector: pBluescript; The
Organ of Corti (OC) was fine dissected from a total of 386
OC as follows: 102 samples from post-natal (P) day 5; 72

```

from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XL1 Blue MRF<sup>+</sup> cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concerto96(TW) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGGTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 147 a 85 c 143 g 139 t  
ORIGIN

## Alignment Scores:

Pred. No.: 4,64e-70 Length: 514  
Score: 602.00 Matches: 111  
Percent Similarity: 93.7% Conservative: 9  
Best Local Similarity: 86.7% Mismatches: 8  
Query Match: 89.0% Indels: 0  
DB: 13 Gaps: 0

US-10-019-455A-6 (1-128) x BQ568498 (1-514)

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DB 5 ATGGCAAGGATATTGATCTTTTGGCTTGGGGCCCTTGTGTTCTATGTCGGCGCATGGT 64  
QY 21 llePheMetAspArgLeuSerLysLysLeuCysAlaAspGluCysValThr 40  
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DB 125 ATTTCTCTGGCAGAGACACAGGAAGATTACATGCCCCAGACTGTAGGTTCATCGATGTC 184  
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80  
DB 185 AAGAAGGGCAGACGATCTATGTTTCTCCAGCTGGTACAGAAAACGAGACTGGAGAG 244  
QY 81 PheTrrAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100  
DB 245 TTTTGGGCTGGCAGTGTATTGTTGTCGACCAACAGGATGAGATGGGAATTCGTAGTTATTTC 304  
QY 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGlnAlaThrLysGluValProThr 120  
DB 305 CCACCAACTTGGTGAAGGAGCAGCGTGTATACAGGAGGCCACCAAGGAGATGCCAACCC 364  
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BQ564134  
BQ564134.1 GI:21467451  
VERSION  
KEYWORDS  
SOURCE  
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AUTHORS  
TITLE  
JOURNAL  
COMMENT  
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/clone\_lib="Mouse Organ of Corti cDNA pBluescript"  
/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both



from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XLI Blue MRF<sup>+</sup> cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGACACGTAAGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT

155 a 87 c 148 g 144 t

ORIGIN

Alignment Scores:

Pred. No.:	4.9e-70	Length:	534
Score:	602.00	Matches:	111
Percent Similarity:	93.75%	Conservative:	9
Best Local Similarity:	86.72%	Mismatches:	8
Query Match:	89.05%	Indels:	0
DB:	13	Gaps:	0

US-10-019-455A-6 (1-128) x BQ564134 (1-534)

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Db	63	GTATTATCGATAAATCTTCTTCTAGAGTTGTGTGCGGATGAGGAGTGTGCTACT	122
Qy	41	IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal	60
Db	123	ATTTCTCTGCAAGACACAGGAGGATTAACAATGCCACGACTGTAGTTTCATCGATGTC	182
Qy	61	LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu	80
Db	183	AGAAAGGGGAGAGATCTATGTTTACTCCAACTGGTAAACAGAAACCGAGCTGGAGAG	242
Qy	81	PheTyrAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe	100
Db	243	TTTGGGCTGGCAGTGTATTATGTTGACCCAGGATGAGATGGAAATTGTAGTTATTTC	302

Qy	101	ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr	120
Db	303	CCACGACACTTGGTGAGGAGGACGCGTGTTATACGAGAGGCCACAGAGATCCCAACC	362
Qy	121	ThrAspIleAspPhePheCysGlu	128
Db	363	ACGGATATTGACTTCTTCTGTGAA	386

RESULT 5  
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LOCUS  
DEFINITION  
g1135f01.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA  
Clone g1135f01 5', mRNA sequence.  
ACCESSION  
BQ569741  
VERSION  
BQ569741.1 GI:21473058  
KEYWORDS  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Kachar, B.  
1 (bases 1 to 560)  
REFERENCE  
EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing  
Unpublished  
JOURNAL  
Contact: Kachar, B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kachar@nidcd.nih.gov  
Plate: 135 row: f column: 01  
Seq primer: M13RPI reverse primer (ABI).  
Location/Qualifiers  
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/mol\_type="mRNA"  
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/clone="g1135f01"  
/sex="male and female"  
/dev\_stage="Post natal day 5 to 13"  
/clone\_lib="Mouse Organ of Corti cDNA pBluescript"  
/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the Micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA)

FEATURES  
source

columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified.

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BASE COUNT      160 a      92 c      154 g      153 t
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Alignment Scores:
Pred. No.:      5,25e-70      Length:      560
Score:          602.00      Matches:      111
Percent Similarity: 93.75%      Conservative: 9
Best Local Similarity: 86.72%      Mismatches: 8
Query Match:      89.05%      Indels:      C
DB:              13      Gaps:      0

US-10-019-455A-6 (1-128) x BQ569741 (1-560)

QY      1 MetAlaArgIleLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20
Db      6 ATGGCAAGATATTCATCTTTTGGTGGGGCCCTTGTGTTCTATGTCGGGGCATGGT 65

QY      21 IlePheMetAspArgLeuAlaSerIlySlysLeuCysAlaAspAspGluCysValTyrThr 40
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QY      41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
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QY      101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120
Db      306 CCCAGCAACTTGGTAGGAGAGCAGCGTGTATACAGAGAGGCCAACCAAGAGATCCCAACC 365

QY      121 ThrAspIleAspPheCysGlu 128
Db      366 ACGGATATTGACTTCTTCTGTGAA 389

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## RESULT 6

BQ564944

LOCUS

BQ564944 608 bp mRNA linear EST 19-JUN-2002

DEFINITION

g127g09.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA

clone g127g09 5', mRNA sequence.

## ACCESSION

BQ564944 GI:21468261

## VERSION

BQ564944.1

## KEYWORDS

EST.

## SOURCE

Mus musculus (house mouse)

## ORGANISM

Mus musculus

## REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

Kachar, B.

1 (bases 1 to 608)

EST analysis of gene expression in the mouse Organ of Corti at the

onset of hearing

Unpublished

Contact: Kachar, B.

Structural Cell Biology

National Institute of Deafness and other Communication Disorders

50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA

Tel: 301-402-1599

Fax: 301-402-1765

Email: kacharb@nidcd.nih.gov

Seg primer: M13RP1 reverse primer (ABI).

Plate: 27 row: 9 column: 09

Location/Qualifiers

1. 608

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/mol\_type="mRNA"

/strain="BALB/c"

/db\_xref="taxon:10090"

/clone="g127g09"

/sex="male and female"

/dev\_stage="Post natal day 5 to 13"

/clone\_lib="Mouse Organ of Corti cDNA pBluescript"

/note="Organ: Organ of Corti; Vector: pBluescript; The

organ of Corti (OC) was fine dissected from a total of 386

OC as follows: 102 samples from post-natal (P) day 5; 72

from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;

14 from P12 and 24 from P13. After killing animals by

cervical dislocation followed by decapitation, the bulla

was removed and opened in Leibowitz medium. The bony

capsule of the cochlea was chipped away, stria vascularis

and spiral ligament were removed and the sensory

epithelium was carefully dissected out of the modiolus.

Total RNA was extracted using the micro Fasttrack kit

(catalog # K1593-02; Invitrogen, Carlsbad, CA), according

to manufacturer's instructions. Reverse transcription and

library construction were carried out with the Uni-Zap XR

vector kit (catalog # 237211, Stratagene) and Uni-Zap XR

Gigapack III Gold Cloning kit (catalog # 237612), both

from Stratagene (La Jolla, CA, USA), according to

manufacturer's instructions. Briefly: 1.5 ug mRNA was

reverse transcribed using a hybrid oligo(dT) linker-primer

that contains an Xho I site. First strand synthesis was

primed with the linker- primer and transcribed using

Moloney murine leukemia virus reverse transcriptase

(MMLV-RT) and 5-methyl dCTP. The second strand was

synthesized with DNA polymerase and Rnase H. Complementary

DNA was blunt ended with Pfu DNA polymerase, ligated with

EcoR I adapters in the presence of ligase and digested

with Xho I. The cDNA was sequentially size fractionated

over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden)

and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA)

columns to enrich for cDNAs greater than 400bp and 1000 bp

, respectively. The cDNA was then directionally ligated to

the Uni-ZAP XR vector, which had been predigested with

EcoR I and Xho I. The phagemid was packaged with Gigapack

III Gold and, upon titration on XL1 Blue MRF' cells, the

yield of the phage library was estimated to be 11,100,000

recombinants. Stratagene's ExAssist interference

resistance helper phage (catalogue # 211203) was adopted

to rescue plasmid DNA from the phages. Upon plating of the

rescued library, individual cDNA clones were selected and

grown in 96-well, 2 ml growth plate. Plasmid DNA was

purified from 200 ul of saturated culture with the

Concert96(TM) plasmid purification kit (Invitrogen,

Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGTATGACC) and 25 $\times$  strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 169 a 107 c 166 g 166 t

ORIGIN

#### Alignment Scores:

Pred. No.:	5.9e-70	Length:	608
Score:	602.00	Matches:	111
Percent Similarity:	93.75%	Conservative:	9
Best Local Similarity:	86.72%	Mismatches:	8
Query Match:	89.05%	Indels:	0
DB:	13	Gaps:	0

US-10-019-455A-6 (1-128) x BQ564944 (1-608)

Qy	1	MetAlaArgIleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly	20
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Db	73	GTATTATGGATAAATCTTCTTAAGAGTTGTGTGGGATGAGAGTGCTGTACTACT	132
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Db	193	AAGAAAGGGCGACGATCTATGTCTTACCCCAAGCTGGTAAACAGAAACGGAGCTGGAGAG	252
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#### RESULT 7

BQ568471  
LOCUS BQ568471 630 bp mRNA linear EST 19-JUN-2002  
DEFINITION G108904.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone g108904 5', mRNA sequence.  
ACCESSION BQ568471  
VERSION BQ568471.1 GI:21471788  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Kachar, B.  
REFERENCE 1 (bases 1 to 630)  
AUTHORS Kachar, B.  
TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing  
JOURNAL Unpublished  
COMMENT Contact: Kachar, B.

Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kachar@nidcd.nih.gov

Plate: 108 row: g column: 04

Seq primer: M13Rpl reverse primer (ABI).

#### FEATURES

##### source

Location/Qualifiers  
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/db\_xref="taxon:10090"  
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/sex="male and female"  
/dev\_stage="Post natal day 5 to 13"  
/clone\_lib="Mouse Organ of Corti; Vector: pBluescript"; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, the stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XLI Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGTATGACC) and 25 $\times$  strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function;

12% are uncharacterized ESTs and 20% are unidentified."

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BASE COUNT      178 a      111 c      167 g      174 t
ORIGIN

Alignment Scores:
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Score:          602.00      Matches:      111
Percent Similarity: 93.75%      Conservative: 9
Best Local Similarity: 86.72%      Mismatches: 8
Query Match:      89.05%      Indels:      0
DB:              13      Gaps:      0

US-10-019-455A-6 (1-128) x BQ568471 (1-630)

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Db      73 GTATTATTGGATAAACTTCTTCTAAGAGATTGTGTGGGATGAGGAGTGTCTATACT 132
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QY      41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
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QY      81 PheTTPAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100
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Db      253 TTTTGGCTGGCAGTGTTTATGGTGACCCAGGATGAGATGGGAATTGTAGGTTATTTC 312
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QY      101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120
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RESULT 8
LOCUS      BB611549      696 bp      mRNA      linear      EST 31-AUG-2001
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ACCESSION      BB611549
VERSION      BB611549.1 GI:15393547
KEYWORDS      EST.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 696)
AUTHORS      Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
            Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
            ,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okada
            Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
            ,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
            Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
            Muramatsu,M. and Hayashizaki,Y.
            RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
            Unpublished
TITLE      Contact: Yoshihide Hayashizaki
JOURNAL      Laboratory for Genome Exploration Research Group, RIKEN Genomic
COMMENT      Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/

```

Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh ,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura ,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara ,Y. and Hayashizaki,Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Yamanaka,I., Kiyosawa,H., Kondo,S., Saito,T., Shinagawa,A., Aizawa ,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K., Arakawa,T., Ishii,Y. and Hayashizaki,Y.

Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct. Func. Genomics 2 pre, 172-186 (2001)

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

e mouse tissues.

## FEATURES

source

Location/Qualifiers

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1..696
/organism="Mus musculus"
/mol_type="mRNA"
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/clone="3110083012"
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/lab_host="SOLR"
/clone_lib="RIKEN full-length enriched, 13 days embryo
head"
/notes="Site 1: XhoI; Site 2: SstI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5',
GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was
prepared by using trihalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 10.0 and subtraction to Rot = 50.0. Second strand
cDNA was prepared with the primer adapter of sequence [5',
GAGAGAGAGATCTCGAGTTAATTAATTAATCCCCCCCCCC 3']. cDNA
was cleaved with XhoI and SstI."

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BASE COUNT 204 a 122 c 176 g 194 t

ORIGIN

## Alignment Scores:

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Percent Similarity: 93.75%      Conservative: 9
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Query Match:      89.05%      Indels:      0
DB:              10      Gaps:      0

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US-10-019-455A-6 (1-128) x BB611549 (1-696)

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QY      1 MetAlaArgIleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20
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Db      84 GTATTATTGGATAAACTTCTTCTAAGAGATTGTGTGGGATGAGGAGTGTCTATACT 143
      |||||.....:|||||.....:|||||.....:|||||.....:|||||
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Db      204 AAGAAAGGGCAGCAGATCTATGTTTACTCCAAAGCTGGTAAACAGAAACCGGAGCTGGAGAG 263
Qy      81 PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100
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Qy      101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGlnAlaThrLysGluValProThr 120
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RESULT 9
BQ565637
LOCUS      gi42903.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
DEFINITION      clone gi42903 5', mRNA sequence.
ACCESSION      BQ565637
VERSION        BQ565637.1 GI:21468954
KEYWORDS       EST.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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```

REFERENCE
AUTHORS      Kachar,B.
TITLE         EST analysis of gene expression in the mouse Organ of Corti at the
              onset of hearing
JOURNAL       Unpublished
COMMENT       Contact: Kachar,B.
              Structural Cell Biology
              National Institute of Deafness and other Communication Disorders
              50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
              Tel: 301-402-1599
              Fax: 301-402-1765
              Email: kachar@nidcd.nih.gov
              Plate: 42 row: 9 column: 03
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              Location/Qualifiers
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                  /clone_lib="Mouse Organ of Corti cDNA pBluescript"
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organ of Corti (OC) was fine dissected from a total of 386
OC as follows: 102 samples from post-natal (P) day 5; 72
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
14 from P12 and 24 from P13. After killing animals by
cervical dislocation followed by decapitation, the bulla
was removed and opened in Leibowitz medium. The bony
capsule of the cochlea was chipped away, stria vascularis
and spiral ligament were removed and the sensory
epithelium was carefully dissected out of the modiolus.
Total RNA was extracted using the micro Fasttrack kit
(catalog # K1593-02; Invitrogen, Carlsbad, CA), according
to manufacturer's instructions. Reverse transcription and
library construction were carried out with the Uni-Zap XR
vector kit (catalog # 237211, Stratagene) and Uni-Zap XR
Gigapack III Gold Cloning kit (catalog # 237612), both
from Stratagene (La Jolla, CA, USA), according to
manufacturer's instructions. Briefly: 1.5 ug mRNA was

```

## FEATURES

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source
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  /mol_type="mRNA"
  /strain="BALB/c"
  /db_xref="taxon:10090"
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  /sex="male and female"
  /dev_stage="Post natal day 5 to 13"
  /clone_lib="Mouse Organ of Corti cDNA pBluescript"
  /note="Organ: Organ of Corti; Vector: pBluescript; The
organ of Corti (OC) was fine dissected from a total of 386
OC as follows: 102 samples from post-natal (P) day 5; 72
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
14 from P12 and 24 from P13. After killing animals by
cervical dislocation followed by decapitation, the bulla
was removed and opened in Leibowitz medium. The bony
capsule of the cochlea was chipped away, stria vascularis
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epithelium was carefully dissected out of the modiolus.
Total RNA was extracted using the micro Fasttrack kit
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Gigapack III Gold Cloning kit (catalog # 237612), both
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manufacturer's instructions. Briefly: 1.5 ug mRNA was

```

```

reverse transcribed using a hybrid oligo(dT) linker-primer
that contains an Xho I site. First strand synthesis was
primed with the linker- primer and transcribed using
MoLoney murine leukemia virus reverse transcriptase
(MMLV-RT) and 5-methyl dCTP. The second strand was
synthesized with DNA polymerase and RNase H. Complementary
DNA was blunt ended with Pfu DNA polymerase, ligated with
EcoR I adapters in the presence of ligase and digested
with Xho I. The cDNA was sequentially size fractionated
over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden)
and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA)
columns to enrich for cDNAs greater than 400bp and 1000 bp
, respectively. The cDNA was then directionally ligated to
the Uni-Zap XR vector, which had been predigested with
EcoR I and Xho I. The phagemid was packaged with Gigapak
III Gold and, upon titration on XLI Blue MRF' cells, the
yield of the phage library was estimated to be 11,100,000
recombinants. Stratagene's ExAssist Interference
resistance helper phage (catalogue # 211203) was adopted
to rescue plasmid DNA from the phages. Upon plating of the
rescued library, individual cDNA clones were selected and
grown in 96-well, 2 ml growth plate. Plasmid DNA was
purified from 200 ul of saturated culture with the
Concert96(TM) plasmid purification kit (Invitrogen,
Carlsbad, CA) as instructed by the manufacturer. ESTs from
the 5' end of the cDNA clones were generated with the
universal M13 reverse primer (CAGGAACAGCTATGACC) and 25¢
strength BigDye terminator sequencing chemistry (Applied
Biosystems, Foster City, CA). Sequencing reactions were
performed on MJ Tetrad thermal cyclers (MJ Research,
Waltham, MA), and analyzed on 3700 automated capillary
sequencers using POP5 polymer (Applied Biosystems, Foster
City, CA). The frequency distribution of the library is
as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10;
1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of
genes are present in GenBank and have known function; 23%
have hits in GenBank, but do not have assigned function;
12% are uncharacterized ESTs and 20% are unidentified."

```

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BASE COUNT      145 a      78 c      131 g      120 t
ORIGIN

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## Alignment Scores:

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Pred. No.:      1.92e-69      Length:      474
Score:          597.00      Matches:    110
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Best Local Similarity: 85.94%      Mismatches: 9
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DB:             13      Gaps:      0

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US-10-019-455A-6 (1-128) x BQ565637 (1-474)

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Db      254 TTTTGGGCTGGCAGTGTATGTTATGGTACCACAGATGAGATGGGAATTGTAGGTTATTTTC 313
Qy      101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120

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## KEYWORDS

SOURCE Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 409)

## REFERENCE

AUTHORS Kachar, B.

TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing

## JOURNAL

COMMENT Unpublished

Contact: Kachar, B.

Structural Cell Biology

National Institute of Deafness and other Communication Disorders

50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA

Tel: 301-402-1599

Fax: 301-402-1765

Email: kachar@nidcd.nih.gov

Plate: 73 row: 9 column: 09

Seq primer: M13RP1 reverse primer (ABI).

## FEATURES

source

1..409

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universal M13 reverse primer (CAGGAACAGCTATGACC) and 25x strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 102 a 75 c 121 g 111 t

## ORIGIN

Alignment Scores:

Pred. No.: 3,42e-66 Length: 409  
Score: 572.00 Matches: 108  
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Query Match: 84.62% Indels: 1  
DB: 13 Gaps: 0

US-10-019-455A-6 (1-128) x BQ566932 (1-409)

Qy 1 MetAlaAaGLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20  
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Qy 60 LlysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyG1 80  
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Db 267 GTTTTGGCTGGCAGTGTATTATGTCACCACGAGATGAGATGGGAATTGTAGGTATT 326  
Qy 100 eProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProTh 120  
Db 327 CCCAGCAACTTGTGTGAAGGAGCAGCGTGTATACCAGAGGCCACCAAGGAGATCCCAAC 386  
Qy 120 rThrAspIleAspPhePheCys 127  
Db 387 CACGGCTATTGACTTCTTCGT 408

## RESULT 12

BQ565411

LOCUS

DEFINITION

BQ565411

VERSION

BQ565411.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BQ565411 490 bp mRNA linear EST 19-JUN-2002  
clone gi37b12.1 Mouse Organ of Corti cDNA pBluescript Mus musculus CDNA  
clone gi37b12.5', mRNA sequence.

BQ565411

BQ565411

BQ565411.1

GI:21468728

Mus musculus (house mouse)

Mus musculus

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Kachar, B.

EST analysis of gene expression in the mouse Organ of Corti at the

onset of hearing

Unpublished

Contact: Kachar, B.

Structural Cell Biology

National Institute of Deafness and other Communication Disorders



50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA

Tel: 301-402-1599

Fax: 301-402-1765

Email: kacharb@nidcd.nih.gov

Plate: 37 row: b column: 12

Seq primer: M13P1 reverse primer (ABI).

Location/Qualifiers

# FEATURES

source

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BASE COUNT

191 a

77 c

109 g

112 t

1 others

## ORIGIN

### Alignment Scores:

Pred. No.: 6.18e-62 Length: 490  
Score: 541.00 Matches: 100  
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Best Local Similarity: 80.65% Mismatches: 12  
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US-10-019-455A-6 (1-128) x BQ565411 (1-490)

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Qy 25 ArgLeuAlaSerLysLysLeuCysAlaAspGluCysValTyrThrIleSerLeuAla 44  
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## RESULT 13

BE236443

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

14645 MARC 4BOV Bos taurus cDNA 5', mRNA sequence. 527 bp mRNA linear EST 25-APR-2001

BE236443

BE236443.1 GI:9021161

EST.

Bos taurus (cow)

Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Bovidae; Bovinae; Bos.

1 (bases 1 to 527)

Smith, T.P.L., Grosche, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,

Casas, E., Wray, J.E., White, J., Cho, J., Fahrrenkrug, S.C., Bennett

, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,

Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and

Keefe, J.W.

Sequence evaluation of four pooled-tissue normalized bovine cDNA

libraries and construction of a gene index for cattle

Genome Res. 11 (4), 626-630 (2001)

21180013

11282978

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt\_trimmed with phred

v0.980904.e. Vector identified by cross\_match with the -minscore 18

and -minmatch 12 options.

PCR Primers

FORWARD: AGAACAACAGTATGACCAT  
BACKWARD: GTTTCCTCCAGTCACGACG  
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Location/Qualifiers

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Library made from pooled tissue from day 20 and day 40  
embryos."

BASE COUNT 173 a 94 c 126 g 134 t  
ORIGIN

Alignment Scores: Length: 527  
Pred. No.: 522.00 Matches: 102  
Score: 83.72% Conservative: 6  
Percent Similarity: 79.07% Mismatches: 7  
Best Local Similarity: 77.22% Indels: 14  
Query Match: 10 Gaps: 2  
DB:

US-10-019-455A-6 (1-128) x BE236443 (1-527)

Qy 1 MetAlaArgIleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20  
Db 35 ATGCAAGATTGGTGTACTTTCTCCAGGCTTGTGCCATATGCTGTGTCATGGA 94  
Qy 21 IlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspGluCysValTyrThr 40  
Db 95 ATATTATGACAGACTTGTGTCAAGAAGCTGTGCAGATGATGATGTCTACT 154  
Qy 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60  
Db 155 ATTCTCTGCCAGAGCTCAAGAGATTACAAATGCTCCGAGCTGTAGATTCAATACGTT 214  
Qy 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAenGlyAlaGlyGlu 80  
Db 215 AAAAAAGCAGCTGGATCTATGTTTACTCAAGCTG----- 250  
Qy 81 PheTrpAlaGlySerValTyrGlyAsp--GlyGlnAspGluMetGlyValValGlyTyr 99  
Db 251 -----GCTATGGCAATCAGTCTCGAGTGAATGAATGGAACCGTGGTTAT 295  
Qy 100 PheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValPro 119  
Db 296 TTTCACCAACCTTGGTCCAGGAACAACATGTGTACCAAGAAGCCACCAAGGAAGTTCT 355  
Qy 120 ThrThrAspLeuAspPhePheCysGlu 128  
Db 356 ACCACGGATATTGACTTTTCTTCGGAG 382

RESULT 14

BY232622 365 bp mRNA linear EST 10-DEC-2002  
LOCUS  
DEFINITION BY232622 RIKEN full-length enriched, adult inner ear Mus musculus  
cDNA clone F930026J20 5', mRNA sequence.

ACCESSION  
VERSION BY232622  
KEYWORDS EST.

SOURCE  
ORGANISM Mus musculus (house mouse)

REFERENCE  
AUTHORS  
1 (bases 1 to 365)  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,  
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamakita, I., Kiyosawa, H.,  
Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C.,  
Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A.,

Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S.,  
Beisel, K. W., Blake, J. A., Bratt, D., Brusic, V., Chothia, C., Corbani,  
L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. P., Forrest,  
A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A.,  
Gough, J., Hammond, S., Gustincich, S., Hirokawa, N., Jackson, I. J.,  
Jarvis, E. D., Kanai, A., Kawai, H., Kawasawa, Y., Kedzierski, R. M.,  
King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons,  
P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki,  
H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Petrea, G.,  
Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ring,  
Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring,  
B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou,  
M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale,  
R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y.,  
Watanabe, Y., Wells, C., Wilming, L. G., Wyshaw-Boris, A., Yanagisawa,  
M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A.,  
Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura,  
M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Iwami, K., Ishii,  
A., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii,  
Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata,  
K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander,  
E. S., Rogers, J., Birney, E. and Hayashizaki, Y.  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
22354683  
12466851  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gs.riken.go.jp/  
URL: http://genome.gsc.riken.go.jp/  
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane,  
T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A.,  
Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K.,  
Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami,  
M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct  
Submission  
Computational Analysis of Full-Length Mouse cDNAs Compared with  
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new  
genes. Genome Res. 10 (10), 1617-1630 (2000)  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
10 (11), 1757-1771 (2000)  
Computer-based methods for the mouse full-length cDNA  
encyclopedia: real-time sequence clustering for construction of a  
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Tissues were provided by Kirk W. Beisel ( Boys Town National  
Research Hospital 555 North 30th Street Omaha, NE 68131 USA ) whose  
assistance we gratefully acknowledge. Please visit our web site  
(http://genome.gsc.riken.go.jp) for further details.  
Location/Qualifiers  
1. 365  
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/mol\_type="mRNA"  
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/clone="F930026J20"  
/tissue\_type="inner ear"  
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FEATURES  
source

BASE COUNT 97 a 60 c 110 g 98 t

## ORIGIN

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 Score: 512.00 Matches: 97  
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 Best Local Similarity: 85.09% Mismatches: 9  
 Query Match: 75.74% Indels: 0  
 DB: 13 Gaps: 0

US-10-019-455A-6 (1-128) x BY232622 (1-365)

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 Qy 21 IlePheMetAspArgLeuAlaSerLysLeuCysAlaAspAspGlyCysValTyrThr 40  
 Db 84 GTATTATGATTAACCTTCTTCTTGAAGTGTGTGCGGATGAGAGTGTCTATACT 143  
 Qy 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60  
 Db 144 ATTCTCTGCGCAAGAGCACAGGAAGATTACAATGCCACACTGTAGTTTCATCGATGC 203  
 Qy 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80  
 Db 204 AAGAAAGGGCAGCAGATCTATGTTTACTCCAAGCTGTAAACAGAAACGGAGCTGGAG 263  
 Qy 81 PheTyrAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100  
 Db 264 TTTGGGGCTGGCAGTGTATTATGTGACCCAGGATGAGATGGGAATTGTAGTTATTC 323  
 Qy 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAla 114  
 Db 324 CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACAGAGGCC 365

## RESULT 15

BQ567343 604 bp mRNA linear EST 19-JUN-2002  
 LOCUS gi88d08.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA  
 DEFINITION clone gi88d08 5', mRNA sequence.

## ACCESSION

BQ567343

## VERSION

BQ567343.1 GI:21470660

## KEYWORDS

EST.

## SOURCE

Mus musculus (house mouse)

## ORGANISM

Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing  
 Unpublished  
 Structural Cell Biology  
 National Institute of Deafness and other Communication Disorders  
 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
 Tel: 301-402-1599  
 Fax: 301-402-1765  
 Email: kachar@nidcd.nih.gov  
 Plate: 88 row: d column: 08

## FEATURES

## source

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 /note="Organ: Organ of Corti; Vector: pBluescript; The

BASE COUNT 178 a 108 c 152 g 166 t  
 ORIGIN

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Pred. No.: 1.37e-56 Length: 604  
 Score: 502.00 Matches: 92  
 Percent Similarity: 96.00% Conservative: 4  
 Best Local Similarity: 92.00% Mismatches: 4  
 Query Match: 74.26% Indels: 0  
 DB: 13 Gaps: 0

US-10-019-455A-6 (1-128) x BQ567343 (1-604)

Qy 29 LysLysLeuCysAlaAspAspGluCysValTyrThrIleSerLeuAlaSerAlaGlnGlu 48

Db 1 AAGAAGTGTGTGCGGATGAGAGTGTCTATACTATTTCTCTGGCAGACGACGAA 60

Qy 49 AspTyrAsnAlaProAspCysArgPheIleAsnValLysGlyGlnIleTyrVal 68

organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's Exassist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAACAGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

Tue Dec 30 10:20:55 2003

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|||||
Db 61 GATTACAATGCCCCAGACTGTAGTTTCATCGATGTCAGAAAGCGGACAGATCTATGTT 120
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Db 121 TACTCCAAGCTGTTAACAGAAAACGGAGCTGGAGAGTTTTGGGCTGGCAGTGTTATGGT 180
|||||
QY 89 AspGlyGlnAspGluMetGlyValValGlyTyrPheProArgAsnLeuVallysGluGln 108
|||||
Db 181 GACCACCAGGATGAGATGGGAATTGTAGGTTATTTCCCCAGCAACTTGGTGAAGGAGCAG 240
|||||
QY 109 ArgValTyrGlnGluAlaThrLysGluValProThrThrAspPhePheCysGlu 128
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Db 241 CGTGTATACCAGAGGCCACCAAGGAGATCCACACCGGATATTGACTTCTCTGTGAA 300
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Search completed: December 29, 2003, 22:00:44  
Job time : 1330.28 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 29, 2003, 16:10:49 ; Search time 154.353 Seconds  
(without alignments)  
2238.558 Million cell updates/sec

Title: US-10-019-455a-6

Perfect score: 676

Sequence: 1 MARILLFLPLGLVAVCAVHG.....RVYQATKEVPTTIDIDFCE 128

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Zgapop 6.0 , Zgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O=/cgn2\_1/USPTO spool/US10019455/runat\_29122003.160347\_230/app\_query.fasta\_1.1770  
-DB=N\_Geneseq\_19Jun03 -QFMT=fastp -SUFFIX=ring -MINMATCH=0.1 -LOOPEXT=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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Database : N\_Geneseq\_19Jun03:\*

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	676	100.0	384	22	AAF59065	Human MLP nucleoti
2	676	100.0	387	24	AAH17583	DNA encoding novel
3	676	100.0	426	22	AAH26341	Human growth regul
4	676	100.0	521	24	ABL95740	Human angiogenesis
5	676	100.0	521	24	ABL88251	Human PRO9873 CDNA
6	676	100.0	521	24	ABK33571	cDNA encoding huma
7	676	100.0	891	22	AAH98228	Human EST-derived
8	676	100.0	891	22	AAH26342	Human growth regul
9	676	100.0	923	22	AAF59083	Human MLP nucleoti
10	676	100.0	1201	22	AAH26343	Human growth regul
11	602	89.1	384	22	AAF59068	Mouse MLP nucleoti
12	602	89.1	947	22	AAF59084	Mouse MLP nucleoti
13	600	88.8	384	22	AAF59098	Rat MLP nucleotide
14	590	87.3	330	22	AAF59079	Human MLP nucleoti
15	547	80.9	330	22	AAF59080	Mouse MLP nucleoti
16	541	80.0	330	22	AAF59099	Rat MLP nucleotide
17	472	69.8	307	22	AAF59093	Rat MLP nucleotide
18	413	61.1	261	22	AAF59092	Rat MLP nucleotide
19	257.5	38.1	459	16	AAQ84050	Sequence encoding
20	257.5	38.1	459	22	AAI70083	Melanoma inhibitor
21	257.5	38.1	459	22	AAH18732	Human antisense ol
22	256.5	37.9	442	24	ABL63602	Breast cancer rela
23	256.5	37.9	442	24	ABL64012	Breast cancer rela
24	255.5	37.8	433	22	AAH47783	Recombinant human
25	255.5	37.8	555	23	ABV59229	Human prostate exp
26	253.5	37.5	330	16	AAQ84061	Sequence encoding
27	232.5	34.4	581	16	AAQ84052	Sequence encoding
28	226.5	33.5	417	22	AAH99775	Human protein enco
29	225.5	33.4	884	22	AAH22459	Human cDNA encodin
30	225.5	33.4	1230	24	ABQ79850	Human TANGO 130 pa
31	225.5	33.4	1263	21	AAZ51245	Human TANGO 130 CD
32	225.5	33.4	1363	24	ABQ79849	Human TANGO 130 po
33	225.5	33.4	4409	23	ABV21035	Human prostate exp
34	225.5	33.4	4409	23	ABV23751	Human prostate exp
35	225.5	33.4	4409	23	ABV26878	Human prostate exp
36	225.5	33.4	4409	23	ABV29625	Human prostate exp
37	225.5	33.4	5724	24	ABQ79852	Human TANGO 130 po
38	225.5	33.4	8121	24	ABQ79851	Human TANGO 130 po
39	217	32.1	2037	22	AAH46220	Human DNA encoding
40	217	32.1	2037	25	ACA57978	Human PRO20088 cDN
41	217	32.1	2037	25	ABX98448	Human cDNA encodin
42	217	32.1	2037	25	ABX98950	Novel human secret
43	217	32.1	2037	25	ACA05995	Human secreted/tra
44	217	32.1	2037	25	ABX98039	Human PRO polynucl
45	217	32.1	2037	25	ABX78823	Human PRO polynucl

# ALIGNMENTS

## RESULT 1

AAF59065  
ID AAF59065 standard; DNA; 384 BP.

XX AAF59065;

XX (first entry)

DT 23-APR-2001

DE Human MLP nucleotide sequence SEQ ID NO:4.  
XX MLP; MTA; melanoma inhibitory activity; cancer; bone disease;  
XX joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
KW cardiant; gene therapy; secretory cell function regulator; promoter;  
KW inhibitor; ds.

XX Homo sapiens.

OS

```

PN WO200102564-A1.
XX
PD 11-JAN-2001.
XX
XX 29-JUN-2000; 2000WO-JF04278.
XX
XX 30-JUN-1999; 99JP-0186718.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
PI Tanaka H;
XX
XX WPI; 2001-159271/16.
DR P-PSDB; AAB69123.
XX
XX Safe, low-toxicity secretory cell function-regulatory protein and
PT encoded DNA, applicable as drugs, in diagnosis and development of
PT promoters and inhibitors for preventing or treating e.g. bone and joint
PT diseases -
XX
XX Example 1; Page 91; 111pp; Japanese.
XX
XX The present invention describes novel MLP proteins and their encoding
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiac
CC activities, and can be used in gene therapy and as secretory cell
CC function regulators. The MLP proteins and DNAs can be used in drugs, in
CC the diagnosis and development of promoters and inhibitors for preventing
CC or treating bone and joint diseases as well as pathologic angiogenesis.
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
CC in the exemplification of the present invention.
XX
XX Sequence 384 BP; 99 A; 70 C; 106 G; 109 T; 0 other;
SQ

```

---

```

AAS17583
ID AAS17583 standard; cDNA; 387 BP.
XX
AC AAS17583;
XX
DT 26-FEB-2002 (first entry)
XX
DE DNA encoding novel secreted protein #12.
XX
XX Secreted protein; cytostatic; immunosuppressive; vulnery; vaccine;
XX antiinflammatory; neuroprotective; nephrotropic; cardiovascular;
XX human; cancer; autoimmune disease; wound healing disorder; infection;
XX haematopoietic disorder; inflammatory disorder; infertility;
XX neurological disease; psychiatric disease; cardiovascular disease;
XX respiratory disease; renal; gastrointestinal; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH 1..387
FT CDS
FT /*tag= a
FT /*product= "Human secreted protein"
XX
XX WO200179454-A1.
XX
XX 25-OCT-2001.
XX
XX 11-APR-2001; 2001WO-US11797.
XX
XX 13-APR-2000; 2000US-196603P.
XX 24-APR-2000; 2000US-199417P.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;
XX
XX WPI; 2002-061975/08.
DR P-PSDB; AAU09871.
XX
XX New secreted proteins or polypeptides, useful for treating e.g. cancer,
XX autoimmune diseases, wound healing disorder, infections, haematopoietic
XX disorders, inflammatory disorders, infertility, cancer -
XX
XX Claim 2; Page 44; 92pp; English.
XX
XX The invention relates to an isolated novel secreted polypeptide (I) and
XX polynucleotide (II). (I) and (II) are useful for treating cancer,
XX autoimmune diseases, wound healing disorder, infections, haematopoietic
XX disorders, inflammatory disorders, infertility, neurological and
XX psychiatric diseases, cardiovascular diseases, respiratory diseases,
XX renal diseases, or gastrointestinal diseases. These may also be used to
XX treat diseases, abnormalities and disorders caused by abnormal
XX expression, production, function and/or metabolism of the genes, as
XX vaccines for inducing immunological response in a mammal, and in
XX screening methods for detecting the effect of added compounds on the
XX production of mRNA and polypeptide in cells. The polypeptides can be used
XX as immunogens to produce antibodies immunospecific for the polypeptides,
XX and to identify membrane-bound or soluble receptors. The polynucleotides
XX may be used as diagnostic reagents, in chromosome localisation studies,
XX and in tissue expression studies. The present sequence represents the
XX coding sequence of novel human secreted protein #12.
XX
XX Sequence 387 BP; 101 A; 70 C; 106 G; 110 T; 0 other;
SQ

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Alignment Scores:
Pred. No.: 7.79e-87 Length: 384
Score: 676.00 Matches: 128
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-10-019-455A-6 (1-128) x AAF59065 (1-384)

Qy 1 MetAlaArgIleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20
Db 1 ATGGCAGAAATATTGTTACTTTCTCCCGGCTCTGTGGCTGTATGCTGTGCATGGA 60

Qy 21 IlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysValTyThr 40
Db ATATTATTGGACCGCTAGCTTCCAGAGAGCTCTGTGCAGATGATGATGCTGTATACT 120

Qy 41 IleSerLeuAlaSerAlaGlnGluAspTyrrAsnAlaProAspCysArgPheIleAsnVal 60
Db ATTTCTCTGGCTAGTGTCTCAAGAGATTATATATGCCCGGACTGTAGATTCAATACGTT 180

Qy 61 LysLysGlyGlnGlnIleTyrrValTyrrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80
Db AAAAAGGCGCAGCATCTATGTGTACTCAAGCTGGTAAAGAAAAATGGAGCTGGAGAA 240

Qy 81 PheTTPAlaGlySerValTyrrGlyAspGlyGlnAspGluMetGlyValValGlyTyrrPhe 100
Db TTTTGGCTGGCAGTGTATTGTTATGGTATGGCCAGGACGAGATGGAGTGTGGGTATTTC 300

Qy 101 ProArgAsnLeuValLysGluGlnArgValTyrrGlnGluAlaThrLysGluValProThr 120
Db CCCAGAACTTGTTCAGGAACAGCGTGTGTACCAGGAAGCTTACCAGGAAGTCCACC 360

Qy 121 ThrAspIleAspPheCysGlu 128
Db ACGGATATTGACTTCTTTCGCGAG 384

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US-10-019-455A-6 (1-128) x AAS17593 (1-387)

```

QY 1 MetAlaArgIleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20
DB 1 ATGGCAAGAATAATTGTTACTTTTCTCCCGGGTCTTGTGGCTGTATGTGCTGTCATGGA 60
QY 21 IlePheMetAspArgLeuAlaSerLysLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40
DB 61 ATATTATATGAGCGCTAGCTTCCCAAGAAGCTCTGTGCAGATGATGAGTGTGTCTATACT 120
QY 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
DB 121 ATTTCCTGGCTAGTGTCTCAAGAAGATTATAATGCCCGGACTGTAGATTCATTACGTT 180
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80
DB 181 AAAAAAGGGCAGCAGATCTATGTGTACTCAAGCTGTAAAGAAATAATGGAGCTGGAGAA 240
QY 81 PheTyrAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100
DB 241 TTTTGGGCTGGCAGTGTATTATGTGTATGGCCAGGACGAGATGGAGTGGGTGTTATTC 300
QY 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120
DB 301 CCAGGAACTTGTCTCAAGGACAGCGTGTGTACCAAGAGCTACCAAGGAAGTCCACC 360
QY 121 ThrAspIleAspPhePheCysGlu 128
DB 361 ACGGATATTGACTTCTTCTGCGAG 384

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# RESULT 3

AAH26341  
ID AAH26341 standard; cDNA; 426 BP.

AC AAH26341;

DT 02-OCT-2001 (first entry)

DE Human growth regulatory-like polypeptide clone 16372272.

KW Growth regulatory-like polypeptide; human; cartilage; melanoma;  
KW neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;  
KW ss.

OS Homo sapiens.

PN WO200155332-A2.

XX 02-AUG-2001.

XX 25-JAN-2001; 2001WO-US02455.

XX 25-JAN-2000; 2000US-0491404.

XX 02-MAY-2000; 2000US-0563786.

PA (HYSE-) HYSEQ INC.

PI Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;  
PI Drmanac RT;

XX WPI; 2001-483233/52.

XX Isolated human growth regulatory-like polypeptide useful for treating  
PT e.g. Alzheimer's disease, cancer, autoimmune disorders,  
PT hyperproliferative disorders, coagulation disorders, and nervous system  
PT disorders -

XX Example 1; Page 114; 119pp; English.

XX The present sequence is that of Hyseq clone identification number  
CC 16372272, which was obtained from a human thymus cDNA library  
CC using standard PCR with primers specific for vector sequences  
CC flanking the inserts, sequencing by hybridisation sequence

CC signature analysis, and Sanger sequencing techniques. This  
CC expressed sequence tag was used in the assembly of a full-length  
CC cDNA sequence (see AAH26343) encoding a novel human growth  
CC regulatory-like polypeptide (GRLP, see AAB82671). The GRLP  
CC belongs to the same protein family as growth regulatory proteins,  
CC growth factors, human melanoma derived growth regulatory protein  
CC precursor (64% similarity and 45% identity over 111 amino acids)  
CC or melanoma inhibitory activity, cattle cartilage-derived and 64%  
CC retinoic acid sensitive protein (CD-RAP, 44% identity and 64%  
CC similarity over 126 amino acids) and other retinoic acid-sensitive  
CC proteins. GRLP polypeptides and polynucleotides of the invention  
CC can be used in the prophylaxis and treatment (including gene therapy)  
CC and diagnosis of disorders and diseases caused by, or involving,  
CC cartilage development and maintenance, inhibition of melanoma cell  
CC growth and tumours, including neuroectodermal tumours such as  
CC gliomas. The polynucleotides can also be used to design probes  
CC and primers, for chromosome and gene mapping, in the recombinant  
CC production of protein, in the generation of antisense, ribozyme and  
CC peptide-nucleic acid molecules, and to produce transgenic animals.  
XX  
SQ Sequence 426 BP; 119 A; 73 C; 113 G; 120 T; 1 other;

Alignment Scores:  
Pred. No.: 9,05e-87 Length: 426  
Score: 676.00 Matches: 128  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 22 Gaps: 0

US-10-019-455A-6 (1-128) x AAH26341 (1-426)

QY 1 MetAlaArgIleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20

DB 19 ATGGCAAGAATAATTGTTACTTTTCTCCCGGGTCTTGTGGCTGTATGTGCTGTCATGGA 78

QY 21 IlePheMetAspArgLeuAlaSerLysLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40

DB 79 ATATTATATGAGCGCTAGCTTCCCAAGAAGCTCTGTGCAGATGATGAGTGTGTCTATCT 138

QY 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60

DB 139 ATTTCCTGGCTAGTGTCTCAAGAAGATTATAATGCCCGGACTGTAGATTCATTACGTT 198

QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80

DB 199 AAAAAAGGGCAGCAGATCTATGTGTACTCAAGCTGTAAAGAAATAATGGAGCTGGAGAA 258

QY 81 PheTyrAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100

DB 259 TTTTGGGCTGGCAGTGTATTATGTGTATGGCCAGGACGAGATGGAGTGGGTGTTATTC 318

QY 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120

DB 319 CCAGGAAGCTTGTCTCAAGGACAGCGTGTGTACCAAGAGCTACCAAGGAAGTCCACC 378

QY 121 ThrAspIleAspPhePheCysGlu 128

DB 379 ACGGATATTGACTTCTTCTGCGAG 402

## RESULT 4

ABL95740

ID ABL95740 standard; cDNA; 521 BP.

XX ABL95740;

XX 19-JUL-2002 (first entry)

XX Human angiogenesis related cDNA PRO9873 SEQ ID NO: 359.

XX Human angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
KW cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;



KW antiarteriosclerotic; gene; ss.  
 XX Homo sapiens.  
 XX WO200208284-A2.  
 XX 31-JAN-2002.  
 XX 09-JUL-2001; 2001WO-US21735.  
 XX 20-JUL-2000; 2000US-219558P.  
 XX 25-JUL-2000; 2000US-220624P.  
 XX 25-JUL-2000; 2000US-220664P.  
 XX 28-JUL-2000; 2000WO-US20710.  
 XX 02-AUG-2000; 2000US-222695P.  
 XX 17-AUG-2000; 2000US-0643657.  
 XX 23-AUG-2000; 2000WO-US23522.  
 XX 24-AUG-2000; 2000WO-US23328.  
 XX 07-SEP-2000; 2000US-230978P.  
 XX 15-SEP-2000; 2000US-000000P.  
 XX 18-SEP-2000; 2000US-0664610.  
 XX 18-SEP-2000; 2000US-0665350.  
 XX 24-OCT-2000; 2000US-242922P.  
 XX 08-NOV-2000; 2000US-0709238.  
 XX 08-NOV-2000; 2000WO-US30952.  
 XX 10-NOV-2000; 2000WO-US30873.  
 XX 01-DEC-2000; 2000WO-US32678.  
 XX 20-DEC-2000; 2000US-0747259.  
 XX 20-DEC-2000; 2000WO-US34956.  
 XX 22-JAN-2001; 2001US-0767609.  
 XX 28-FEB-2001; 2001US-0796498.  
 XX 28-FEB-2001; 2001WO-US06520.  
 XX 01-MAR-2001; 2001WO-US06666.  
 XX 09-MAR-2001; 2001US-0802706.  
 XX 14-MAR-2001; 2001US-0808689.  
 XX 22-MAR-2001; 2001US-0816744.  
 XX 05-APR-2001; 2001US-0828366.  
 XX 10-MAY-2001; 2001US-0854208.  
 XX 10-MAY-2001; 2001US-0854280.  
 XX 25-MAY-2001; 2001US-0866028.  
 XX 25-MAY-2001; 2001US-0866034.  
 XX 25-MAY-2001; 2001WO-US17092.  
 XX 30-MAY-2001; 2001US-0870574.  
 XX 30-MAY-2001; 2001WO-US17443.  
 XX 01-JUN-2001; 2001WO-US17800.  
 XX 20-JUN-2001; 2001WO-US19692.  
 XX 28-JUN-2001; 2001WO-US00000.  
 XX (GETH ) GENENTECH INC.  
 XX (BAKE/) BAKER K P.  
 XX (FERR/) FERRARA N.  
 XX (GERB/) GERBER H.  
 XX (GERR/) GERRITSEN M E.  
 XX (GODD/) GODDARD A.  
 XX (GODO/) GODOWSKI P J.  
 XX (GURN/) GURNEY A L.  
 XX (HILL/) HILLAN K J.  
 XX (MARS/) MARSTERS S A.  
 XX (PANJ/) PAN J.  
 XX (PAON/) PAONI N F.  
 XX (STEP/) STEPHAN J F.  
 XX (WATA/) WATANABE C K.  
 XX (WILL/) WILLIAMS P M.  
 XX (WOOD/) WOOD W I.  
 XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;  
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
 XX WPI; 2002-171999/22.  
 DR P-PSDB; ABB95602.  
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
 PT

PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 XX infarction), endothelial or angiogenic disorders in a mammal -  
 XX Claim 1; Fig 359; 567pp; English.  
 XX The present invention provides the protein and coding sequences of human  
 CC PRO proteins. These are useful for treating or diagnosing a  
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac  
 CC hypertrophy, trauma, cancer, age-related macular degeneration,  
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
 CC angina, myocardial infarctions, thrombophlebitis, lymphomatoid tumour  
 CC angiogenesis (such as breast carcinoma and liver carcinoma), tumour  
 CC healing. The present sequence is a coding sequence of the invention.  
 XX SQ Sequence 521 BP; 167 A; 86 C; 131 G; 137 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 1-21e-86 Length: 521  
 Score: 676.00 Matches: 128  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 24 Indels: 0  
 DB: Gaps: 0  
 US-10-019-455A-6 (1-128) x ABL95740 (1-521)  
 Qy 1 MetAlaArgIleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20  
 Db 38 ATGGCAAGAAATATTGTACTTTCTCCCGGCTTGTGGCTGTATGTGCTGTCATGGA 97  
 Qy 21 IlePheMetAspArgIleuAlaSerLysValLysLeuCysAlaAspAspGluCysValThr 40  
 Db 98 ATATTATGGACCCCTAGCTTCCAGAGATTTATTAATGCCCGGACTCTAGATTCAATTAACGTT 157  
 Qy 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60  
 Db 158 ATTTCTCTGGCTAGTCTCAAGAGATTATTAATGCCCGGACTCTAGATTCAATTAACGTT 217  
 Qy 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyValGlyGlu 80  
 Db 218 AAAAAGGCGCAGCATCTATGTACTCAAGCTGGTAAAGAAATGGAGCTGGAGAA 277  
 Qy 81 PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100  
 Db 278 TTTTGGGCTGGCAGTGTATTATGGTATGCCAGACGAGATGGAGTCTGGGTATTATTC 337  
 Qy 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120  
 Db 338 CCCAGGAACCTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTTCACCACC 397  
 Qy 121 ThrAspIleAspPhePheCysGlu 128  
 Db 398 ACGGATATTGACTTCTTCTGCGAG 421  
 RESULT 5  
 ABL88251  
 ID ABL88251 standard; cDNA; 521 BP.  
 XX ABL88251;  
 AC ABL88251;  
 XX 16-MAY-2002 (first entry)  
 DT Human PRO9873 cDNA sequence SEQ ID NO:359.  
 XX Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;  
 KW vulnery; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
 KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
 KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
 KW age-related macular degeneration; arterial restenosis; angina;  
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
 KW wound healing; chromosome mapping; gene mapping; gene; ss.

OS Homo sapiens.  
PN WO200200690-A2.  
XX 03-JAN-2002.  
XX 20-JUN-2001; 2001WO-US19692.  
XX 23-JUN-2000; 2000US-213637P.  
PR 20-JUL-2000; 2000US-219556P.  
PR 25-JUL-2000; 2000US-220624P.  
PR 25-JUL-2000; 2000US-220664P.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 02-AUG-2000; 2000US-222695P.  
PR 17-AUG-2000; 2000US-0643657.  
PR 23-AUG-2000; 2000WO-US23322.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 07-SEP-2000; 2000US-230978P.  
PR 18-SEP-2000; 2000US-0664610.  
PR 18-SEP-2000; 2000US-0665350.  
PR 24-OCT-2000; 2000US-242922P.  
PR 08-NOV-2000; 2000US-0709238.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000US-0747259.  
PR 20-DEC-2000; 2000WO-US34956.  
PR 22-JAN-2001; 2001US-0767609.  
PR 22-FEB-2001; 2001US-0796498.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-MAR-2001; 2001WO-US06666.  
PR 09-MAR-2001; 2001US-0802706.  
PR 14-MAR-2001; 2001US-0808689.  
PR 22-MAR-2001; 2001US-0816744.  
PR 05-APR-2001; 2001US-0828366.  
PR 10-MAY-2001; 2001US-0854208.  
PR 10-MAY-2001; 2001US-0854280.  
PR 25-MAY-2001; 2001US-0866028.  
PR 25-MAY-2001; 2001US-0866034.  
PR 25-MAY-2001; 2001WO-US17092.  
PR 30-MAY-2001; 2001US-0870574.  
PR 30-MAY-2001; 2001WO-US17443.  
PR 01-JUN-2001; 2001WO-US17800.  
XX (GETH ) GENENTECH INC.  
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;  
PI Godowski PJ, Gurney AL, Hillan KU, Marsters SA, Pan J, Paoni NF;  
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
XX WPI; 2002-090516/12.  
DR P-PSDB; ABB84996.  
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
PT infarction), endothelial or angiogenic disorders in a mammal -  
XX Claim 2; Fig 359; 565pp; English.  
PS  
XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to  
CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,  
CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic  
CC activities, and can be used in gene therapy. The PRO polynucleotides,  
CC proteins, agonists and antagonists are useful for treating or diagnosing  
CC a cardiovascular, endothelial or angiogenic disorder in a mammal,  
CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular  
CC degeneration, atherosclerosis, hypertension, arterial restenosis,  
CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,  
CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver  
CC carcinoma) and wound healing. The PRO polynucleotides have applications  
CC in molecular biology, including use as hybridisation probes, and in  
CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and  
CC probes used in the exemplification of the present invention.

XX SQ Sequence 521 BP; 167 A; 86 C; 131 G; 137 T; 0 other;  
XX Alignment Scores:  
XX Pred. No.: 1,21e-86 Length: 521  
XX Score: 676.00 Matches: 128  
XX Percent Similarity: 100.00% Conservative: 0  
XX Best Local Similarity: 100.00% Mismatches: 0  
XX Query Match: 100.00% Indels: 0  
XX DB: 24 Gaps: 0  
XX US-10-019-455A-6 (1-128) x ABL88251 (1-521)  
QY 1 MetAlaArgIleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20  
DB 38 ATGGCAAGAAATATTGTACTTTCTCCGGGCTTTGTGGCTGTATGTCTGTGCATGGA 97  
QY 21 IlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspGluCysValTyrThr 40  
DB 98 ATATTTATGGACCGTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGTGTCTATACT 157  
QY 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60  
DB 158 ATTTCTCTGGCTAGTGCTCAAGAAGATTATAATGCCCGGACTGTAGATTCATTACGTT 217  
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80  
DB 218 AAAAAAGGCGCAGCATCTATGTACTCAAGAGCTGTATAAAGAAATGGAGCTGGAGAA 277  
QY 81 PheTyrAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100  
DB 278 TTTTGGCTGGCAGTGTTTATGTGTATGCCAGCAGATGGAGTCGTGGTATTATTC 337  
QY 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120  
DB 338 CCCAGGAACCTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTTCCACC 397  
QY 121 ThrAspIleAspPheCysGlu 128  
DB 398 ACGGATATTGACTTCTCTCGAG 421  
XX RESULT 6  
XX ABLK33571  
ID ABLK33571 standard; cDNA; 521 BP.  
XX AC ABLK33571;  
XX DT 08-MAY-2002 (first entry)  
XX DE cDNA encoding human PRO protein, Seq ID No 71.  
XX KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;  
KW breast cancer; prostate tumour; rectal tumour; liver tumour;  
KW pericyte cell proliferation; chondrocyte cell proliferation;  
KW tumour necrosis factor-alpha; gene; ss.  
XX OS Homo sapiens.  
XX PN WO200208288-A2.  
XX 31-JAN-2002.  
XX 29-JUN-2001; 2001WO-US21066.  
XX 20-JUL-2000; 2000US-219556P.  
PR 25-JUL-2000; 2000US-220585P.  
PR 25-JUL-2000; 2000US-220605P.  
PR 25-JUL-2000; 2000US-220607P.  
PR 25-JUL-2000; 2000US-220624P.  
PR 25-JUL-2000; 2000US-220638P.  
PR 25-JUL-2000; 2000US-220664P.  
PR 25-JUL-2000; 2000US-220666P.  
PR 26-JUL-2000; 2000US-220893P.

PR	28-JUL-2000; 2000WO-US20710.	QY	81	PheTTPAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe	100
PR	23-AUG-2000; 2000WO-US23522.	DB	278	TTTTGGGCTGGCAGTGTATTAATGTTGGTGGCAGACAGAGTGGTGGTATTTTC	337
PR	24-AUG-2000; 2000WO-US23328.				
PR	15-SEP-2000; 2000US-000000P.				
PR	10-NOV-2000; 2000WO-US30873.	QY	101	ProArgAsnLeuVallysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr	120
PR	28-NOV-2000; 2000US-233646P.	DB	338	CCAGGAACTTGGTCAAGGAACAGCGTGTGTACCGAGAGCTACCAAGGAAGTCCACACC	397
PR	01-DEC-2000; 2000WO-US32678.				
PR	20-DEC-2000; 2000US-0747259.	QY	121	ThrAspIleAspPhePheCysGlu	128
PR	28-DEC-2000; 2000WO-US34956.	DB	398	ACGGATATTGACTTCTTCTCGGAG	421
PR	20-FEB-2001; 2001WO-US06520.				
PR	10-MAY-2001; 2001US-0854280.				
PR	23-MAY-2001; 2001WO-US17092.				
XX	(GETH ) GENENTECH INC.	RESULT 7			
PA	Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski FU;	AAH98228			
XX	Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;	ID	AAH98228	standard; cDNA; 891 BP.	
PI		XX	AC	AAH98228;	
XX		XX	AC		
DR	WPI; 2002-172001/22.	DT	12-OCT-2001	(first entry)	
DR	P-PSDB; AAU83627.	XX			
XX		DE			
XX		DE			
PT	One hundred and twenty two nucleic acids encoding PRO polypeptides,	XX			
PT	useful for treating a PRO related disorder and for diagnosing tumours	KW			
PT	such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal	KW			
PT	tumour or liver tumour -	KW			
XX		XX			
PS	Claim 2; Figure 71; 359pp; English.	OS			
XX		XX			
CC	The invention relates to one hundred and twenty two nucleic acids	XX			
CC	encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides	XX			
CC	encode human secreted proteins. The PRO nucleic acids, polypeptides,	PN	WO200154477-A2.		
CC	agonists and antagonists are useful for treating a PRO related disorder.	PD	02-AUG-2001.		
CC	The PRO polypeptides are useful for diagnosing tumours, especially lung	XX			
CC	cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or	XX			
CC	liver tumour. The PRO polypeptides are useful for stimulating the	XX			
CC	proliferation of, or gene expression, in pericyte cells, for stimulating	XX			
CC	the proliferation or differentiation of chondrocyte cells, for	XX			
CC	stimulating the release of tumour necrosis factor-alpha from human blood,	XX			
CC	for stimulating or inhibiting the proliferation of normal human dermal	XX			
CC	fibroblast cells. The PRO polypeptide may also be used as molecular	XX			
CC	weight markers and for tissue typing. The PRO nucleic acids have	XX			
CC	applications in molecular biology, including use as hybridisation probes,	XX			
CC	and in chromosome and gene mapping. ABK33536-ABK33657 represent human	XX			
CC	PRO protein coding sequences of the invention.	XX			
XX		XX			
SQ	Sequence 521 BP; 167 A; 86 C; 131 G; 137 T; 0 other;	XX			
		XX			
Alignment Scores:		XX			
Pred. No.:	1.21e-86	XX			
Score:	676.00	XX			
Percent Similarity:	100.00%	XX			
Best Local Similarity:	100.00%	XX			
Query Match:	100.00%	XX			
DB:	24	XX			
		XX			
US-10-019-455A-6 (1-128) x ABK33571 (1-521)		XX			
QY	1 MetAlaArgIleLeuLeuLeuPheIeuProGlyLeuValAlaValCysAlaValHisGly	XX			
DB	38 ATGCCAAGAAATATTGTACTTTTCTCCCGGGTCTTGTGGCTGTATGCTGTCATGGA	XX			
		XX			
QY	21 IlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysValTyrThr	XX			
DB	98 ATATTATGGACCGCTAGCTTCCAGAGAGCTCTGTGCAGATGATGATGTTCTACT	XX			
		XX			
QY	41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal	XX			
DB	158 ATTTCTCTGGCTAGTGTCTCAAGAGATATTAATGCCCGGACTGTAGATTCAATACGTT	XX			
		XX			
QY	61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu	XX			
DB	218 AAAAAAGGGCAGCAGATCTATGTGTACTCAAAAGCTGGTAAAGAAATGGAGCTGGAGAA	XX			
		XX			

Alignment Scores:  
 Pred. No.: 2.64e-86 Length: 891  
 Score: 676.00 Matches: 128  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 22 Gaps: 0  
 US-10-019-455A-6 (1-128) x AAH98228 (1-891)

```
QY 1 MetAlaArgIleLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20
DB 19 ATGGCAAGAATATTGTTACTTTCTCCCGGCTCTTGCGCTGTATGCTGTGCATGGA 78
QY 21 IlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspGluCysValTyrThr 40
DB 79 ATATTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTATACT 138
QY 41 IleSerLeuAlaSerAlaGlnGlnArgTyrAsnAlaProAspCysArgPheIleAsnVal 60
DB 139 ATTTCTCTGGCTAGTGTCTCAAGAGATTATAATGCCCGGACTGTAGATTCAATTAACGTT 198
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80
DB 199 AAAAAAGGCACAGCATCTATGTACTCAAGAGCTGTAAAGAAATGGAGCTGGAGAA 258
QY 81 PheTyrAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100
DB 259 TTTTGGGCTGGCAGTGTATTATGGTATGCCAGGACGAGATGGAGTGTGGTATTATTC 318
QY 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120
DB 319 CCCAGAACTTGGTCAAGAACAGCGGTGTATCCAGGAAGCTTACCAGGAAGTTCCACC 378
QY 121 ThrAspIleAspPhePheCysGlu 128
DB 379 ACGGATATTGACTTCTTCTGGCAG 402

RESULT 8
AAH26342
ID AAH26342 standard; cDNA; 891 BP.
XX
AC AAH26342;
XX
DT 02-OCT-2001 (first entry)
XX
DE Human growth regulatory-like polypeptide partial cDNA clone.
KW Growth regulatory-like polypeptide; human; cartilage; melanoma;
KW neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;
KW ss.
XX
OS Homo sapiens.
XX
FN WO200155332-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US02455.
XX
PR 25-JAN-2000; 2000US-0491404.
XX
PR 02-MAY-2000; 2000US-0563786.
XX
PA (HYSE-) HYSEQ INC.
PI Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;
PI Drmanac RT;
PI
XX WPI; 2001-483233/52.
XX
PT Isolated human growth regulatory-like polypeptide useful for treating
PT e.g. Alzheimer's disease, cancer, autoimmune disorders,
PT hyperproliferative disorders, coagulation disorders, and nervous system
PT disorders -
XX
PS Claim 1; Page 115; 119pp; English.
XX
CC The present sequence is that of a novel nucleic acid that was
CC assembled from human thymus cDNA library-derived Hyseq clone
CC identification number 16372272 (see AAH26341). A recursive
CC algorithm was used to extend the clone by pulling additional
CC sequences from different databases. A full-length sequence (see
```

```
CC AAH26343) encoding novel human growth regulatory-like polypeptide
CC (GRP, see AAH26371) was subsequently obtained. Human GRP
CC belongs to the same protein family as growth regulatory proteins,
CC growth factors, human melanoma derived growth regulatory protein
CC precursor (64% similarity and 45% identity over 111 amino acids)
CC or melanoma inhibitory activity, cattle cartilage-derived
CC retinoic acid sensitive protein (CD-RAP, 44% identity and 64%
CC similarity over 126 amino acids) and other retinoic acid-sensitive
CC proteins. GRP polypeptides and polynucleotides of the invention
CC can be used in the prophylaxis, treatment (including gene therapy)
CC and diagnosis of disorders and diseases caused by, or involving,
CC cartilage development and maintenance, inhibition of melanoma cell
CC growth and tumours, including neuroectodermal tumours such as
CC gliomas. The polynucleotides can also be used to design probes
CC and primers, for chromosome and gene mapping, in the recombinant
CC production of protein, in the generation of antisense, ribozyme and
CC peptide-nucleic acid molecules, and to produce transgenic animals.
XX
SQ Sequence 891 BP; 272 A; 146 C; 214 G; 259 T; 0 other;
XX

Alignment Scores:
Pred. No.: 2,648-86 Length: 891
Score: 676.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-10-019-455A-6 (1-128) x AAH26342 (1-891)

QY 1 MetAlaArgIleLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20
DB 19 ATGGCAAGAATATTGTTACTTTCTCCCGGCTCTTGCGCTGTATGCTGTGCATGGA 78
QY 21 IlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspGluCysValTyrThr 40
DB 79 ATATTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTATACT 138
QY 41 IleSerLeuAlaSerAlaGlnGlnArgTyrAsnAlaProAspCysArgPheIleAsnVal 60
DB 139 ATTTCTCTGGCTAGTGTCTCAAGAGATTATAATGCCCGGACTGTAGATTCAATTAACGTT 198
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80
DB 199 AAAAAAGGCACAGCATCTATGTACTCAAGAGCTGTAAAGAAATGGAGCTGGAGAA 258
QY 81 PheTyrAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100
DB 259 TTTTGGGCTGGCAGTGTATTATGGTATGCCAGGACGAGATGGAGTGTGGTATTATTC 318
QY 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120
DB 319 CCCAGAACTTGGTCAAGAACAGCGGTGTATCCAGGAAGCTTACCAGGAAGTTCCACC 378
QY 121 ThrAspIleAspPhePheCysGlu 128
DB 379 ACGGATATTGACTTCTTCTGGCAG 402

RESULT 9
AAF59083
ID AAF59083 standard; DNA; 923 BP.
XX
AC AAF59083;
XX
DT 23-APR-2001 (first entry)
XX
DE Human MLP nucleotide sequence SEQ ID NO:29.
XX
KW MLP; MTA; melanoma inhibitory activity; cancer; bone disease;
KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
KW cardiant; gene therapy; secretory cell function regulator; promoter;
KW inhibitor; ds.
XX
```

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OS Homo sapiens.
XX WO200102564-A1.
XX PD 11-JAN-2001.
XX 29-JUN-2000; 2000WO-JP04278.
XX 30-JUN-1999; 99JP-0186718.
XX (TAKEDA ) TAKEDA CHEM IND LTD.
XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
XX Tanaka H;
XX WPI; 2001-159271/16.
XX Safe, low-toxicity secretory cell function-regulatory protein and
XX encoded DNA, applicable as drugs, in diagnosis and development of
XX promoters and inhibitors for preventing e.g. bone and joint
XX diseases -
XX Example 1; Page 99-100; 111pp; Japanese.
XX The present invention describes novel MLP proteins and their encoding
XX DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
XX activities, and can be used in gene therapy and as secretory cell
XX function regulators. The MLP proteins and DNAs can be used in drugs, in
XX the diagnosis and development of promoters and inhibitors for preventing
XX or treating bone and joint diseases as well as pathologic angiogenesis.
XX AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
XX in the exemplification of the present invention.
XX
XX Sequence 923 BP; 303 A; 147 C; 213 G; 260 T; 0 other;
XX
Alignment Scores:
Pred. No.: 2,77e-86 Length: 923
Score: 676.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0
US-10-019-455A-6 (1-128) x AAF59083 (1-923)
QY 1 MetAlaArgIleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20
DB 34 ATGGCAAGAAATATTGTACTTTTCTCCCGGCTTGTGGCTGTATGTGTCATGGA 93
QY 21 IlePheMetAspArgLeuAlaSerLysLeuCysAlaAspGluCysValTyrThr 40
DB 94 ATATTATGACCGCTAGCTTCCAGAAAGATTATAATGCCCGAGCTAGATTCATTACGTT 153
QY 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
DB 154 ATTTCTGTGCTAGTGTCTCAAGAGATTATAATGCCCGAGCTAGATTCATTACGTT 213
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80
DB 214 AAAAAAGGGCAGCAGATCTATGTGTACTCAAGCTGGTAAAGAAAATGGAGCTGGAGAA 273
QY 81 PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100
DB 274 TTTTGGCTGGAGTGTTATGGTGAATGGCAGCAGATGGAGTCGGTGGGTATTTC 333
QY 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120
DB 334 CCCAGGAACCTGGTCAAGAACACAGCGGTGTACACGGAAGCTACCAAGGAAGTCCACC 393
QY 121 ThrAspIleAspPheCysGlu 128
DB 394 ACGGATATTGACTTCTTCTCGGAG 417

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RESULT 10
AAH26343
ID AAH26343 standard; cDNA; 1201 BP.
XX AC AAH26343;
XX 02-OCT-2001 (first entry)
XX Human growth regulatory-like polypeptide cDNA.
XX Growth regulatory-like polypeptide; human; cartilage; melanoma;
XX neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;
XX ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX CDS 33..419
XX FT /tag= a
XX FT sig_peptide 33..101
XX FT /tag= b
XX FT mat_peptide 102..416
XX FT /tag= c
XX WO200155332-A2.
XX 02-AUG-2001.
XX 25-JAN-2001; 2001WO-US02455.
XX 25-JAN-2000; 2000US-0491404.
XX 02-MAY-2000; 2000US-0563786.
XX (HYSE-) HYSEQ INC.
XX Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;
XX Drmanac RT;
XX WPI; 2001-483233/52.
XX P-PSDB; AAB82671.
XX Isolated human growth regulatory-like polypeptide useful for treating
XX e.g. Alzheimer's disease, cancer, autoimmune disorders,
XX hyperproliferative disorders, coagulation disorders, and nervous system
XX disorders -
XX Claim 1; Page 115-116; 119pp; English.
XX The present sequence is that of a novel nucleic acid encoding
XX human growth regulatory-like polypeptide (GRLP, see AAB82671).
XX The sequence was assembled using human thymus cDNA library-derived
XX Hyseq clone identification number 16372272 (see AAH26341) as seed,
XX using software programs to pull additional sequences from Hyseq's
XX proprietary database containing expressed sequence tag sequences,
XX and by gel sequencing using primers to extend both 5' and 3' ends.
XX The predicted protein has a mol.wt. of 14 kDa unglycosylated. GRLP
XX belongs to the same protein family as growth regulatory proteins,
XX growth factors, human melanoma derived growth regulatory protein
XX precursor (64% similarity and 45% identity over 111 amino acids)
XX or melanoma inhibitory activity, cattle cartilage-derived
XX retinoic acid sensitive protein (CD-RAP, 44% identity and 64%
XX similarity over 126 amino acids) and other retinoic acid-sensitive
XX proteins. GRLP polypeptides and polynucleotides of the invention
XX can be used in the prophylaxis, treatment (including gene therapy)
XX and diagnosis of disorders and diseases caused by, or involving,
XX cartilage development and maintenance, inhibition of melanoma cell
XX growth and tumours, including neuroectodermal tumours such as
XX gliomas. The polynucleotides can also be used to design probes
XX and primers, for chromosome and gene mapping, in the recombinant
XX production of protein, in the generation of antisense, ribozyme and
XX peptide-nucleic acid molecules, and to produce transgenic animals.
XX They may also have cytokine and cell proliferation or
XX differentiation activity, stem cell growth factor activity,

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CC haematopoiesis regulating activity, tissue growth activity,  
 CC immunosuppressive or immunostimulant activity, activin/inhibin  
 CC activity, chemotactic/chemokinetic activity, haemostatic and  
 CC thrombolytic activity, use in cancer diagnosis and therapy,  
 CC drug screening, receptor/ligand activity, antiinflammatory  
 CC activity, and treatment of leukaemia, nervous system disorders,  
 CC arthritis and inflammation.

XX  
 SQ Sequence 1201 BP; 357 A; 188 C; 275 G; 381 T; 0 other;

Alignment Scores:  
 Pred. No.: 4.06e-86 Length: 1201  
 Score: 676.00 Matches: 128  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 22 Gaps: 0

US-10-019-455A-6 (1-128) x AAH26343 (1-1201)

QY 1 MetAlaArgIleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20  
 DB 33 ATGGCAAGAAATATGTACTTTTCTCCCGGGCTTGTGGCTGTATGTGTCATGGA 92  
 QY 21 IlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspGluCysValTyrThr 40  
 DB 93 ATATTTATGGACGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTATACT 152  
 QY 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60  
 DB 153 ATTTCCTCGGTAGTCTCAAGAAGATTATAATGCCCGGACTGTAGATTCAATACGTT 212  
 QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80  
 DB 213 AAAAAGGCGACGAGATCTATGTGACTCAAGCTGTAAAGAAATGAGCTGGAGAA 272  
 QY 81 PheTyrAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100  
 DB 273 TTTTGGCTGGCAGTGTATTTATGGTATGCCAGGACGAGATGGAGTCTGGTTATTTC 332  
 QY 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120  
 DB 333 CCCAGAACTTGGTCAAGAACAGCGTGTGTACCCAGGAAGCTACCAAGGAAGTTCCACC 392  
 QY 121 ThrAspIleAspPheCysGlu 128  
 DB 393 ACGGATATTGACTTCTTCTGCGAG 416

RESULT 11  
 AAF59068  
 ID AAF59068 standard; DNA; 384 BP.

XX  
 AC AAF59068;

XX  
 DT 23-APR-2001 (first entry)

DE Mouse MLP nucleotide sequence SEQ ID NO:10.

XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
 KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
 KW cardiant; gene therapy; secretory cell function regulator; promoter;  
 KW inhibitor; ds.

XX  
 OS Mus musculus.

XX  
 PN WO200102564-A1.

XX  
 PD 11-JAN-2001.

XX  
 PF 29-JUN-2000; 2000WO-JP04278.

XX  
 PR 30-JUN-1999; 99JP-0186718.

XX

PA (TAKE ) TAKEDA CHEM IND LTD.

XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
 PI Tanaka H;

XX WPI; 2001-159271/16.

DR P-PSDB; AAB69125.

XX

PT Safe, low-toxicity secretory cell function-regulatory protein and  
 PT encoded DNA, applicable as drugs, in diagnosis and development of  
 PT promoters and inhibitors for preventing or treating e.g. bone and joint  
 PT diseases

XX Claim 11; Page 93; 111pp; Japanese.

CC The present invention describes novel MLP proteins and their encoding  
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
 CC activities, and can be used in gene therapy and as secretory cell  
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
 CC the diagnosis and development of promoters and inhibitors for preventing  
 CC or treating bone and joint diseases as well as pathologic angiogenesis.  
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
 CC in the exemplification of the present invention.

SQ Sequence 384 BP; 98 A; 68 C; 111 G; 107 T; 0 other;

Alignment Scores:

Pred. No.: 2.79e-76 Length: 384  
 Score: 602.00 Matches: 111  
 Percent Similarity: 93.75% Conservative: 9  
 Best Local Similarity: 86.72% Mismatches: 8  
 Query Match: 89.05% Indels: 0  
 DB: 22 Gaps: 0

US-10-019-455A-6 (1-128) x AAF59068 (1-384)

QY 1 MetAlaArgIleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20  
 DB 1 ATGGCAAGAAATATGTACTTTTCTCCCGGGCTTGTGGCTGTATGTGTCATGGA 60  
 QY 21 IlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspGluCysValTyrThr 40  
 DB 61 GTATTTATGGATAAACTTCTTCTAAGAAGTGTGTGCGGATGAGAGTGTGTCTATACT 120  
 QY 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60  
 DB 121 ATTTCCTCGCAAGACGACAGGAAGATTACAATGCCCGGACTGTAGTTCATCGATGC 180  
 QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80  
 DB 181 AAGAAGGCGACGAGATCTATGTCTTACTCCAGCTGGTAACAGAAACGAGCTGGAGAG 240  
 QY 81 PheTyrAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100  
 DB 241 TTTTGGCTGGCAGTGTATTTATGGTACCACGAGGATGAGATGGGAATTGAGTTATTTC 300  
 QY 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120  
 DB 301 CCCAGAACTTGGTGAAGGAGCAGCGTGTATACCCAGGAGGCCACCAAGGAGATCCCAACC 360  
 QY 121 ThrAspIleAspPheCysGlu 128  
 DB 361 ACGGATATTGACTTCTTCTGTGAA 384

RESULT 12

AAF59084

ID AAF59084 standard; DNA; 947 BP.

XX  
 AC AAF59084;

XX  
 DT 23-APR-2001 (first entry)

DE Mouse MLP nucleotide sequence SEQ ID NO:30.

```
XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
KW cardiant; gene therapy; secretory cell function regulator; promoter;
KW inhibitor; ds.
XX
OS Mus musculus.
XX
XX WO200102564-A1.
XX
XX 11-JAN-2001.
XX
XX 29-JUN-2000; 2000WO-JP04278.
XX
XX 30-JUN-1999; 99JP-0186718.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
PI Tanaka H;
XX
XX WPI; 2001-159271/16.
XX
XX Safe, low-toxicity secretory cell function-regulatory protein and
PT encoded DNA, applicable as drugs, in diagnosis and development of
PT promoters and inhibitors for preventing or treating e.g. bone and joint
PT diseases -
XX
XX Example 2; Page 100-101; 111pp; Japanese.
XX
XX The present invention describes novel MLP proteins and their encoding
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
CC activities, and can be used in gene therapy and as secretory cell
CC function regulators. The MLP proteins and DNAs can be used in drugs, in
CC the diagnosis and development of promoters and inhibitors for preventing
CC or treating bone and joint diseases as well as pathologic angiogenesis.
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
CC in the exemplification of the present invention.
XX
XX Sequence 947 BP; 279 A; 158 C; 221 G; 289 T; 0 other;
SQ
Alignment Scores:
Pred. No.: 1-03e-75 Length: 947
Score: 602.00 Matches: 111
Percent Similarity: 93.75% Conservative: 9
Best Local Similarity: 86.72% Mismatches: 8
Query Match: 89.05% Indels: 0
DB: 22 Gaps: 0
US-10-019-455A-6 (1-126) x AAF59084 (1-947)
QY 1 MetAlaArgIleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20
DB 11 ATGGCAAGGATATGATTCTTTTGGCTTGGGGGCTTGTGTCTATGTCGGCGCATGTT 70
QY 21 IlePheMetAspArgLeuAlaSerLysLeuCysAlaAspGluCysValTyrThr 40
DB 71 GTATTATGGATAAATCTTCTTAGAGAGTTGTGTGGGATGAGAGTGTGTCTACT 130
QY 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
DB 131 ATTTCTCTGCAAGAGACACAGGAAGATTACAATGCCAGACTGTAGGTTCATCGATGTC 190
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80
DB 191 AAAAAAGGCGACAGATCTATGTTTACTCCAGCTGGTAACAGAAACCGAGCTGGAGAG 250
QY 81 PheTIPAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100
DB 251 TTTTGGCTGGCAGTGTATTATGTTGACCCAGAGATGAGATGGGAATTGTAGGTATTTC 310
QY 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnAlaThrLysGluValProThr 120
DB 111
XX 311 CCAGCAACTTGGTGAAGGACGCGTGTATACCAGGAGGCCACCAAGAGATCCCAACC 370
QY 121 ThrAspIleAspPheCysGlu 128
DB 371 ACGGATATTGACTTCTTCTGTGAA 394
RESULT 13
AAF59098
ID AAF59098 standard; DNA; 384 BP.
XX
XX AAF59098;
XX
XX 23-APR-2001 (first entry)
XX
XX Rat MLP nucleotide sequence SEQ ID NO:46.
XX
XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
KW cardiant; gene therapy; secretory cell function regulator; promoter;
KW inhibitor; ds.
XX
XX Rattus sp.
XX
XX WO200102564-A1.
XX
XX 11-JAN-2001.
XX
XX 29-JUN-2000; 2000WO-JP04278.
XX
XX 30-JUN-1999; 99JP-0186718.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
PI Tanaka H;
XX
XX WPI; 2001-159271/16.
XX
XX P-PSDB; AAB69130.
XX
XX Safe, low-toxicity secretory cell function-regulatory protein and
PT encoded DNA, applicable as drugs, in diagnosis and development of
PT promoters and inhibitors for preventing or treating e.g. bone and joint
PT diseases -
XX
XX Claim 13; Page 105-106; 111pp; Japanese.
XX
XX The present invention describes novel MLP proteins and their encoding
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
CC activities, and can be used in gene therapy and as secretory cell
CC function regulators. The MLP proteins and DNAs can be used in drugs, in
CC the diagnosis and development of promoters and inhibitors for preventing
CC or treating bone and joint diseases as well as pathologic angiogenesis.
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
CC in the exemplification of the present invention.
XX
XX Sequence 384 BP; 98 A; 72 C; 109 G; 105 T; 0 other;
SQ
Alignment Scores:
Pred. No.: 5.37e-76 Length: 384
Score: 600.00 Matches: 111
Percent Similarity: 93.75% Conservative: 9
Best Local Similarity: 86.72% Mismatches: 8
Query Match: 88.76% Indels: 0
DB: 22 Gaps: 0
US-10-019-455A-6 (1-128) x AAF59098 (1-384)
QY 1 MetAlaArgIleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20
DB 1 ATGGCAAGGATATGATTCTTTTGGCTTGGGGGCTTGTGTCTATGTCGGCGCATGTC 60
QY 21 IlePheMetAspArgLeuAlaSerLysLeuCysAlaAspGluCysValTyrThr 40
DB 111
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Db 61 ATGTTATGATATAAATCTTCTTAAGAAGTTGTGTGCAGATGAGGAGTGTGTCTATACC 120
Qy 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
Db 121 ATTTCTCTGGCAGACAGACAGGAAGACTTACAATGCCCGGAGCTGTAGGTTTCATCAATGTC 180
Qy 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80
Db 181 AAGAAAGGGCAGCAGATCTATGTTTATTCGAAGCTGGTAAACAGAAATGGAGCTGGGGCA 240
Qy 81 PheTyrAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100
Db 241 TTCTGGGCTGCAGCTGTTATGGTGACCAACAGATGAGATGGGAATGTGGTTATTTTC 300
Qy 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120
Db 301 CCCAGCAACTTGGTTAGAGAGCAACGAGTGTACCAGGAGGCCACCAAGAGGATTCACAACC 360
Qy 121 ThrAspIleAspPheCysGlu 128
Db 361 ACGGATATTGACTTCTTCTGTGGAA 384

RESULT 14
AAF59079
ID AAF59079 standard; DNA; 330 BP.
XX
AC AAF59079;
XX
DT 23-APR-2001 (first entry)
XX
DE Human MLP nucleotide sequence SEQ ID NO:23.
XX
KW MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
KW cardiant; gene therapy; secretory cell function regulator; promoter;
KW inhibitor; ds.
XX
OS Homo sapiens.
XX
PN WO200102564-A1.
XX
PD 11-JAN-2001.
XX
PF 29-JUN-2000; 2000WO-JP04278.
XX
PR 30-JUN-1999; 99JP-0186718.
XX
PA (TAKE ) TAKEDA CHEM IND LTD.
XX
PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
PI Tanaka H;
DR WPI; 2001-159271/16.
DR P-PSDB; AAB69126.
XX
PT Safe, low-toxicity secretory cell function-regulatory protein and
PT encoded DNA, applicable as drugs, in diagnosis and development of
PT promoters and inhibitors for preventing or treating e.g. bone and joint
PT diseases -
XX
PS Claim 8; Page 97; 11pp; Japanese.
XX
The present invention describes novel MLP proteins and their encoding
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
CC activities, and can be used in gene therapy and as secretory cell
CC function regulators. The MLP proteins and DNAs can be used in drugs, in
CC the diagnosis and development of promoters and inhibitors for preventing
CC or treating bone and joint diseases as well as pathologic angiogenesis.
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
CC in the exemplification of the present invention.
XX
SQ Sequence 330 BP; 91 A; 60 C; 91 G; 88 T; 0 other;

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Pred. No.: 1.15e-74 Length: 330
Score: 590.00 Matches: 110
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 87.28% Indels: 0
DB: 22 Gaps: 0

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Qy 39 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 58
Db 61 TATACTATTCTCTGGCTAGTGTCTCAAGAAGATTATTAATGCCCGGAGCTGTAGATTCAAT 120
Qy 59 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 78
Db 121 AAGTTTAAAGAGGGCAGCAGATCTATGTGTACTCAAAAGCTGGTAAAGAAAATGGAGCT 180
Qy 79 GlyGluPheTyrAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 98
Db 181 GGAGAATTTTGGGCTGGCAGTGTATTATGGTGATGCCAGGACGAGATGGGAGTCTGTGGT 240
Qy 99 TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 118
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Qy 119 ProThrThrAspIleAspPheCysGlu 128
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RESULT 15
AAF59080
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AC AAF59080;
XX
DT 23-APR-2001 (first entry)
XX
DE Mouse MLP nucleotide sequence SEQ ID NO:25.
XX
KW MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
KW cardiant; gene therapy; secretory cell function regulator; promoter;
KW inhibitor; ds.
XX
OS Mus musculus.
XX
PN WO200102564-A1.
XX
PD 11-JAN-2001.
XX
PF 29-JUN-2000; 2000WO-JP04278.
XX
PR 30-JUN-1999; 99JP-0186718.
XX
PA (TAKE ) TAKEDA CHEM IND LTD.
XX
PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
PI Tanaka H;
DR WPI; 2001-159271/16.
DR P-PSDB; AAB69127.
XX
PT Safe, low-toxicity secretory cell function-regulatory protein and
PT encoded DNA, applicable as drugs, in diagnosis and development of
PT promoters and inhibitors for preventing or treating e.g. bone and joint
PT diseases -
XX
PS Claim 10; Page 98; 11pp; Japanese.

```

XX The present invention describes novel MLP proteins and their encoding  
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
CC activities, and can be used in gene therapy and as secretory cell  
CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
CC the diagnosis and development of promoters and inhibitors for preventing  
CC or treating bone and joint diseases as well as pathologic angiogenesis.  
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
CC in the exemplification of the present invention.  
XX  
SQ Sequence 330 BP; 91 A; 60 C; 92 G; 87 T; 0 other;

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Query Match: 80.92% Indels: 0  
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US-10-019-455A-6 (1-128) x AAF59080 (1-330)

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QY	39	TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle	58
DB	61	TATACTATTCTCTGGCAAGAGCACAGGAGATTACAATGCCCCAGACTGTAGGTTTCATC	120
QY	59	AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla	78
DB	121	GATGTCAGAAAGGGCAGCAGATCTATGTTTACTTCAAGCTGGTAAACAGAAACGGAGCT	180
QY	79	GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly	98
DB	181	GGAGAGTTTGGGCTGGCAGTGTATTATGGTGACCACCAGGATCAGATGGGAATTGTAGGT	240
QY	99	TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal	118
DB	241	TATTTCCCAACCACTTGGTGAAGGAGCAGCGTGTATACCAGGAGGCCACCAAGGAGATC	300
QY	119	ProThrThrAspIleAspPheCysGlu	128
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Job time : 157.353 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 29, 2003, 19:57:30 ; Search time 287.193 Seconds  
(without alignments)  
1527.048 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2244575 seqs, 1713117285 residues

Total number of hits satisfying chosen parameters: 4489150

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-LOPCPI=0 -LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=ptct -THR MAX=100  
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-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
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Database : Published Applications NA:\*

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- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
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- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*
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- 13: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq2:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	676	100.0	521	13	US-10-216-163-71	Sequence 71, Appl
3	676	100.0	521	13	US-10-218-785-71	Sequence 71, Appl
4	676	100.0	521	13	US-10-219-063-71	Sequence 71, Appl
5	676	100.0	521	13	US-10-219-066-71	Sequence 71, Appl
6	676	100.0	521	13	US-10-219-067-71	Sequence 71, Appl
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9	676	100.0	521	13	US-10-219-073-71	Sequence 71, Appl
10	676	100.0	521	13	US-10-219-475-71	Sequence 71, Appl
11	676	100.0	521	13	US-10-219-480-71	Sequence 71, Appl
12	676	100.0	521	13	US-10-219-483-71	Sequence 71, Appl
13	676	100.0	521	13	US-10-219-525-71	Sequence 71, Appl
14	676	100.0	521	13	US-10-219-526-71	Sequence 71, Appl
15	676	100.0	521	13	US-10-219-530-71	Sequence 71, Appl
16	676	100.0	521	13	US-10-219-532-71	Sequence 71, Appl
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22	676	100.0	521	13	US-10-223-082-359	Sequence 359, App
23	676	100.0	521	15	US-10-227-884-71	Sequence 71, Appl
24	676	100.0	521	15	US-10-230-163-71	Sequence 71, Appl
25	676	100.0	521	15	US-10-230-338-71	Sequence 71, Appl
26	676	100.0	521	15	US-10-218-631-71	Sequence 71, Appl
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29	676	100.0	521	15	US-10-218-849-71	Sequence 71, Appl
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33	676	100.0	521	15	US-10-219-003-71	Sequence 71, Appl
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37	676	100.0	521	15	US-10-219-479-71	Sequence 71, Appl
38	676	100.0	521	15	US-10-219-481-71	Sequence 71, Appl
39	676	100.0	521	15	US-10-230-260-71	Sequence 71, Appl
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ALIGNMENTS

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US-10-216-038-1  
; Sequence 1, Application US/10216038  
; Publication No. US20030124573A1  
; GENERAL INFORMATION:  
; APPLICANT: Mize, Nancy K  
; APPLICANT: Boyle, Bryan J  
; APPLICANT: Ford, John E  
; APPLICANT: Arterburn, Matthew C  
; APPLICANT: Tang, Y Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Drmanac, Radoje T  
; APPLICANT: Song, Yong  
; APPLICANT: Sjastad, Michael  
; TITLE OF INVENTION: Methods and Materials Relating to No. US20030124573A1e1 Growth )  
; FILE REFERENCE: HYS-7CIP  
; CURRENT APPLICATION NUMBER: US/10/216,038  
; CURRENT FILING DATE: 2002-08-08  
; PRIOR APPLICATION NUMBER: US 09/563,786  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: US 09/491,404  
; PRIOR FILING DATE: 2000-01-25  
; NUMBER OF SEQ ID NOS: 8

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; SEQ ID NO 1
; LENGTH: 426
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (426)..(426)
; OTHER INFORMATION: n = A, T, G, or C
US-10-216-038-1
Alignment Scores:
Pred. No.: 9,95e-94 Length: 426
Score: 676.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0
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QY 1 MetAlaArgTleLeuLeuLeuValAlaValCysAlaValHisGly 20
DB 19 ATGCGCAAGATATGTTACTTTTCTCCCGGGTCTTGTGCTGTATGCTGTGCAATGGA 78
QY 21 IlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysValTyrThr 40
DB 79 ATATTATATGACCGCTAGCTTCCNAGAAGCTCTGTGCAGATGATGAGTGTGTCTATACT 138
QY 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
DB 139 ATTTCTCTGGCTAGTGTCTCAAGAAGATTTAATGCCCGGACTGTAGATTCAATTAACGTT 198
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80
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QY 121 ThrAspIleAspPhePheCysGlu 128
DB 379 ACGGATATTGACTTCTTCGGAG 402
RESULT 2
US-10-216-163-71
; Sequence 71, Application US/10216163
; Publication No. US20030149239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530FIC3
; CURRENT APPLICATION NUMBER: US/10/216,163
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
;
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 426
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (426)..(426)
; OTHER INFORMATION: n = A, T, G, or C
US-10-216-038-1
Alignment Scores:
Pred. No.: 9,95e-94 Length: 426
Score: 676.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0
US-10-019-455A-6 (1-128) x US-10-216-163-71 (1-521)
QY 1 MetAlaArgTleLeuLeuLeuValAlaValCysAlaValHisGly 20
DB 38 ATGCGCAAGATATGTTACTTTTCTCCCGGGTCTTGTGCTGTATGCTGTGCAATGGA 97
QY 21 IlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysValTyrThr 40
DB 98 ATATTATATGACCGCTAGCTTCCNAGAAGCTCTGTGCAGATGATGAGTGTGTCTATACT 157
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; Publication No. US20030187201A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530FIC3
; CURRENT APPLICATION NUMBER: US/10/218,765
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
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APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
TITLE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3530PIC19  
CURRENT APPLICATION NUMBER: US/10/218,765  
CURRENT FILING DATE: 2002-08-12  
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PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
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PRIOR FILING DATE: 1998-06-25  
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PRIOR FILING DATE: 1998-09-18  
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PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/101477  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101738  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101741  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101786  
PRIOR FILING DATE: 1998-09-25  
PRIOR APPLICATION NUMBER: 60/101916  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101922  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/106178  
PRIOR FILING DATE: 1998-10-28  
PRIOR APPLICATION NUMBER: 60/106248  
PRIOR FILING DATE: 1998-10-29  
PRIOR APPLICATION NUMBER: 60/106464  
PRIOR FILING DATE: 1998-10-30  
PRIOR APPLICATION NUMBER: 60/106905  
PRIOR FILING DATE: 1998-11-03  
PRIOR APPLICATION NUMBER: 60/108787  
PRIOR FILING DATE: 1998-11-17  
PRIOR APPLICATION NUMBER: 60/108801  
PRIOR FILING DATE: 1998-11-17  
PRIOR APPLICATION NUMBER: 60/108849  
PRIOR FILING DATE: 1998-11-18  
PRIOR APPLICATION NUMBER: 60/112422  
PRIOR FILING DATE: 1998-12-15  
PRIOR APPLICATION NUMBER: 60/113296  
PRIOR FILING DATE: 1998-12-22  
PRIOR APPLICATION NUMBER: 60/113605  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: 60/113621  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: 60/115558  
PRIOR FILING DATE: 1999-01-12  
PRIOR APPLICATION NUMBER: 60/115565  
PRIOR FILING DATE: 1999-01-12  
PRIOR APPLICATION NUMBER: 60/115733  
PRIOR FILING DATE: 1999-01-12  
PRIOR APPLICATION NUMBER: 60/119549  
PRIOR FILING DATE: 1999-02-10  
PRIOR APPLICATION NUMBER: 60/123618  
PRIOR FILING DATE: 1999-03-10  
PRIOR APPLICATION NUMBER: 60/125259  
PRIOR FILING DATE: 1999-03-19  
PRIOR APPLICATION NUMBER: 60/125775

Qy	81	PheTpnAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe	100
Db	278	TTTTGGGCTGGCAGTGTATTATGGTGAATGGCCAGGACCGAGATGGGAGTCGTGGTTATTC	337
Qy	101	ProArgAsnLeuValLysGluInArgValTyrGlnGluAlaThrLysGluValProThr	120
Db	338	CCCAGGAACTTGGTCAAGGAACAGCGTGTGTATCCAGGAAGCTACCAAGGAAGTTCCACC	397
Qy	121	ThrAspIleAspPheCysGlu	128
Db	398	ACGGATATTGACTTCTTCTGCGAG	421
RESULT 4			
US-10-219-063-71			
; Sequence 71, Application US/10219063			
; Publication No. US20030187202A1			
; GENERAL INFORMATION:			
; APPLICANT: Baker, Kevin P.			
; APPLICANT: Desnoyers, Luc			
; APPLICANT: Gerritsen, Mary			
; APPLICANT: Goddard, Audrey			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Grimaldi, J. Christopher			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Smith, Victoria			
; APPLICANT: Stephan, Jean-Philippe F.			
; APPLICANT: Watanabe, Colin L.			
; APPLICANT: Wood, William I.			
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC			
; FILE REFERENCE: P3530PIC24			
; CURRENT APPLICATION NUMBER: US/10/219,063			
; PRIOR FILING DATE: 2002-08-13			
; PRIOR APPLICATION NUMBER: 10/119,480			
; PRIOR FILING DATE: 2002-04-09			
; PRIOR APPLICATION NUMBER: 60/059113			
; PRIOR FILING DATE: 1997-09-17			
; PRIOR APPLICATION NUMBER: 60/062287			
; PRIOR FILING DATE: 1997-10-17			
; PRIOR APPLICATION NUMBER: 60/063549			
; PRIOR FILING DATE: 1997-10-28			
; PRIOR APPLICATION NUMBER: 60/064103			
; PRIOR FILING DATE: 1997-10-31			
; PRIOR APPLICATION NUMBER: 60/069873			
; PRIOR FILING DATE: 1997-12-17			
; PRIOR APPLICATION NUMBER: 60/078910			
; PRIOR FILING DATE: 1998-03-20			
; PRIOR APPLICATION NUMBER: 60/079294			
; PRIOR FILING DATE: 1998-03-25			
; PRIOR APPLICATION NUMBER: 60/079656			
; PRIOR FILING DATE: 1998-03-26			
; PRIOR APPLICATION NUMBER: 60/079728			
; PRIOR FILING DATE: 1998-03-27			
; Remaining Prior Application data removed - See File Wrapper or PALM.			
; NUMBER OF SEQ ID NOS: 246			
; SEQ ID NO 71			
; LENGTH: 521			
; TYPE: DNA			
; ORGANISM: Homo Sapien			
US-10-219-063-71			
Alignment Scores:			
Pred. No.:	1,34e-93	Length:	521
Score:	676.00	Matches:	128
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	13	Gaps:	0
US-10-019-455A-6 (1-128) x US-10-219-765-71 (1-521)			
Qy	1	MetAlaArgIleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly	20
Db	38	ATGGCAAGATATGTACTTTCTCCGGGCTCTGGCTGTATGTGTGTGCTATGGA	97
Qy	21	IlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysValTyrThr	40
Db	98	ATATTATATGGACCGCTCTAGCTTCCAAAGCTCTGTGCAGATGATGATGTGTCTACT	157
Qy	41	IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal	60
Db	158	ATTTCCTCTGGCTAGTGTCTAAGAGATTATATCCCGGAGCTAGATTCAATTAAGTT	217
Qy	61	LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu	80
Db	218	AAAAAGGCAGCAGATCTATGTACTCAAAAGCTGGTAAAGAAATGGAGCTGGAGAA	277
US-10-019-455A-6 (1-128) x US-10-219-063-71 (1-521)			
Qy	1	MetAlaArgIleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly	20
Db	38	ATGGCAAGATATGTACTTTCTCCGGGCTCTGGCTGTATGTGTGTGCTATGGA	97
Qy	21	IlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysValTyrThr	40
Db	98	ATATTATATGGACCGCTCTAGCTTCCAAAGCTCTGTGCAGATGATGATGTGTCTACT	157
Qy	41	IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal	60
Db	158	ATTTCCTCTGGCTAGTGTCTAAGAGATTATATCCCGGAGCTAGATTCAATTAAGTT	217
Qy	61	LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu	80
Db	218	AAAAAGGCAGCAGATCTATGTACTCAAAAGCTGGTAAAGAAATGGAGCTGGAGAA	277

Db	38	ATGCCAAGAAATATTGTGTACTTTTCTCCCGGGCTCTGTGGCTGATGTGCTGTGCATGGA	97
Qy	21	IlePheMetAspArgLeuAlaSerIlysLysLeuCysAlaAspAspGluCysValTyrThr	40
Db	98	ATAATTTATGGACCGTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGTGTCTATACT	157
Qy	41	IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal	60
Db	158	ATTTCCTCTGGCTAGTGTCCAAGAGATTATAATGCCCGGACTGTAGATTCTATTAAACGTT	217
Qy	61	LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu	80
Db	218	AAAAAAGGCGACGACAGACTATGTGTACTCAAAAGCTGGTAAAAAGAAATGGAGCTGGAGAA	277
Qy	81	PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe	100
Db	278	TTTTTGGGCTGGCAGTGTTTATGGTGATGGCCACGACGAGATGGGAGTGTGGGGTTATTTC	337
Qy	101	ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr	120
Db	338	CCCAGGAACTTGGTCAAGSAACAGCGTGTGTACCAAGGAAGCTACCAAGGAAGTTCCACC	397
Qy	121	ThrAspIleAspPhePheCysGlu	128
Db	398	ACGGATATTGACTTCTTCTGTGCAG	421

RESULT 5  
US-10-219-066-71  
; Sequence 71, Application US/10219066  
; Publication No. US20030187203A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

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US-10-019-066-71

Alignment Scores:
Pred. No.:      1.34e-93      Length:      521
Score:          676.00      Matches:    128
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:    0
DB:              13      Gaps:      0

US-10-019-455A-6 (1-128) x US-10-219-066-71 (1-521)

Qy 1 MetAlaArgIleLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20
Db 38 ATGCAAGAATATTGTACTTTCTCCCGGCTTGTGGCTGTATGTCTGTGCATGGA 97
Qy 21 IlePheMetAspArgLeuAlaSerIlySlyLeuCysAlaAspGluCysValTyrThr 40
Db 98 ATATTATTAGGACCGTCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTATACT 157
Qy 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
Db 158 ATTCTCTGGCTAGTGGCTCAAGAGATTATAATGCCCGGACTGTAGATTATTAAACGTT 217
Qy 61 LysIlyGlyGlnGlnIleTyrValTyrSerIlySlyLeuValIlySlyGluAsnGlyAlaGlyGlu 80
Db 218 AAAAAAGGCGACGACAGATCTATGTGTACTCAAAAGCTGTGTAAAGAAAAATCGAGCTGCAGAA 277
Qy 81 PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100
Db 278 TTTTGGGCGTGGCAGTGTTATTGGTGATGCGCAGGACGAGATGGGAGTCTGTGGGTATTATTC 337
Qy 101 ProArgAsnLeuValIlySlyGlnGlnArgValTyrGlnGluAlaThrIlySlyGluValProThr 120
Db 338 CCCAGGAACTTGGTCAAGAACACGCGTGTGTACCAAGAGAGCTACCAAGAGAAAGTTCCACC 397
Qy 121 ThrAspIleAspPheCysGlu 128
Db 398 ACGGATATTGACTTCTTCTCGGAG 421

RESULT 6
US-10-219-067-71
; Sequence 71, Application US/10219067
; Publication No. US20030187204A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe P.
; APPLICANT: Watanabe, Colin I.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P530P1C51
; CURRENT APPLICATION NUMBER: US/10/219,067
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17

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```
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-067-71

Alignment Scores:
Pred. No.: 1,34e-93 Length: 521
Score: 676.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-019-455A-6 (1-128) x US-10-219-067-71 (1-521)
QY 1 MetAlaArgIleLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20
DB 38 ATGGCAAGAATATTGTACTTTTCCCTCCGGGTCCTGTGCTGTATGTGTGTCATGGA 97
QY 21 IlePheMetAspArgIleuAlaSerLysLeuCysAlaAspGluCysValTyrThr 40
DB 98 ATATTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTATACT 157
QY 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
DB 158 ATTCTCTGGCTAGTCTCAAGAAGATTATATATGCCCGGACGTGTAGATTCAATTAAGTT 217
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80
DB 218 AAAAAAGGGCAGCAGATCTATGTGTACTCAAGCTGTGTAAGCTGTAAGAAATGGAGCTGGAGAA 277
QY 81 PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100
DB 278 TTTTGGCTGGCAGTGTATTATGTGTATGGCCAGACGATGGAGTCTGGGGTTATTTC 337
QY 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120
DB 338 CCCAGGAACCTTGTCAAGGAACAGCGTGTGTACCAAGAGCTACCAAGGAAGTCCACC 397
QY 121 ThrAspIleAspPhePheCysGlu 128
DB 398 ACGGATATTGACTTCTTCTCGCAG 421

RESULT 7
US-10-219-068-71
; Sequence 71, Application US/10219068
; Publication No. US20030187205A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C31
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; CURRENT APPLICATION NUMBER: US/10/219,068
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-068-71

Alignment Scores:
Pred. No.: 1,34e-93 Length: 521
Score: 676.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-019-455A-6 (1-128) x US-10-219-068-71 (1-521)
QY 1 MetAlaArgIleLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20
DB 38 ATGGCAAGAATATTGTACTTTTCCCTCCGGGTCCTGTGCTGTATGTGTGTCATGGA 97
QY 21 IlePheMetAspArgIleuAlaSerLysLeuCysAlaAspGluCysValTyrThr 40
DB 98 ATATTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTATACT 157
QY 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
DB 158 ATTCTCTGGCTAGTCTCAAGAAGATTATATATGCCCGGACGTGTAGATTCAATTAAGTT 217
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80
DB 218 AAAAAAGGGCAGCAGATCTATGTGTACTCAAGCTGTGTAAGCTGTAAGAAATGGAGCTGGAGAA 277
QY 81 PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100
DB 278 TTTTGGCTGGCAGTGTATTATGTGTATGGCCAGACGATGGAGTCTGGGGTTATTTC 337
QY 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120
DB 338 CCCAGGAACCTTGTCAAGGAACAGCGTGTGTACCAAGAGCTACCAAGGAAGTCCACC 397
QY 121 ThrAspIleAspPhePheCysGlu 128
DB 398 ACGGATATTGACTTCTTCTCGCAG 421

RESULT 8
US-10-219-069-71
; Sequence 71, Application US/10219069
; Publication No. US20030187206A1
; GENERAL INFORMATION:
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Tue Dec 30 10:20:54 2003

APPLICANT: Baker, Kevin P.  
APPLICANT: Desnoyers, Luc  
APPLICANT: Gerritsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3530PIC40  
CURRENT APPLICATION NUMBER: US/10/219,069  
CURRENT FILING DATE: 2002-08-13  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 246  
SEQ ID NO 71  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-219-069-71

Alignment Scores:  
Pred. No.: 1,34e-93 Length: 521  
Score: 676.00 Matches: 128  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0

US-10-019-455A-6 (1-128) x US-10-219-069-71 (1-521)  
QY 1 MetAlaArgIleLeuLeuLeuValAlaValCysAlaValHisGly 20  
DB 38 ATGCGAAGATATGTTTCTCCCGGGCTTGTGCTGTATGCTGTGCTATGCAATGGA 97  
QY 21 IlePheMetAspArgLeuAlaSerLysLeuCysAlaAspGluCysValTyrThr 40  
DB 98 ATATTATGACCGCTAGCTTCCAGAAAGCTCTGTCAGATGATGATGCTGTACTACT 157  
QY 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60  
DB 158 ATTTCTCTGGCTAGTGTCTCAAGAAGATTATATGCGCGGACTGTAGATTCAATTAACGTT 217  
QY 61 LysIleGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAenGlyAlaGlyGlu 80  
DB 218 AAAAAAGGGCAGCAGATCTATGTACTCAAGCTGTATAAAGAAATGGAGCTGGAGAA 277  
QY 81 PheTyrAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100  
DB 278 TTTTGGCTGGCAGTGTATTATGTTGATGGCAGCAGATGGAGTGGTGGGTATTTC 337

QY 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120  
DB 338 CCCAGGAACCTTGGTCAAGGAACAGCGTGTGTACCGAAGACTACCAAGAGATTCCACC 397  
QY 121 ThrAspIleAspPheCysGlu 128  
DB 398 ACCGATATGACTTCTTCTGCGAG 421  
RESULT 9  
US-10-219-073-71  
Sequence 71, Application US/10219073  
Publication No. US20030187207A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Desnoyers, Luc  
APPLICANT: Gerritsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3530PIC52  
CURRENT APPLICATION NUMBER: US/10/219,073  
CURRENT FILING DATE: 2002-08-14  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 246  
SEQ ID NO 71  
LENGTH: 521  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-219-073-71

Alignment Scores:  
Pred. No.: 1,34e-93 Length: 521  
Score: 676.00 Matches: 128  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0

US-10-019-455A-6 (1-128) x US-10-219-073-71 (1-521)  
QY 1 MetAlaArgIleLeuLeuLeuValAlaValCysAlaValHisGly 20  
DB 38 ATGCGAAGATATGTTTCTCCCGGGCTTGTGCTGTATGCTGTGCTATGCAATGGA 97  
QY 21 IlePheMetAspArgLeuAlaSerLysLeuCysAlaAspGluCysValTyrThr 40

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Db      98 ATATTTATGACCGCTAGCTCCACAGAGCTCTGTGCAGATGATGAGTGTCTATACT 157
Qy      41 ILeSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
Db      158 ATTTCTCTGGCTAGTCTCAAGAAGATTATAATGCCCGGAGCTGTAGATTCAATTAACGTT 217
Qy      61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80
Db      218 AAAAAAGGGCAGCAGATCTATGTGTACTCAAGCTGTATAAAGAAAATGGAGCTGGAGAA 277
Qy      81 PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100
Db      278 TTTTGGCTGGCAGTGTATTATGCTGATGCCAGCAGATGGAGTGTGGGTTATTTC 337
Qy      101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120
Db      338 CCCAGGAACCTGTGTCAGGAACAGCGTGTGTACCAAGAGTGTACCAAGGAAGTCCACC 397
Qy      121 ThrAspIleAspPhePheCysGlu 128
Db      398 ACGGATATTGACTTCTTCTCGGAG 421

```

## RESULT 10

```

US-10-219-475-71
; Sequence 71, Application US/10219475
; Publication No. US20030187208A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C49
; CURRENT APPLICATION NUMBER: US/10/219,475
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR FILING DATE: 1997-09-17
; PRIOR FILING DATE: 1997-09-17
; PRIOR FILING DATE: 1997-10-17
; PRIOR FILING DATE: 1997-10-28
; PRIOR FILING DATE: 1997-10-31
; PRIOR FILING DATE: 1997-12-17
; PRIOR FILING DATE: 1998-03-20
; PRIOR FILING DATE: 1998-03-25
; PRIOR FILING DATE: 1998-03-26
; PRIOR FILING DATE: 1998-03-27
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-475-71
; Alignment Scores:

```

```

Pred. No.: 1.34e-93 Length: 521
Score: 676.00 Matches: 128
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-019-455A-6 (1-128) x US-10-219-475-71 (1-521)

Qy      1 MetAlaArgIleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20
Db      38 ATGCCAAGAATATTGTTACTTTCTCCCGGGCTTGTGGCTGTATGCTGTGTCATGGA 97
Qy      21 IlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysValTyrThr 40
Db      98 ATATTTATGGACCGCTAGCTTCCAGAGACTCTGTGCAGATGATGAGTGTGCTACT 157
Qy      41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
Db      158 ATTTCTCTGGCTAGTCTCAAGAAGATTATAATGCCCGGAGCTGTAGATTCAATTAACGTT 217
Qy      61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80
Db      218 AAAAAAGGGCAGCAGATCTATGTGTACTCAAGCTGTATAAAGAAAATGGAGCTGGAGAA 277
Qy      81 PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100
Db      278 TTTTGGCTGGCAGTGTATTATGCTGATGCCAGCAGATGGAGTGTGGGTTATTTC 337
Qy      101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120
Db      338 CCCAGGAACCTGTGTCAGGAACAGCGTGTGTACCAAGAGTGTACCAAGGAAGTCCACC 397
Qy      121 ThrAspIleAspPhePheCysGlu 128
Db      398 ACGGATATTGACTTCTTCTCGGAG 421

```

## RESULT 11

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US-10-219-480-71
; Sequence 71, Application US/10219480
; Publication No. US20030187209A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C38
; CURRENT APPLICATION NUMBER: US/10/219,480
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294

```

; PRIOR FILING DATE: 1998-03-25  
 ; PRIOR APPLICATION NUMBER: 60/079656  
 ; PRIOR FILING DATE: 1998-03-26  
 ; PRIOR APPLICATION NUMBER: 60/079728  
 ; PRIOR FILING DATE: 1998-03-27  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 246  
 ; SEQ ID NO 71  
 ; LENGTH: 521  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 US-10-219-480-71

Alignment Scores:  
 Pred. No.: 1,34e-93 Length: 521  
 Score: 676.00 Matches: 128  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 13 Gaps: 0

US-10-019-455A-6 (1-128) x US-10-219-480-71 (1-521)

Qy	1	MetAlaArgIleLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly	20
Db	38	ATGGCAAGAAATATTGTTACTTTCTCCCGGGTCTTGGCTGTATGCTGTGCATGGA	97
Qy	21	IlePheMetAspArgLeuAlaSerIlySlyLeuCysAlaAspAspGluCysValThr	40
Db	98	ATAATTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTATACT	157
Qy	41	IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal	60
Db	158	ATTTCTCTGGCTAGTGTCTCAAGAGAAATATATGATCCCGGAGCTGTAGATTCAATTAACGTT	217
Qy	61	LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu	80
Db	218	AAAAAAGGCGACAGATCTATGTGTACTCAAGCTGGTAAAGAAATGGAGCTGGAGAA	277
Qy	81	PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe	100
Db	278	TTTTGGGCTGGCAGTGTATTATGTTGATGCCAGGACGAGATGGGAGTGGTGGTTATTTC	337
Qy	101	ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr	120
Db	338	CCCAGGAACTTGGTCAAGAGAACAGCGTGTGTACCCAGGAGCTTACCAAGAAAGTCCCACC	397
Qy	121	ThrAspIleAspPheCysGlu	128
Db	398	ACGGATATTGACTTCTTCTGCGAG	421

RESULT 12

US-10-219-483-71  
 ; Sequence 71, Application US/10219483  
 ; Publication No. US20030187210A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Gerritsen, Mary  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stephan, Jean-Philippe P.  
 ; APPLICANT: Watanabe, Colin L.  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P3530PIC43  
 ; CURRENT APPLICATION NUMBER: US/10/219,483  
 ; CURRENT FILING DATE: 2002-08-13  
 ; PRIOR APPLICATION NUMBER: 10/119,480

; PRIOR FILING DATE: 2002-04-09  
 ; PRIOR APPLICATION NUMBER: 60/059113  
 ; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/062287  
 ; PRIOR FILING DATE: 1997-10-17  
 ; PRIOR APPLICATION NUMBER: 60/063549  
 ; PRIOR FILING DATE: 1997-10-28  
 ; PRIOR APPLICATION NUMBER: 60/064103  
 ; PRIOR FILING DATE: 1997-10-31  
 ; PRIOR APPLICATION NUMBER: 60/069873  
 ; PRIOR FILING DATE: 1997-12-17  
 ; PRIOR APPLICATION NUMBER: 60/078910  
 ; PRIOR FILING DATE: 1998-03-20  
 ; PRIOR APPLICATION NUMBER: 60/079294  
 ; PRIOR FILING DATE: 1998-03-25  
 ; PRIOR APPLICATION NUMBER: 60/079656  
 ; PRIOR FILING DATE: 1998-03-26  
 ; PRIOR APPLICATION NUMBER: 60/079728  
 ; PRIOR FILING DATE: 1998-03-27  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 246  
 ; SEQ ID NO 71  
 ; LENGTH: 521  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 US-10-219-483-71

US-10-019-455A-6 (1-128) x US-10-219-483-71 (1-521)

Qy	1	MetAlaArgIleLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly	20
Db	38	ATGGCAAGAAATATTGTTACTTTCTCCCGGGTCTTGGCTGTATGCTGTGCATGGA	97
Qy	21	IlePheMetAspArgLeuAlaSerIlySlyLeuCysAlaAspAspGluCysValThr	40
Db	98	ATAATTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTATACT	157
Qy	41	IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal	60
Db	158	ATTTCTCTGGCTAGTGTCTCAAGAGAAATATATGATCCCGGAGCTGTAGATTCAATTAACGTT	217
Qy	61	LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu	80
Db	218	AAAAAAGGCGACAGATCTATGTGTACTCAAGCTGGTAAAGAAATGGAGCTGGAGAA	277
Qy	81	PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe	100
Db	278	TTTTGGGCTGGCAGTGTATTATGTTGATGCCAGGACGAGATGGGAGTGGTGGTTATTTC	337
Qy	101	ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr	120
Db	338	CCCAGGAACTTGGTCAAGAGAACAGCGTGTGTACCCAGGAGCTTACCAAGAAAGTCCCACC	397
Qy	121	ThrAspIleAspPheCysGlu	128
Db	398	ACGGATATTGACTTCTTCTGCGAG	421

RESULT 13

US-10-219-525-71  
 ; Sequence 71, Application US/10219525  
 ; Publication No. US20030187211A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Gerritsen, Mary

APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
TITLE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3530PIC29  
CURRENT APPLICATION NUMBER: US/10/219,525  
CURRENT FILING DATE: 2002-08-13  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 246  
SEQ ID NO 71  
LENGTH: 521  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-219-525-71

Alignment Scores:  
Pred. No.: 1,34e-93 Length: 521  
Score: 676.00 Matches: 128  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0  
US-10-019-455A-6 (1-128) x US-10-219-525-71 (1-521)  
QY 1 MetAlaArgIleLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20  
DB 38 ATGGCAAGAAATATTGTTACTTCTCCCGGCTCTGTGGCTGTATGCTGTGCATGGA 97  
QY 21 IlePheMetAspArgLeuAlaSerLysLeuCysAlaAspGluCysValTyrThr 40  
DB 98 ATATTATGGACCGTCTAGCTCCAGAGAGCTCTGCAGATGATGAGTGTCTTACT 157  
QY 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60  
DB 158 ATTTCTCTGGCTAGTGTCTCAAGAGATTAATATGCCCCGAGCTGTAGATTCAATAGCTT 217  
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80  
DB 218 AAAAAGGGCAGCATCTATGTGACTCAAGCTGGTAAAGAAATGGAGCTGGAGAA 277  
QY 81 PheTTPAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100  
DB 278 TTTTGGCTGGCAGTGTATTGATGATGATGATGATGATGATGATGATGATGATGATGAT 337  
QY 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGlnAlaThrLysGluValProThr 120

DB 338 CCCAGGAACCTTGGTCAAGGAACAGCGTGTGTACCAAGGAAGCTACCAAGGAAGTTCCACC 397  
QY 121 ThrAspIleAspPhePheCysGlu 128  
DB 398 ACGGATATTGACTTCTTCTCTCGGAG 421  
RESULT 14  
US-10-219-526-71  
Sequence 71, Application US/10219526  
Publication No. US20030187212A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Desnoyers, Luc  
APPLICANT: Gerritsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
TITLE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3530PIC41  
CURRENT APPLICATION NUMBER: US/10/219,526  
CURRENT FILING DATE: 2002-08-13  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 246  
SEQ ID NO 71  
LENGTH: 521  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-219-526-71  
Alignment Scores:  
Pred. No.: 1,34e-93 Length: 521  
Score: 676.00 Matches: 128  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0  
US-10-019-455A-6 (1-128) x US-10-219-526-71 (1-521)  
QY 1 MetAlaArgIleLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20  
DB 38 ATGGCAAGAAATATTGTTACTTCTCCCGGCTCTGTGGCTGTATGCTGTGCATGGA 97  
QY 21 IlePheMetAspArgLeuAlaSerLysLeuCysAlaAspGluCysValTyrThr 40  
DB 98 ATATTATGGACCGTCTAGCTTCTCCAGAGAGCTCTGTGCAGATGATGAGTGTCTTACT 157

QY 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProaspCysArgPheIleAsnVal 60  
DB 158 ATTTCTCTGGCTAGTCTCAAGAAGATTATATAATGCCCGGACTGTAGATTCAATTAACGTT 217  
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80  
DB 218 AAAAAAGGGCAGCAGATCTATGTGTACTCAAGCTGGTAAAGAAATGGAGCTGGAGAA 277  
QY 81 PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100  
DB 278 TTTTGGCTGCGCAGTGTATTATGTGTATGGCCAGACGAGATGGAGTCGTGGGTATTTC 337  
QY 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120  
DB 338 CCCAGGAACCTTGTCTCAAGCAACAGCGTGTACCAAGAACTACCAAGGAAGTTCCACC 397  
QY 121 ThrAspIleAspPhePheCysGlu 128  
DB 398 ACGGATATTGACTTCTTCTCGGAG 421

RESULT 15

US-10-219-530-71  
; Sequence 71, Application US/10219530  
; Publication No. US20030187213A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3530FIC54  
; CURRENT APPLICATION NUMBER: US/10/219,530  
; CURRENT FILING DATE: 2002-08-14  
; PRIOR APPLICATION NUMBER: 10/119,480  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/069873  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 246  
; SEQ ID NO 71  
; LENGTH: 521  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-219-530-71

Alignment Scores:  
Pred. No.: 1.34e-93 Length: 521  
Score: 676.00 Matches: 128  
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0  
US-10-019-455A-6 (1-128) x US-10-219-530-71 (1-521)  
QY 1 MetAlaArgIleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20  
DB 38 ATGGCAAGAAATATTGTACTTTTCTCCCGGGTCTTGTGGCTGTATGTGCTGTCATGGA 97  
QY 21 IlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysValTyrThr 40  
DB 98 ATATTTATGGACCGTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGTGTGTCTACT 157  
QY 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProaspCysArgPheIleAsnVal 60  
DB 158 ATTTCTCTGGCTAGTGTCTCAAGAAGATTATATAATGCCCGGACTGTAGATTCAATTAACGTT 217  
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80  
DB 218 AAAAAAGGGCAGCAGATCTATGTGTACTCAAGCTGGTAAAGAAATGGAGCTGGAGAA 277  
QY 81 PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100  
DB 278 TTTTGGCTGCGCAGTGTATTATGTGTATGGCCAGACGAGATGGAGTCGTGGGTATTTC 337  
QY 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120  
DB 338 CCCAGGAACCTTGTCTCAAGGAACAGCGTGTACCAAGAACTACCAAGGAAGTTCCACC 397  
QY 121 ThrAspIleAspPhePheCysGlu 128  
DB 398 ACGGATATTGACTTCTTCTCGGAG 421

Search completed: December 30, 2003, 02:01:00  
Job time : 289.193 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 29, 2003, 16:24:24 ; Search time 40.6947 Seconds  
(without alignments)  
1388.315 Million cell updates/sec

Title: US-10-019-455A-6  
Perfect score: 676  
Sequence: 1 MARILLFLPGLVAVCAVHG.....RVQEQATKEVFTDIDFFCE 128

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-O=/cgn2\_1/USPTO\_spool/US10019455/runat\_29122003\_160348\_277/app\_query.fasta\_1.1770  
-DB=Issued Patents NA -QFMT=fastap -SUPFIX=rni -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR\_SCORE=ptc -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEA=SIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10019455 @CGN 1.1 142 @runat\_29122003\_160348\_277 -NCPUS=6 -ICPU=3  
-NO\_WMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:  
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/PTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	257.5	38.1	459	1	US-08-578-649-1
2	253.5	37.5	230	1	US-08-578-649-18
3	232.5	34.4	581	1	US-08-578-649-4
4	210.5	31.1	305	1	US-08-578-649-8
5	190	28.1	596	1	US-08-578-649-24
6	164.5	24.3	3565	1	US-08-578-649-3
7	86.5	12.8	2757	1	US-08-306-691B-48
8	86.5	12.8	2757	5	PCT-US93-06251-79
9	86.5	12.8	4762	4	US-09-300-958A-30
10	85.5	12.6	2793	1	US-07-646-537B-1
11	79	11.7	467	4	US-09-300-958A-28
12	78.5	11.6	5398	3	US-09-356-952-11

13	78	11.5	1878	3	US-08-996-139-14	Sequence 14, Appl
14	78	11.5	1878	3	US-08-995-659-14	Sequence 14, Appl
15	78	11.5	1878	3	US-08-215-649A-14	Sequence 14, Appl
16	78	11.5	1878	4	US-09-577-780-14	Sequence 14, Appl
17	78	11.5	1878	4	US-09-577-800-14	Sequence 14, Appl
18	78	11.5	1878	4	US-09-466-496-14	Sequence 14, Appl
19	78	11.5	1878	4	US-09-871-856-14	Sequence 14, Appl
20	78	11.5	1878	4	US-09-871-231-14	Sequence 14, Appl
21	76	11.2	1579	4	US-09-071-035-83	Sequence 83, Appl
22	76	11.2	1680	4	US-09-071-035-81	Sequence 81, Appl
23	71.5	10.6	1664976	4	US-08-916-421B-1	Sequence 1, Appl
24	70.5	10.4	1992	4	US-09-134-078-57	Sequence 57, Appl
25	70.5	10.4	2043	4	US-09-134-078-11	Sequence 11, Appl
26	70.5	10.4	1664976	4	US-08-916-421B-1	Sequence 1, Appl
27	68	10.1	2873	4	US-08-916-421B-1	Sequence 1, Appl
28	68	10.1	11864	4	US-08-961-527-61	Sequence 193, Appl
29	67	9.9	4403765	3	US-09-103-840A-2	Sequence 61, Appl
30	67	9.9	4411529	3	US-09-103-840A-1	Sequence 2, Appl
31	66.5	9.8	1457	3	US-09-444-053-3	Sequence 1, Appl
32	66.5	9.8	2595	4	US-09-619-353-13	Sequence 3, Appl
33	66.5	9.8	3981	4	US-09-328-352-760	Sequence 13, Appl
34	66.5	9.8	8651	4	US-08-961-527-181	Sequence 760, Appl
35	66	9.8	747	4	US-08-630-915A-39	Sequence 181, Appl
36	66	9.8	840	1	US-08-434-285-7	Sequence 39, Appl
37	66	9.8	840	1	US-08-459-967-7	Sequence 7, Appl
38	66	9.8	840	1	US-08-460-327-7	Sequence 7, Appl
39	66	9.8	840	1	US-08-459-871-7	Sequence 7, Appl
40	66	9.8	840	3	US-09-024-532-1	Sequence 1, Appl
41	66	9.8	840	4	US-09-104-623A-1	Sequence 1, Appl
42	66	9.8	840	4	US-09-019-532-1	Sequence 1, Appl
43	66	9.8	840	4	US-09-417-359A-1	Sequence 1, Appl
44	66	9.8	1110	1	US-08-434-255-5	Sequence 5, Appl
45	66	9.8	1110	1	US-08-459-967-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1

US-08-578-649-1  
; Sequence 1, Application US/08578649  
; Patent No. 5770366  
; GENERAL INFORMATION:  
; APPLICANT: Ulrich Bogdan  
; APPLICANT: Reinhard Butner  
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felfe & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: Wordperfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/578,649  
; FILING DATE: 29-July-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE P 43 24 247.2  
; FILING DATE: 20-July-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Andrew L. Tiajolloff  
; REGISTRATION NUMBER: 31,575  
; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 688-9200  
; TELEFAX: (212) 838-3884



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; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 459 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 40..432
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 40..111
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 112..432
; US-08-578-649-1
Alignment Scores:
Pred. No.: 2,06e-28 Length: 459
Score: 257.50 Matches: 56
Percent Similarity: 60.29% Conservative: 26
Best Local Similarity: 41.18% Mismatches: 41
Query Match: 38.09% Indels: 13
DB: 1 Gaps: 5
US-10-019-455A-6 (1-128) x US-08-578-649-1 (1-459)
QY 1 MetAlaArgIleLeuLeuPheLeuProGlyLeuValAlaValCysAla----- 17
DB 40 ATGGCCCGGTCCCTGGTGGCTT-----GGTGCATCATCTGTGCTGCTCTCTCC 93
QY 18 -----ValHisGlyIlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAsp 34
DB 94 GGACCTGGTGTCCAGGGGTGTCTCTATGCCCAAGCTGGTACCGGAAGCTGTGTGGGAC 153
QY 35 AspGluCysValTyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAsp 54
DB 154 CAGGAGTCAGCCACCTATCTCCATGGCTGTGGCCCTTCAGGAGTACATGGCCCGGAC 213
QY 55 CysArgPheIleAsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLys 74
DB 214 TGCCGATTCCTGACCATTCACCGGGCCCAAGTGTGTGTCTCTCCAGCTG----- 267
QY 75 GluAsnGlyAlaGlyGlu-----PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGlu 93
DB 268 ---AAGGGCCGTGGCGGCTCTCTGGGAGGAGCGGTTTCAGGAGATTTACTATGGAGAT 324
QY 94 MetGlyVal---ValGlyTyrPhePheProArgAsnLeuValLysGluGlnArgValTyrGln 112
DB 325 CTGGCTGCTCGCTGGGCTATTTCCCGAGTAGCATTTGTCGAGAGGAGGACGACCTGAAA 384
QY 113 GluAlaThrLysGluValProThrThrAspIleAspPheCysGlu 128
DB 385 CCTGGCAATCGATGTGAAGACAGACAAATGGGATTTCTACTGCCAG 432
RESULT 2
US-08-578-649-18
; Sequence 18, Application US/08578649
; Patent No. 5770366
; GENERAL INFORMATION:
; APPLICANT: Ulrich Bogdan
; APPLICANT: Reinhard Buttner
; APPLICANT: Brigitte Kaluza
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/578,649
; FILING DATE: 29-July-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 24 247.2
; FILING DATE: 20-July-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Andrew L. Tiajoloiff
; REGISTRATION NUMBER: 31,575
; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 330 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 7..327
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: 4..6
; OTHER INFORMATION: /function= "Startcodon Met"
; US-08-578-649-18
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Pred. No.: 4,85e-28 Length: 330
Score: 233.50 Matches: 49
Percent Similarity: 64.81% Conservative: 21
Best Local Similarity: 45.37% Mismatches: 33
Query Match: 37.50% Indels: 5
DB: 1 Gaps: 3
US-10-019-455A-6 (1-128) x US-08-578-649-18 (1-330)
QY 23 MetAspArgLeuAlaSerLysLysLeuCysAlaAspGluCysValTyrThrIleSer 42
DB 13 ATGCCAAATTTAGCAGATCGTAAATTATGTGCAGATCAGGAGTGCAGCCCTATCTCC 72
QY 43 LeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnValLys 62
DB 73 ATGGCTGTGGCCCTTCAGGACTACATGGCCCCCGACTGCGGATTCCTGACCATTCACCG 132
QY 63 GlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu---Phe 81
DB 133 GGCCAAAGTGTGTATGTCTTCTCCAAAGCTG-----AAGGGCCGTGGCGGCTCTTC 183
QY 82 TrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyVal---ValGlyTyrPhe 100
DB 184 TGGGAGGAGGAGCGTTTCAGGAGATTTACTATGGAGATTCCTGCTGCTCGGCTATTTCC 243
QY 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120
DB 244 CCAGTAGCATTTGTCGAGAGGAGGACGACCCCTGAAACCTGGCAAGTCGATGTGAAGACA 303
QY 121 ThrAspIleAspPheCysGlu 128
DB 304 GACAAATGGGATTTCTACTGCCAG 327
RESULT 3
US-08-578-649-4
; Sequence 4, Application US/08578649
; Patent No. 5770366

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QY 30 LysLeuCysAlaAspAspGluCysValTyrThrIleSerLeuAlaSerAlaGlnGluAsp 49
DB 7 AAGTTTCGGGGGATCAGAGTGCAGCACCTATCTCCATGGCTGTGGCCCTTCAGGAC 66
QY 50 TyrAsnAlaProAspCysArgPheIleAsnValLysGlyGlnGlnIleTyrValTyr 69
DB 67 TACATGGCCCGGACTGCGGATTCCTGACCATTCACCGGGCCCAAGTGGTGTATGCTTC 126
QY 70 SerLysLeuValLysGluAsnGlyAlaGlyGlu---PheTrpAlaGlySerValTyrGly 88
DB 127 TCCAAGCTG-----AAGGGCGCTGGGGGCTCTCTCGGAGGCGAGCGTTCAGGGA 177
QY 89 AspGlyGln---AspGluMetGlyValValGlyTyrPheProArgAsnLeuValLysGlu 107
DB 178 GATTACTATGAGATCTGGTCTCGCTGGCTGGCTATTTCCCAAGTAGCATTTGCCGAG 237
QY 108 GlnArgValTyrGlnGluAlaThrLysGluValProThrThrAspIleAspPhe 126
DB 238 GACCAGACCTGAAACCTGGCAAGTCGATGTGAAGACAGATAAATGGGATTTCTAC 294
RESULT 5
US-08-578-649-24
; Sequence 24, Application US/08578649
; Patent No. 5770366
; GENERAL INFORMATION:
; APPLICANT: Ulrich Bogdan
; APPLICANT: Reinhard Buttner
; APPLICANT: Brigitte Kaluza
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESS: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/578,649
; FILING DATE: 29-July-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 24 247.2
; FILING DATE: 20-July-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Andrew L. Tiajoloif
; REGISTRATION NUMBER: 31,575
; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 596 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(40..111, 40..166, 214..347, 393..503, 549
; LOCATION: ..569)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 40..111
; FEATURE:
; NAME/KEY: exon

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; LOCATION: 40..166
; FEATURE: exon
; NAME/KEY: 214..347
; LOCATION: 214..347
; FEATURE: exon
; NAME/KEY: 393..503
; LOCATION: 393..503
; FEATURE: exon
; NAME/KEY: 549..569
; LOCATION: 549..569
; FEATURE: exon
; NAME/KEY: one-of(194, 369, 527)
; LOCATION: one-of(194, 369, 527)
; OTHER INFORMATION: /note="N in positions 194, 369
; OTHER INFORMATION: and 527 denotes an indefinite number and sequence
; OTHER INFORMATION: of nucleotides "
US-08-578-649-24
Alignment Scores:
Pred. No.: 2,1e-18 Length: 596
Score: 190.00 Matches: 57
Percent Similarity: 45.36% Conservative: 26
Best Local Similarity: 31.15% Mismatches: 39
Query Match: 28.11% Indels: 62
DB: 1 Gaps: 9
US-10-019-455A-6 (1-128) x US-08-578-649-24 (1-596)
QY 1 MetAlaArgIleIleuLeuLeuPheLeuProGlyLeuValAlaValCysAla----- 17
DB 40 ATGCCCCGGTCCCTGGTGGCTT-----GGTGCAATCATCTTGTGTCTGCCTTCC 93
QY 18 -----ValHisGlyIlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAsp 34
DB 94 GGACCTGGTGTGAGGGGTGCTCTATGCTCAAGCTGACCGAAGCTGTGTGGGAC 153
QY 35 AspGluCysValTyr----- 39
DB 154 CAGGAGTGCAGCG-TAAGAATGGGAGGGTGAAGTGGGNCCTTCTATTCTTCCCTA 212
QY 40 ---ThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 58
DB 213 GACCCCTATCTCCATGGCTGTGGCCCTTCAGGACTACATGCCCCCGGACTGCCGATTCCTG 272
QY 59 AsnValLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 78
DB 273 ACCATTCAACGGGGCCAGTGTGTATGTCTTCTCAAGCTG-----AAGGGCGGT 323
QY 79 GlyGlu---PheTrpAlaGlySer----- 85
DB 324 GGGCGGCTCTTCTGGGAGGCGCGTGGTCTTGGAGAGTGAANAGCTTTAACTCCT 383
QY 86 -----ValTyrGlyAspGlyGlnAspGluMetGlyVal---ValGlyTyrPhePro 101
DB 384 CTTCCCGAGGTTTCAGGGAGATTACTATGAGATCTGGCTGTCTCGCTGGGCTATTTCGCC 443
QY 102 ArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThrThr 121
DB 444 AGTAGCATTTGCGAGAGGAGCCAGACCCCTGAACACCTGGCAAGCTGATGTG---AAGACA 500
QY 122 AspIle-----AspPhe----- 125
DB 501 GACGTGGAGTGTATGGGGCTGGCANTTTCCCTTTCTCTTTTTCAGAAATGGGATTC 560
QY 126 PheCysGlu 128
DB 561 TACTGCCAG 569
RESULT 6
US-08-578-649-3
; Sequence 3, Application US/08578649
; Patent No. 5770366
; GENERAL INFORMATION:

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[illegible]

DB:	1	Gaps:	3
US-10-019-455A-6 (1-128) x US-08-306-691B-48 (1-2757)			
QY	44	AlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnValLysGly	63
DB	2325	GCACAAAGCCCGTATGACTTCTGCGCCCGTGAACCGTTTCAGAGTGTGCTCAAGGAGGT	2384
QY	64	GlnGlnIleTyrValTyrSerLysLeuValLysGlnGluAsnGlyAlaGlyGluPheTrpAla	83
DB	2385	GACATCATC-----AAGATCCTTAACAAGAAAGGACAGCAAGGCTGTGGCGCA	2432
QY	84	GlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPheProArgAsn	103
DB	2433	GGGAGATCTATGGCCG-----TATTCTGAA	2495
QY	104	LeuValLysGlnGlnArgValTyrGlnGlu	113
DB	2472	TACGTGGAGGAAGAT-----TATTCTGAA	2495
RESULT 8			
PCT-US93-06251-79			
; Sequence 79, Application PC/TUS9306251			
; GENERAL INFORMATION:			
; APPLICANT: Wickstrom, Eric and Rife, Jason P.			
; TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing			
; NUMBER OF SEQUENCES: 93			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER			
; STREET: 400 Garden City Plaza			
; CITY: Garden City			
; STATE: NY			
; COUNTRY: USA			
; ZIP: 11530			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Patent In Release #1.0, Version #1.25			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: PCT/US93/06251			
; FILING DATE: 19930630			
; CLASSIFICATION:			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Digiglio, Frank S.			
; REGISTRATION NUMBER: 31,346			
; REFERENCE/DOCKET NUMBER: 8586			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: 516-742-4343			
; TELEFAX: 516-742-4366			
; TELEX: 230 901 SANS UR			
; INFORMATION FOR SEQ ID NO: 79:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 2757 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: double			
; TOPOLOGY: linear			
; MOLECULE TYPE: DNA (genomic)			
PCT-US93-06251-79			
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Score:	86.50	Matches:	23
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US-10-019-455A-6 (1-128) x PCT-US93-06251-79 (1-2757)			
QY	44	AlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnValLysGly	63

/ TITLE OF INVENTION: Vav Proto-Oncogene Protein  
/ NUMBER OF SEQUENCES: 14  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESS: Bristol-Myers Squibb Company  
/ STREET: P.O. Box 4000  
/ CITY: Princeton  
/ STATE: New Jersey  
/ COUNTRY: U.S.A.  
/ ZIP: 08543-4000  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/07/646,537B  
/ FILING DATE:  
/ CLASSIFICATION: 435  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Gaul, Timothy J.  
/ REGISTRATION NUMBER: 33,111  
/ REFERENCE/DOCKET NUMBER: DC10  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (609) 921-5901  
/ TELEFAX: (609) 921-4526  
/ INFORMATION FOR SEQ ID NO: 1:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 2793 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: double  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: cDNA  
/ HYPOTHETICAL: NO  
/ FEATURE:  
/ NAME/KEY: CDS  
/ LOCATION: 14..2545  
/ US-07-646-537B-1

Alignment Scores:  
Pred. No.: 0.0355 Length: 2793  
Score: 85.50 Matches: 22  
Percent Similarity: 51.43% Conservative: 14  
Best Local Similarity: 31.43% Mismatches: 21  
Query Match: 12.65% Indels: 13  
DB: 1 Gaps: 3

US-10-019-455A-6 (1-128) x US-07-646-537B-1 (1-2793)

QY 44 AlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnValLysLysGly 63  
Db 2369 GCCAAGCCCGTACGACTCTGTGCCGGGACAGGTGCGAACTGTCCTTAAGAGGGT 2428  
QY 64 GlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGluPheTrpAla 83  
Db 2429 GATATCATC-----AAGATCCTCAATAAGAGGACAGCAAGCGTGGTGGCGT 2476  
QY 84 GlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPheProArgAsn 103  
Db 2477 GGGCAGATTCACGGCGG-----ATCGGTGGTTCCTTCTTAAC 2515  
QY 104 LeuValLysGluGlnArgValTyrGlnGlu 113  
Db 2516 TATGTGGAGGAGAC-----TATTCGGA 2539

RESULT 11

US-09-300-958A-28  
/ Sequence 28, Application US/09300958A  
/ Patent No. 6495319  
/ GENERAL INFORMATION:  
/ APPLICANT: McClelland, Michael  
/ APPLICANT: Welsh, John  
/ APPLICANT: Trenkle, Thomas  
/ TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of

/ TITLE OF INVENTION: Using Same  
/ FILE REFERENCE: P-PH 3457  
/ CURRENT APPLICATION NUMBER: US/09/300,958A  
/ CURRENT FILING DATE: 1999-04-27  
/ PRIOR APPLICATION NUMBER: 60/083,331  
/ PRIOR FILING DATE: 1998-04-27  
/ PRIOR APPLICATION NUMBER: 60/098,070  
/ PRIOR FILING DATE: 1998-08-27  
/ PRIOR APPLICATION NUMBER: 60/118,624  
/ PRIOR FILING DATE: 1999-02-04  
/ NUMBER OF SEQ ID NOS: 85  
/ SOFTWARE: PatentIn Ver. 2.0  
/ SEQ ID NO 28  
/ LENGTH: 467  
/ TYPE: DNA  
/ ORGANISM: Homo sapiens  
/ FEATURE:  
/ NAME/KEY: unsure  
/ LOCATION: (428)  
/ NAME/KEY: unsure  
/ LOCATION: (462)  
/ US-09-300-958A-28

Alignment Scores:  
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Score: 79.00 Matches: 23  
Percent Similarity: 50.00% Conservative: 16  
Best Local Similarity: 29.49% Mismatches: 27  
Query Match: 11.69% Indels: 12  
DB: 4 Gaps: 3

US-10-019-455A-6 (1-128) x US-09-300-958A-28 (1-467)

QY 46 AlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnValLysLysGlyGlnGln 65  
Db 152 GCTCGGTATGACTCTCTGCAAGAGATATGAGAGAGTTCCTCTGTGTGAAGAGGATGTG 211  
QY 66 IleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGluPheTrpAlaGlySer 85  
Db 212 GTGAAGATTTCACAAAGATG-----AGTGCAATGGCTGGTGGAGAGAGAA 259  
QY 86 ValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPheProArgAsnLeuVal 105  
Db 260 GTAATGGCAGG-----GTGGGTGGTTCATCCACATATGTG 298  
QY 106 LysGluGlnArgValTyrGlnGluAlaThrLysGluValProThrThrAspIle 123  
Db 299 ---GGAAGGAGGATGAATAAATCAATCCCGTGTTCACCCCTGCACCAAAATT 349

RESULT 12

US-09-356-952-11  
/ Sequence 11, Application US/09356952  
/ Patent No. 6117663  
/ GENERAL INFORMATION:  
/ APPLICANT: Boriack-Sjodin, Ann  
/ APPLICANT: Margarit, S. M.  
/ APPLICANT: Bor-Sogii, Dafna  
/ APPLICANT: Cole, Philip  
/ APPLICANT: Kuriyan, John  
/ TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE  
/ FILE REFERENCE: 600-1-228N  
/ CURRENT APPLICATION NUMBER: US/09/356,952  
/ CURRENT FILING DATE: 1999-07-19  
/ EARLIER APPLICATION NUMBER: 60/093,631  
/ EARLIER FILING DATE: 1998-07-21  
/ NUMBER OF SEQ ID NOS: 14  
/ SOFTWARE: PatentIn Ver. 2.0  
/ SEQ ID NO 11  
/ LENGTH: 5398  
/ TYPE: DNA  
/ ORGANISM: Saccharomyces cerevisiae  
/ US-09-356-952-11





STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/995,659  
FILING DATE: 22 DECEMBER 1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 60/064,671  
FILING DATE: 14 OCTOBER 1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/813,509  
FILING DATE: 07 MARCH 1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/772,330  
FILING DATE: 23 DECEMBER 1996  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2852-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1878 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Murine  
IMMEDIATE SOURCE:  
LIBRARY: Murine Fetal Liver Epithelium  
CLONE: muRANK  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1875  
US-08-995-659-14

Alignment Scores:  
Pred. No.: 0.245 Length: 1878  
Score: 78.00 Matches: 30  
Percent Similarity: 39.44% Conservative: 26  
Best Local Similarity: 21.13% Mismatches: 48  
Query Match: 11.54% Indels: 38  
DB: 3 Gaps: 5

US-10-019-455A-6 (1-128) x US-08-995-659-14 (1-1878)

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Db 649 GTTCTGCTCTCTCTCATCTCTGTGGTAGTAGTGGCTGCCATCATCTTCGGCGTTTACTAC 708  
Qy 24 AspArg----- 25  
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Qy 26 ---LeuAlaSerLysLysLeuCysAlaAspGluCysValThrIleSerLeuAla 44  
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Qy 65 GlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGluPheTrp----- 82  
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Qy 83 -----AlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100  
Db 922 TGTGGCGCAGGTGGGCCCTGGGCAGAGTCAGAGATTCTAGGACGTT----- 969  
Qy 101 ProArgAsnLeuValLysGlnGlnArgValTyrGlnGluAlaThrLysGluValProThr 120  
Db 970 -----ACACTGTCAGCGAGGTTCAGAGCGGAGGAGACCTCTCGAGGAAGATCCCA 1023  
Qy 121 ThrAsp 122  
Db 1024 GAGGAT 1029  
RESULT 15  
US-09-215-649A-14  
; Sequence 14, Application US/09215649A  
; Patent No. 6271349  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Dirk M.  
; Galibert, Laurent  
; Maraskovsky, Eugene  
; TITLE OF INVENTION: Receptor Activator of NF-kappaB  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation, Law Department  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/215,649A  
FILING DATE: 17-Dec-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/996,139  
FILING DATE: <Unknown>  
APPLICATION NUMBER: USSN 08/813,509  
FILING DATE: 07 MARCH 1997  
APPLICATION NUMBER: USSN 08/772,330  
FILING DATE: 23 DECEMBER 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2851-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1878 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Murine  
IMMEDIATE SOURCE:

Search completed: December 29, 2003, 22:04:58  
Job time : 52.6947 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 22:08:26 ; Search time 1216 Seconds  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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- 1: gb.ba.\*
- 2: gb.htg.\*
- 3: gb.lin.\*
- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pl.\*
- 9: gb.pr.\*
- 10: gb.ro.\*
- 11: gb.sts.\*
- 12: gb.sy.\*
- 13: gb.un.\*
- 14: gb.vi.\*
- 15: em.ba.\*
- 16: em.fun.\*
- 17: em.hum.\*
- 18: em.in.\*
- 19: em.mu.\*
- 20: em.om.\*
- 21: em.or.\*
- 22: em.ov.\*
- 23: em.pat.\*
- 24: em.ph.\*
- 25: em.pl.\*
- 26: em.ro.\*
- 27: em.sts.\*
- 28: em.un.\*
- 29: em.vi.\*
- 30: em.htg.hum.\*
- 31: em.htg.inv.\*
- 32: em.htg.other.\*
- 33: em.htg.mus.\*
- 34: em.htg.pin.\*
- 35: em.htg.rod.\*
- 36: em.htg.mam.\*
- 37: em.htg.vrt.\*
- 38: em.sy.\*
- 39: em.htgo.hum.\*
- 40: em.htgo.mus.\*
- 41: em.htgo.other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	384	100.0	384	6	BD010802	BD010802 Novel pol
2	384	100.0	384	6	BD093103	BD093103 Novel pol
3	384	100.0	521	6	AX358818	AX358818 Sequence
4	384	100.0	521	6	AX362311	AX362311 Sequence
5	384	100.0	521	6	AX454774	AX454774 Sequence
6	384	100.0	521	6	AX491252	AX491252 Sequence
7	384	100.0	846	9	AF233261	AF233261 Homo sapi
8	384	100.0	865	9	AF243505	AF243505 Homo sapi
9	384	100.0	923	6	BD010820	BD010820 Novel pol
10	384	100.0	923	6	BD093121	BD093121 Novel pol
11	384	100.0	1422	9	HS242452	AJ242552 Homo sapi
12	330	85.9	330	6	BD010816	BD010816 Novel pol
13	330	85.9	330	6	BD093117	BD093117 Novel pol
14	287	74.7	384	6	BD010805	BD010805 Novel pol
15	287	74.7	384	6	BD093106	BD093106 Novel pol
16	287	74.7	929	10	AF243504	AF243504 Mus muscu
17	287	74.7	947	6	BD010821	BD010821 Novel pol
18	287	74.7	947	6	BD093122	BD093122 Novel pol
19	287	74.7	958	10	MM024393	AJ243339 Mus muscu
20	287	74.7	1054	10	AF233333	AF233333 Mus muscu
21	285.4	74.3	384	6	BD010835	BD010835 Novel pol
22	285.4	74.3	384	6	BD093136	BD093136 Novel pol
23	252.2	65.7	330	6	BD010817	BD010817 Novel pol
24	252.2	65.7	330	6	BD093118	BD093118 Novel pol
25	249	64.8	330	6	BD010836	BD010836 Novel pol
26	249	64.8	330	6	BD093137	BD093137 Novel pol
27	217.4	56.6	307	6	BD010830	BD010830 Novel pol
28	217.4	56.6	307	6	BD093131	BD093131 Novel pol
29	193.8	50.5	261	6	BD010829	BD010829 Novel pol
30	193.8	50.5	261	6	BD093130	BD093130 Novel pol
31	190.2	49.5	484	5	AF233518	AF233518 Gallus ga
32	142	37.0	232	9	HS252325	AJ252325 Homo sapi
33	142	37.0	121151	9	HS705D16	AL034428 Human DNA
34	134	34.9	466	5	AF233519	AF233519 Rana cate
35	116.4	30.3	358	9	HS252324	AJ252324 Homo sapi
36	114.8	23.9	144765	2	EX510362	BX510362 Mus muscu
37	112.4	29.3	215581	2	AC106161	AC106161 Rattus no
38	109	28.4	259	9	HS252326	AJ252326 Homo sapi
39	67.2	17.5	545	10	RNU67884	U67884 Rattus norv
40	64.8	16.9	396	9	BT007044	BT007044 Homo sapi
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42	64.8	16.9	433	6	AX253435	AX253435 Sequence
43	64.8	16.9	459	6	A42942	A42942 Sequence 1
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45	64.8	16.9	459	6	AX252508	AX252508 Sequence

ALIGNMENTS

RESULT 1	BD010802	BD010802	384 bp	DNA	linear	PAT 31-JAN-2002
LOCUS	BD010802	Novel polypeptide and DNA thereof.				
DEFINITION	BD010802	Novel polypeptide and DNA thereof.				
ACCESSION	BD010802					
VERSION	BD010802.1	GI:18639175				
KEYWORDS	JP 2001069994-A/3.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1 (bases 1 to 384)					
AUTHORS	Ito, Y., Nishi, K., Ogi, K., Mogi, S., Noguchi, Y., Yoshimura, K. and Tanaka, H.					
TITLE	Novel polypeptide and DNA thereof					

JOURNAL	Patent: JP 2001069994-A 3 21-MAR-2001; TAKEDA CHEMICAL INDUSTRIES LTD	TITLE	Novel polypeptide and its DNA
COMMENT	OS Homo sapiens (human) PN JP 2001069994-A/3 PD 21-MAR-2001 PF 29-JUN-2000 JP 2000195911 PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI SHINICHI MOGI PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC A61P19/08, PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC G01N33/53// PC C12P21/08, C12N15/00, A61K37/02, C12N5/00 CC FH Key Location/Qualifiers FT source 1..384 FT /organism='Homo sapiens (human)'. FT Location/Qualifiers	COMMENT	OS Homo sapiens (human) PN WO 0102564-A/3 PD 11-JAN-2001 PF 29-JUN-2000 WO 2000JP004278 PR 30-JUN-1999 JP 99P 186718 PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI MOGI, PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA PC C12N15/12, C12N5/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC A61K38/17, PC A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7088/(C12P21/02, C12R1:19) CC FH Key Location/Qualifiers
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Qy	1 ATGCGAAGAATATGTTACTTTTCCTCCCGGCTCTTGCGCTGTATGTGCTGTCATGGA 60	Qy	1 ATGCGAAGAATATGTTACTTTTCCTCCCGGCTCTTGCGCTGTATGTGCTGTCATGGA 60
Db	1 ATGCGAAGAATATGTTACTTTTCCTCCCGGCTCTTGCGCTGTATGTGCTGTCATGGA 60	Db	1 ATGCGAAGAATATGTTACTTTTCCTCCCGGCTCTTGCGCTGTATGTGCTGTCATGGA 60
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Qy	121 ATTCTCTGCGTAGTGTCTCAAGAAGATTATAATGCCCGGACTGTAGATTCAATTAACGTT 180	Qy	121 ATTCTCTGCGTAGTGTCTCAAGAAGATTATAATGCCCGGACTGTAGATTCAATTAACGTT 180
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Qy	181 AAAAAAGGCGAGAGATCTATGTACTCAAGCTGTGTAAGAAATGAGAGCTGGAGAA 240	Qy	181 AAAAAAGGCGAGAGATCTATGTACTCAAGCTGTGTAAGAAATGAGAGCTGGAGAA 240
Db	181 AAAAAAGGCGAGAGATCTATGTACTCAAGCTGTGTAAGAAATGAGAGCTGGAGAA 240	Db	181 AAAAAAGGCGAGAGATCTATGTACTCAAGCTGTGTAAGAAATGAGAGCTGGAGAA 240
Qy	241 TTTTGGGCTGCGAGTGTATGTTGATGGCCAGACGAGATGGAGTCGTGGGTATTTC 300	Qy	241 TTTTGGGCTGCGAGTGTATGTTGATGGCCAGACGAGATGGAGTCGTGGGTATTTC 300
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Qy	301 CCCAGGAACCTTGGTCAAGGAACAGCGTGTGTACCAAGAAAGTACCAAGGAAGTTCCCAACC 360	Qy	301 CCCAGGAACCTTGGTCAAGGAACAGCGTGTGTACCAAGAAAGTACCAAGGAAGTTCCCAACC 360
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RESULT 2	BD093103	RESULT 3	AX358818
LOCUS	BD093103	LOCUS	AX358818
DEFINITION	Novel polypeptide and its DNA.	DEFINITION	Sequence 71 from Patent WO0193983.
ACCESSION	BD093103	ACCESSION	AX358818
VERSION	BD093103.1 GI:22638691	VERSION	AX358818.1 GI:18675310
KEYWORDS	WO 0102564-A/3.	KEYWORDS	
SOURCE	Homo sapiens (human)	SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens	ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 384)	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,	AUTHORS	

REFERENCE 1  
AUTHORS Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A.,  
Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,  
Watanabe,C.K. and Wood,W.I.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
JOURNAL Patent: WO 0193983-A 71 13-DEC-2001;  
Genentech Inc. (US)  
FEATURES Location/Qualifiers  
source 1. .521  
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Best Local Similarity 100.0%; Pred. No. 3.4e-107;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 38 ATGGCAAGAATATTGTTACTTTTCTCCCGGCTCTTGCGGTGTATGTGCTGTGATGGA 97  
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DB 98 ATATTATGGACCGTCTAGCTTCCAAAGAGCTCTGTGCGATGATGATGCTCTTACT 157  
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DB 158 ATTTCTCTGGCTAGTGTCTCAAGAAGATTATATGCTCCCGGCTGTAGATTCATTAACT 217  
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DB 398 ACGGATATTGACTTCTTCTGCGAG 421  
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LOCUS Sequence 71 from Patent WO0208288.  
DEFINITION AX362311  
ACCESSION AX362311  
VERSION AX362311.1 GI:18694613  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A.,  
Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,  
Watanabe,C.K. and Wood,W.I.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
JOURNAL Patent: WO 0208288-A 71 31-JAN-2002;  
Genentech, Inc. (US)  
FEATURES Location/Qualifiers  
source 1. .521  
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ORIGIN  
Query Match 100.0%; Score 384; DB 6; Length 521;  
Best Local Similarity 100.0%; Pred. No. 3.4e-107;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGGCAAGAATATTGTTACTTTTCTCCCGGCTCTTGCGGTGTATGTGCTGTGATGGA 60  
DB 38 ATGGCAAGAATATTGTTACTTTTCTCCCGGCTCTTGCGGTGTATGTGCTGTGATGGA 97  
QY 61 ATATTATGGACCGTCTAGCTTCCAAAGAGCTCTGTGCGATGATGATGCTCTTACT 120  
DB 98 ATATTATGGACCGTCTAGCTTCCAAAGAGCTCTGTGCGATGATGATGCTCTTACT 157  
QY 121 ATTTCTCTGGCTAGTGTCTCAAGAAGATTATATGCTCCCGGCTGTAGATTCATTAACT 180  
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QY 301 CCCAGAACTTGGTCAAGAACAGCGTGTGTACCAAGAGCTACCAAGAAAGTTCACCACC 360  
DB 338 CCCAGAACTTGGTCAAGAACAGCGTGTGTACCAAGAGCTACCAAGAAAGTTCACCACC 397  
QY 361 ACGGATATTGACTTCTTCTGCGAG 384  
DB 398 ACGGATATTGACTTCTTCTGCGAG 421  
RESULT 5  
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LOCUS Sequence 359 from Patent WO0208284.  
DEFINITION AX454774  
ACCESSION AX454774  
VERSION AX454774.1 GI:21714011  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,  
Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,  
Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.  
and Ye,W.  
TITLE Compositions and methods for the diagnosis and treatment of  
disorders involving angiogenesis  
JOURNAL Patent: WO 0208284-A 359 31-JAN-2002;  
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone  
(US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ;  
Audey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;  
Hillan, Kenneth J. (US) ; Marsters, Scott A. (US) ; Pan, James (US)  
; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;  
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William  
I. (US)  
FEATURES Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 3.4e-107;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Db	45	ATGGCAAGAAATATTGTTACTTTTCTCCCGGCTCTGTGGCTGTATGTGTGTCATGGA	104	Query Match	100.0%;	Score 384;	DB 9;	Length 865;
Qy	61	ATATTTATGACCGCTCTAGCTTCCAGAAGCTCTGTGCAGATGATGATGTCTATACT	120	Best Local Similarity	100.0%;	Pred. No. 3.6e-107;		
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Qy	121	ATTTCTCTGGCTAGTGTCTCAAGAAGATTATAATGCCCGGACTGTAGATTCATTAAAGTT	180				Indels	0;
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Qy	181	AAAAAGGGCAGCAGATCTATGTCTACTCAAGCTGGTAAAGAAAATGGAGCTGGAGAA	240					
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Qy	241	TTTTGGGCTGGCAGTGTATTATGTGTGGCCAGACAGATGGAGTGGTGGTTATTC	300					
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Qy	301	CCCAGGAACCTTGGTCAAGGAACAGGCTGTACCAAGGAAGCTACCAAGGAAGTTCCAC	360					
Db	345	CCCAGGAACCTTGGTCAAGGAACAGGCTGTGTACCAAGGAAGCTACCAAGGAAGTTCCAC	404					
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Db	405	ACGGATATTGACTTCTTCTGCGAG	428					
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AF243505		865 bp	mRNA	linear				
LOCUS								
DEFINITION								
ACCESSION								
VERSION								
KEYWORDS								
SOURCE								
ORGANISM								
REFERENCE								
AUTHORS								
TITLE								
JOURNAL								
MEDLINE								
PUBMED								
REFERENCE								
AUTHORS								
TITLE								
JOURNAL								
FEATURES								
source								
gene								
CDS								
BASE COUNT								
ORIGIN								



	/db_xref="taxon:9606"
BASE COUNT	303 a    147 c    213 g    260 t
ORIGIN	
Query Match	100.0%; Score 384; DB 6; Length 923;
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Matches 384; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
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QY	61 APTATTATGGACCGTCTAGCTCTCCAAGAAGCCTCTGCCAGATCATTAACA 120 
Dd	94 ATATTATGGACCGTCTAGCTCTCCAAGAAGCCTCTGCCAGATCATTAACA 153 
QY	121 ATTCTCTGGCTAGTAGCTCTCAAAGAAGATTAATATGCCCGGAACTAACC 180 
Dd	154 ATTCTCTGGCTAGTAGCTCTCAAAGAAGATTAATATGCCCGGAACTAACC 213 
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Dd	214 AAAAAGGCGCACAGATCTATGTGTA CTCAAAGCTGGTAAAAAGAAAATCG 273 
QY	241 TTTTGGCTGGCAGTGTATGGTGTATGGCCAGGACAGATGGGAGTCGTGGT 300 
Dd	274 TTTTGGCTGGCAGTGTATGGTGTATGGCCAGGACAGATGGGAGTCGTGGT 333 
QY	301 CCAGAACCTTGGTCAAGGAACAGCGCTGTATCCAGGAAGCTACCAAGAA 360 
Dd	334 CCAGGAACCTTGGTCAAGGAACAGCGGTGTATCCAGGAAGCTACCAAGNA 393 
QY	361 ACCGATATTGACTTCTTCTGCGGAG 384 
Dd	394 AC GGATATTGACTTCTTCTGCGGAG 417 
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LOCUS	HSA242552 1422 bp mRNA linear PRI 29-JAN-2001
DE' INITION	Homo sapiens mRNA for melanoma inhibitory activity like protein (MIAL gene).
ACCESSION	AJ242552
VERSION	AJ242552.1 GI:12619172
KEYWORDS	melanoma inhibitory activity like protein; Mial gene.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 Rendtorff,N.D., Frodin,M., Attie-Bitach,T., Vekemans,M. and Tommerup N. Identification and characterization of an inner ear-expressed human melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent polymorphism that abolishes translation Genomics 71 (1), 40-52 (2001) 21100875 PUBMED 11161796
TITLE	2 (Bases 1 to 1422) Rendtorff,N.D. Direct Submission Submitted (21-MAY-1999) Rendtorff N.D., Department of Medical Genetics, Institute of Medical Biochemistry and Genetics, Blegdamvej 3, 2200 Copenhagen N, DENMARK Revised by author 03-AUG-1999 Related sequence: AJ243939 (Mus musculus mRNA) Related sequences: AJ252324 to AJ252327 (genomic sequence). Location/Qualifiers
JOURNAL MEDLINE PUBMED	1. 1422 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /chromosome="20"
REMARK COMMENT FEATURES source	



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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model  
Run on: December 30, 2003, 01:02:37 ; Search time 1278.03 Seconds  
(without alignments)  
7302.593 Million cell updates/sec

Title: US-10-019-455A-4  
Perfect score: 384  
Sequence: 1 atggsaagaatattgtact.....atattgacttttttgcgag 384

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues  
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
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16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pin:\*  
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22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_pmg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match %	Length DB ID	Description
1	287	74.7	398 13	BQ570035
2	287	74.7	488 13	BQ564607
3	287	74.7	514 13	BQ568498
4	287	74.7	534 13	BQ564134

5	287	74.7	560	13	BQ569741
6	287	74.7	608	13	BQ564944
7	287	74.7	630	13	BQ568471
8	287	74.7	696	10	BB611549
9	285.4	74.3	474	13	BQ565637
10	285.4	74.3	684	13	BQ563768
11	271.8	70.8	409	13	BQ566932
12	260.4	67.8	490	13	BQ565411
13	253	65.9	365	13	BY232622
14	236.6	61.6	604	13	BQ567343
15	234.8	61.1	527	10	BE236443
16	198.6	51.7	795	13	BU748241
17	192.8	50.2	280	13	BQ568785
18	192.4	50.1	485	13	BQ565179
19	164.6	42.9	588	13	BQ566776
20	157.4	41.0	349	9	AW021345
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24	119.4	31.1	533	9	AL925854
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29	109	28.4	593	9	AL717905
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32	107.2	27.9	492	9	AA222797
33	101.4	26.4	633	14	CD360404
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36	83.6	21.8	646	13	BQ563767
37	82	21.4	576	12	BI492218
38	67.2	17.5	424	14	CB796570
39	67.2	17.5	544	13	BQ208982
40	67.2	17.5	594	14	CA509768
41	66.4	17.3	507	12	BM674250
42	66	17.2	533	14	W74647
43	64.8	16.9	373	10	BF691795
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ALIGNMENTS

RESULT 1	BQ570035	398 bp	mRNA	linear	EST 19-JUN-2002	
LOCUS	g1143b10.y1	Mouse Organ of Corti	cdna	pBluescript	Mus musculus	cdna
DEFINITION	Clone g1143b10 5', mRNA sequence.					
ACCESSION	BQ570035					
VERSION	BQ570035.1	GI:21473352				
KEYWORDS	EST.					
SOURCE	Mus musculus (house mouse)					
ORGANISM	Mus musculus					
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
REFERENCE	1 (bases 1 to 398)					
AUTHORS	Kachar, B.					
TITLE	EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing					
JOURNAL	Unpublished					
COMMENT	Contact: Kachar, B. Structural Cell Biology National Institute of Deafness and other Communication Disorders 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA Tel: 301-402-1599 Fax: 301-402-1765 Email: kachar@nidcd.nih.gov Plate: 143 row: b column: 10 Seq primer: M13RPI reverse primer (ABI).					
FEATURES	Location/Qualifiers					

source

1. 398  
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 /clone="g1143b10"  
 /sex="male and female"  
 /dev\_stage="Post natal day 5 to 13"  
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 /note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the Micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMuLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGTACGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 105 a 69 c 116 g 108 t  
 ORIGIN  
 Query Match 74.7%; Score 287; DB 13; Length 398;  
 Best Local Similarity 84.3%; Pred. No. 1.6e-75;  
 Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

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Db 13 ATGGCAAGATATTGTTACTTTTCTGGGGCGCTTGTGGTTCTATGTGCCGGCATGGT 72  
 QY 61 ATATTATTGAGCCGCTGTAGCTTCCAGAGAGCTCTGTGCAGATGATGAGTGTCTATACT 120  
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 QY 181 AAAAAAGGCGCAGCAGATCTATGTGTACTCAAGCTGTGTAAAGAAAATGGAGCTGGAGAA 240  
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# RESULT 2 BQ564607 LOCUS

DEFINITION  
 g119h02.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA

ACCESSION  
 BQ564607

VERSION  
 BQ564607.1

KEYWORDS  
 EST.

SOURCE  
 Mus musculus (house mouse)

ORGANISM  
 Mus musculus

REFERENCE  
 1 (bases 1 to 488)

AUTHORS  
 Kachar,B.

TITLE  
 EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing

JOURNAL  
 Unpublished

COMMENT  
 Contact: Kachar,B.  
 Structural Cell Biology  
 National Institute of Deafness and other Communication Disorders  
 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
 Tel: 301-402-1599  
 Fax: 301-402-1765  
 Email: kacharb@nidcd.nih.gov

Seq primer: M13RPI reverse primer (ABI).

Location/Qualifiers

1. 488

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="BALB/c"

/db\_xref="taxon:10090"

/clone="g119h02"

/sex="male and female"

/dev\_stage="Post natal day 5 to 13"

/clone\_lib="Mouse Organ of Corti cDNA pBluescript"

/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory

Tue Dec 30 10:20:46 2003

epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XLI Blue MRF<sup>+</sup> cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 143 a 83 c 135 g 127 t  
ORIGIN  
Query Match 74.7%; Score 287; DB 13; Length 488;  
Best Local Similarity 84.3%; Pred. No. 1.7e-75;  
Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;  
QY 1 ATGGCAAGATATGTTACTTTCTCCCGGGCTTGTGGCTGTATGCTGTGCAATGGA 60  
DB 7 ATGGCAAGATATGTTACTTTCTTGGCTTGGGGCTTGTGGTCTATGTCGGGCGATGGT 66  
QY 61 ATATTATGACCGCTAGCTTCCCAAGAGCTCTGTGCGAGATCATGAGTGTGCTATACT 120  
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DB 187 AAGAAAGGCGAGACATCTATGTTTACTTCCAAAGCTGTGTACAGAAACCGAGCTGGAG 246  
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QY 301 CCAGGACTTGTCTAGGACAGCGTGTGTACCAGGAAGCTACCAAGGAGTTCCACCC 360  
DB 307 CCAGCAACTTGTGTGAAGGAGCGCGTGTATACGAGGCCAAGAGATCCCAACC 366  
QY 361 ACGGATATTGACTTCTTCTCGGA 383  
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ACCESSION BO568498  
VERSION BO568498.1 GI:21471815  
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SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 514)  
AUTHORS Kachar,B.  
TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing  
JOURNAL Unpublished  
COMMENT Contact: Kachar,B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kacharb@nidcd.nih.gov  
Plate: 109 Row: c Column: 02  
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/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated



over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoRI and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on XLI Blue MRF<sup>+</sup> cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 µl of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 147 a 85 c 143 g 139 t  
ORIGIN  
Query Match 74.7%; Score 287; DB 13; Length 514;  
Best Local Similarity 84.3%; Pred. No. 1.8e-75;  
Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;  
QY 1 ATGCGAAGATATGTTACTTTTCTCCCGGCTTGTGCTGTATGCTGTGTCATGGA 60  
Db 5 ATGCGAAGGATATGTTACTTTTCTTGGGGGCTTGTGCTGTATGCTGTGTCATG 64  
QY 61 ATATTATGACCGTCTAGCTTCCAGAGCTCTGTCAGATGATGATGCTGTATGCT 120  
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Db 185 AAGAAGGCGACGATCTATGTTTACTCAAGCTGCTTAAAGAAATGAGCTGGAG 244  
QY 241 TTTTGGCTGCGAGTGTATGTTGTTGATGGCCAGACGAGATGGGAGTCGTGGT 300  
Db 245 TTTTGGCTGCGAGTGTATGTTGTTGATGGCCAGACGAGATGGGAGTCGTGGT 304  
QY 301 CCCAGGAACCTTGGTCAAGGAACACGGTGTGTACAGGAAGCTACAGGAAGTCCACC 360  
Db 305 CCCAGGAACCTTGGTCAAGGAACACGGTGTGTACAGGAAGCTACAGGAAGTCCACC 364  
QY 361 ACGGATATTGACTTCTTCTGGA 383  
Db 365 ACGGATATTGACTTCTTCTGGA 387

RESULT 4  
BQ564134  
LOCUS  
DEFINITION  
BQ564134  
ACCESSION  
BQ564134.1  
VERSION  
BQ564134.1  
KEYWORDS  
EST.  
BQ564134  
gillid01.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA  
clone gillid01 5', mRNA sequence.  
BQ564134.1 GI:21467451

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 534)  
Kachar,B.  
EST analysis of gene expression in the mouse Organ of Corti at the  
onset of hearing  
Unpublished  
Contact: Kachar,B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kachar@nidcd.nih.gov  
Plate: 11 row: d column: 01  
Seq primer: M13RP1 reverse primer (ABI).  
Location/Qualifiers  
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/note="Organ: Organ of Corti; Vector: pBluescript; The  
organ of Corti (OC) was fine dissected from a total of 386  
OC as follows: 102 samples from post-natal (P) day 5; 72  
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;  
14 from P12 and 24 from P13. After killing animals by  
cervical dislocation followed by decapitation, the bulla  
was removed and opened in Leibowitz medium. The bony  
capsule of the cochlea was chipped away, stria vascularis  
and spiral ligament were removed and the sensory  
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Total RNA was extracted using the micro Fasttrack kit  
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Gigapak III Gold Cloning kit (catalog # 237612), both  
from Stratagene (La Jolla, CA, USA), according to  
manufacturer's instructions. Briefly: 1.5 µg mRNA was  
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that contains an Xho I site. First strand synthesis was  
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Moloney murine leukemia virus reverse transcriptase  
(MMLV-RT) and 5-methyl dCTP. The second strand was  
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DNA was blunt ended with pfu DNA polymerase, ligated with  
EcoRI adapters in the presence of ligase and digested  
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over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden)  
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the Uni-ZAP XR vector, which had been predigested with  
EcoRI and Xho I. The phagemid was packaged with Gigapak  
III Gold and, upon titration on XLI Blue MRF<sup>+</sup> cells, the  
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recombinants. Stratagene's ExAssist Interference  
resistance helper phage (catalogue # 211203) was adopted  
to rescue plasmid DNA from the phages. Upon plating of the  
rescued library, individual cDNA clones were selected and  
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purified from 200 µl of saturated culture with the  
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Carlsbad, CA) as instructed by the manufacturer. ESTs from  
the 5' end of the cDNA clones were generated with the  
universal M13 reverse primer (CAGGAACAGCTATGACC) and 25%

Tue Dec 30 10:20:46 2003

strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 155 a 87 c 148 g 144 t

Query Match 74.7%; Score 287; DB 13; Length 534;  
Best Local Similarity 84.3%; Pred. No. 1.8e-75;  
Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 ATGGCAAGATATTGTTACTTTCTCCCGGCTTGTGGCTGATGTGCTGCTGATGGA 60  
DB 3 ATGGCAAGATATTGTTACTTTCTCCCGGCTTGTGGCTGATGTGCTGCTGATGGA 62  
QY 61 ATATTATGGACGCTAGCTTCAAGAGCTCTGCGAGATGATGCTGTCTATACT 120  
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QY 181 AAAAAAGGCGACAGATCTATGTACTCAAGCTGTAAAGAAATGGAGCTGGAGAA 240  
DB 183 AAGAAAGGCGACAGATCTATGTACTCAAGCTGTAAAGAAATGGAGCTGGAGAG 242  
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DB 243 TTTTGGCTGGCAGTGTATGCTGATGCCAGGACGAGTGGAGTGTAGTTATTTC 302  
QY 301 CCCAGGAATCTGGTCAAGGAACAGCGTGTGTACCGAAGCTTACCAAGAACTTCCACC 360  
DB 303 CCCAGCACTTGTGAAGGACGAGCGTGTATACCGAGGCGCCACCAAGAGATCCCAACC 362  
QY 361 ACGGATATTGACTTCTCTGTGGA 383  
DB 363 ACGGATATTGACTTCTCTGTGGA 385

RESULT 5  
BQ569741 560 bp mRNA linear EST 19-JUN-2002  
LOCUS g1135f01.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA  
DEFINITION clone g1135f01 5', mRNA sequence.  
ACCESSION BQ569741  
VERSION BQ569741.1 GI:21473058  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE 1 (bases 1 to 560)  
AUTHORS Kachar, B.  
TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing  
JOURNAL Unpublished  
COMMENT Contact: Kachar, B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kachar@nidcd.nih.gov  
Plate: 135 row: f column: 01  
Seq primer: M13RPL reverse primer (ABI).

FEATURES  
source

Location/Qualifiers  
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/mol\_type="mRNA"  
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/clone="g1135f01"  
/sex="male and female"  
/dev\_stage="Post natal day 5 to 13"  
/clone\_lib="Mouse Organ of Corti cDNA pBluescript"  
/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bulla capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA) according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been preligated with the III Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 1,100,000 recombinants. Stratagene's EXAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 160 a 92 c 154 g 153 t

Query Match 74.7%; Score 287; DB 13; Length 560;

Best Local Similarity 84.3%; Pred. No. 1.8e-75;  
Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 ATGCGAAGATATTGTTACTTTTCTCCCGGCTCTGTGCTGTATGCTGTGTCATGGA 60  
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 Db 6 ATGCGAAGATATTGATTCTTTCTGCGGGCTTGTGTTCTATGTGCGGGCATGTT 65  
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 QY 61 ATATTATGGACCGCTTAGCTTCCAAAGCTCTGTGCGAGATGATGATGTTCTATCT 120  
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 QY 361 ACGGATATTGACTTCTTCTGCGA 383  
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 Db 366 ACGGATATTGACTTCTTCTGCGA 388  
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RESULT 6  
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 clone g127g09 5', mRNA sequence.  
 ACCESSION BQ564944  
 VERSION BQ564944.1 GI:21468261  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Eulagidae; Murinae; Mus.  
 1 (bases 1 to 608)  
 Kachar,B.  
 EST analysis of gene expression in the mouse Organ of Corti at the  
 onset of hearing  
 JOURNAL Unpublished  
 COMMENT Contact: Kachar,B.  
 Structural Cell Biology  
 National Institute of Deafness and other Communication Disorders  
 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
 Tel: 301-402-1599  
 Fax: 301-402-1765  
 Email: kacharb@nidcd.nih.gov  
 Plate: 27 row: G1 column: 09  
 Seq primer: M13R1 reverse primer (ABI).  
 Location/Qualifiers  
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 /mol\_type="mRNA"  
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 /clone\_lib="Mouse Organ of Corti cDNA pBluescript"  
 /note="Organ of Corti; Vector: pBluescript; The  
 organ of Corti (OC) was fine dissected from a total of 386  
 OC as follows: 102 samples from post-natal (P) day 5; 72  
 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;  
 14 from P12 and 24 from P13. After killing animals by  
 cervical dislocation followed by decapitation, the bulla  
 was removed and opened in Leibowitz medium. The bony  
 capsule of the cochlea was chipped away, stria vascularis

## FEATURES

BASE COUNT 169 a 107 c 166 g 166 t  
 ORIGIN  
 Query Match 74.7%; Score 287; DB 13; Length 608;  
 Best Local Similarity 84.3%; Pred. No. 1.9e-75;  
 Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;  
 QY 1 ATGCGAAGATATTGTTACTTTTCTCCCGGCTCTGTGCTGTATGCTGTGTCATGGA 60  
 |||||  
 Db 13 ATGCGAAGATATTGATTCTTTTCTGCGGGCTTGTGTTCTATGTGCGGGCATGTT 72  
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 QY 61 ATATTATGGACCGCTTAGCTTCCAAAGCTCTGTGCGAGATGATGATGTTCTATCT 120  
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 QY 181 AAAAAGGCGACAGATCTATGTCTACTCAAGCTGTGTAAGAAATAAGAGCTGGAGAA 240  
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 Db 193 AAGAAAGGCGACAGATCTATGTTTACTCCAAAGCTGTAAACAGAAAACGAGCTGGAG 252  
 |||||  
 QY 241 TTTTGGGCTGCAGTGTATGTTGATGGCGGACAGAGATGGAGTCTGGGTATTTTC 300  
 |||||

and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on XLI Blue MRF<sup>+</sup> cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert36(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTATGACC) and 25x strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

253 TTTTGGGCTGGCAGTGTATTATGGTGACACACAGATGAGATGGGAATTGTAGGTATTTC 312

301 CCCAGGACTGGTCAAGGACACAGTGTGTACCAAGGAAGTACCAAGGAAGTTCACAC 360

313 CCCAGCACTTGGTGAAGGACAGCGTGTATACCAAGGAGGCCACCAAGGAGATCCAC 372

361 ACGGATATTGACTTCTTCTGCGA 383

373 ACGGATATTGACTTCTTCTGCGA 395

RESULT 7

LOCUS BQ568471 630 bp mRNA linear EST 19-JUN-2002

DEFINITION gi108g04.yl Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA

ACCESSION BQ568471

VERSION BQ568471.1 GI:21471788

KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Kachar,B.

TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing

JOURNAL Unpublished

COMMENT Contact: Kachar,B. Structural Cell Biology National Institute of Deafness and other Communication Disorders 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA Tel: 301-402-1599 Fax: 301-402-1765 Email: kachar@nidcd.nih.gov Plate: 108 row: g column: 04 Seq primer: M3RPI reverse primer (ABI).

Location/Qualifiers

1. .630

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="BALB/c"

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/clone="g1108g04"

/sex="male and female"

/dev\_stage="Post natal day 5 to 13"

/clone\_lib="Mouse Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested

BASE COUNT 178 a 111 c 167 g 174 t

ORIGIN

Query Match 74.7%; Score 287; DB 13; Length 630;

Best Local Similarity 84.3%; Pred. No. 1.9e-75;

Mismatches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 ATGGCAAGAAATATTGTTACTTTTCTCCCGGGCTTGTGGCTGTATGTGTGTCATGGA 60

Db 13 ATGGCAAGAAATATTGTTACTTTTCTCCCGGGCTTGTGGCTGTATGTGTGTCATGGA 72

QY 61 ATATTATGACCGCTAGCTTCCAAAGAGTCTGTGCGAGATGATGAGTGTGTCTACT 120

Db 73 GTATTATGATAAATCTTCTTCTAAGAAGTGTGTGCGAGTGTGTGTCTACT 132

QY 121 ATTCTCTGGCTAGTCTCAAGAGATTTATATCCCGGACGTAGATTCTATTACGTT 180

Db 133 ATTCTCTGGCAGAGACACAGGAAGATTACAATGCCAGACTGTAGTTTCATCGATGC 192

QY 181 AAAAAAGGCGACGAGATCTATGTACTCAAAAGCTGGTAAAGAAATGGAGCTGGAGAA 240

Db 193 AAGAAAGGCGACGAGATCTATGTTTACTCCAAGCTGGTAAACAGAAACGCGCTGGAGAG 252

QY 241 TTTTGGGCTGGCAGTGTATTATGTTATGCGCAGAGATGGAGTGTGGGTATTTC 300

Db 253 TTTTGGGCTGGCAGTGTATTATGTTATGCGCAGAGATGGAGTGTGGGTATTTC 312

QY 301 CCAGCAACTTGTTCAGGACAGCGCTGTACAGGAAGCTACCAAGGAAGTTCACAC 360

Db 313 CCAGCAACTTGTTCAGGACAGCGCTGTATACAGGAAGCTACCAAGGAAGTTCACAC 372

QY 361 ACGGATATTGACTTCTTCTGCGA 383

Db 373 ACGGATATTGACTTCTTCTGCGA 395

RESULT 8

LOCUS BB611549

DEFINITION BB611549 RIKEN full-length enriched, 13 days embryo head Mus

ACCESSION BB611549

VERSION BB611549.1 GI:15393547

696 bp mRNA linear EST 31-AUG-2001

musculus cDNA clone 3110083012 5', mRNA sequence.

[illegible]

/clone\_lib="Mouse Organ of Corti cDNA pBluescript"  
/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dClP. The second strand was synthesized with DNA polymerase and Knaase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on Xli Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's Exassist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert-96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACGTAAGACC) and 25x strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 145 a 78 c 131 g 120 t  
ORIGIN  
Query Match 74.3%; Score 285.4; DB 13; Length 474;  
Best Local Similarity 84.1%; Pred. No. 5.1e-75;  
Matches 322; Conservative 0; Mismatches 61; Indels 0; Gaps 0;  
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DB 374 ACGGATATGACTTCTCTGCGA 396  
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DEFINITION gi06c09.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA  
ACCESSION BQ563768  
VERSION BQ563768.1 GI:21466749  
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SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 684)  
AUTHORS Kachar,B.  
TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing  
JOURNAL Unpublished  
COMMENT Contact: Kachar,B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kachar@nidcd.nih.gov  
Plate: 06 row: c column: 09  
Seq primer: M13RPI reverse primer (ABI).  
Location/Qualifiers  
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/dev\_stage="Post natal day 5 to 13"  
/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to



manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-Rn) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been pre-digested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XLI Blue MRF<sup>+</sup> cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stragatene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTATGACC) and 25x strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 194 a 120 c 178 g 192 t  
ORIGIN  
Query Match 74.3%; Score 285.4; DB 13; Length 684;  
Best Local Similarity 84.1%; Pred. No. 6.1e-75;  
Matches 32; Conservative 0; Mismatches 61; Indels 0; Gaps 0;  
QY 1 ATGCGAAGAAATATGTTATCTTTCTCCCGGGTCTTGTGGCTGTATGCTGTGATGGA 60  
DB 13 ATGCGAGGATATGTTATCTTTCTCCCGGGTCTTGTGGCTGTATGCTGTGATGGA 72  
QY 61 ATATTTATGACCGTCTAGCTTCCAAAGAGCTCTGTGCAGATGATGATGCTGTATCTACT 120  
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QY 121 ATTTCTCTGGCTAGTCTCAAGAGATTATATGCCCCGAGCTGTAGATTCAATTAAGTT 180  
DB 133 ATTTCTCTGGCAGACAGAGAGATTACATGCCCCAGAGCTGTAGGTTTCAATGATGTC 192  
QY 181 AAAAAAGGCGACAGATCTATGTTACTCAAGCTGTGTAAGAAAGAAAGAGAGAGAGAGAG 240  
DB 193 AAGAAAGGCGACAGATCTATGTTACTCAAGCTGTGTAAGAAAGAGAGAGAGAGAGAG 252  
QY 241 TTTTGGGCTGGCAGTGTATGTTATGTTATGTTATGTTATGTTATGTTATGTTATGTTAT 300  
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QY 301 CCAGAGAACTTGTCTAGAGACAGCGTGTACCGAGAGAGAGAGAGAGAGAGAGAGAGAG 360  
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LOCUS  
DEFINITION  
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VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES  
source

BQ566932 409 bp mRNA linear EST 19-JUN-2002  
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clone gi73909 5', mRNA sequence.  
BQ566932 GI:21470249  
BQ566932.1  
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Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Kachar, B.  
1 (base 1 to 409)  
Esr analysis of gene expression in the mouse Organ of Corti at the  
onset of hearing  
Unpublished  
Contact: Kachar, B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: Kachar@nidcd.nih.gov  
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Location/Qualifiers  
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organ of Corti (OC) was fine dissected from a total of 386  
OC as follows: 102 samples from post-natal (P) day 5; 72  
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;  
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columns to enrich for cDNAs greater than 400bp and 1000 bp  
, respectively. The cDNA was then directionally ligated to  
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EcoR I and Xho I. The phagemid was packaged with Gigapack  
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recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200  $\mu$ l of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACACGCTATACC) and 25 $\mu$ g strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 13% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified." 75 c 121 g 111 t

BASE COUNT	102 a	75 c	121 g	111 t	ORIGIN
Query Match	70.8%;	Score 271.8;	DB 13;	Length 409;	
Best Local Similarity	83.6%;	Pred. No. 6.1e-71;			
Matches 320; Conservative	0;	Mismatches 62;	Indels 1;	Gaps 1;	
Qy	1	ATGCGAAGAATAATGTACTTTTCTCCCGGGTCTTGCGCTGTPATGCTGTCATGGGA	60		
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Qy	240	ATTTTGGGCTGGCAGTGTTTATGTGTATGGCCAGGACGAGATGGGAGTCTGGGTATTATT	299		
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Qy	300	CCCCAGGAACCTTGTCAAGGAACAGCGTGTCTTACCAGGAAGCTACCAAGGAAGTTCCCCAC	359		
Db	327	CCCCAGCAACTTGTGTAGGAGCAGCGTGTATACCGAGGCGCCACCAAGGAGATCCCAAC	386		
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**RESULT 12**

BQ565411	490 bp mRNA linear EST 19-JUN-2002
LOCUS	gi37b12.v1 Mouse Organ of Corti cDNA pbluescript Mus musculus cdNA
DEFINITION	clone gi37b12 5', mRNA sequence.
ACCESSION	BQ565411
VERSION	BQ565411.1 GI:21468728
KEYWORDS	EST.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 490)
AUTHORS	Kachar, B.
TITLE	EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing

genes are present in GenBank and have know function: 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT	191 a	77 c	109 g	112 t	1 others
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Db	208 TTTCTCTGGCAAGAGCACAGGAAAATTAACAATGCCCAACTGTAGGTTTCATCGATGCA 267				
QY	182 AAAAGGCGCAGCATCTGTGTACTCAAGCTGTAAAGAAATGGAGCTGGAGAAT 241				
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QY	242 TTTGGGCTGGCAGTGTATTATGTCATGCCAGGACGAGATGGGAGTCGTGGTTATTTC 301				
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DEFINITION	BY232622 RIKEN full-length enriched, adult inner ear Mus musculus				
ACCESSION	BY232622				
VERSION	BY232622.1				
KEYWORDS	EST.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 365)				
	Okazaki, Y., Furuno, M., Sasakawa, T., Adachi, J., Bono, H., Kondo, S., Nishida, I., Osato, N., Saito, R., Suzuki, H., Yananaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D., Corbani, Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Brad, D., Brusic, V., Chothia, C., Forrest, L.B., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawai, H., Kawasawa, Y., Kedzierzki, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pette, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Sempke, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wyntshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura				

M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, M., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.  
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
22354583  
12466851  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehito-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gsc.riken.go.jp/  
URL: http://genome.gsc.riken.go.jp/  
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission  
Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
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RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)  
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Tissues were provided by Kirk W. Beisel (Boys Town National Research Hospital 555 North 30th Street Omaha, NE 68131 USA) whose assistance we gratefully acknowledge. Please visit our web site (http://genome.gsc.riken.go.jp) for further details.  
(http://genome.gsc.riken.go.jp) for further details.

## FEATURES

Location/Qualifiers  
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Best Local Similarity 83.9%; Pred. No. 2.7e-65;  
Matches 286; Conservative 0; Mismatches 55; Indels 0; Gaps 0;  
QY 1 ATGGCAAGAATATTGTTACTTTCTCCCGGGCTTTGGGCTGTATGTGTCGATGGA 60  
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Job time : 1283.36 secs

REFERENCE 1 (bases 1 to 527)  
AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Perlea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and Keale,J.W.  
TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle  
JOURNAL Genome Res. 11 (4), 626-630 (2001)  
MEDLINE 21180013  
PUBMED 11282978  
COMMENT Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390  
Email: smith@email.marc.usda.gov  
Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross\_match with the -minscore 18 and -minmatch 12 options.  
PCR Primers  
FORWARD: AGGAACAGCTATGACCAT  
BACKWARD: GTTTCCTCAGTCACGAGG  
Plate: 54 row: C column: 18  
Seq primer: ATTAGGTGACACTATAG.

FEATURES  
source  
1..527  
Location/Qualifiers  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/clone\_lib="MARC 4BOV"  
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;  
Library made from pooled tissue from day 20 and day 40 embryos."  
embryos. 173 a 94 c 126 g 134 t

BASE COUNT 173 a 94 c 126 g 134 t  
ORIGIN  
Query Match 61.1%; Score 234.8; DB 10; Length 527;  
Best Local Similarity 79.7%; Pred. No. le-59;  
Matches 306; Conservative 0; Mismatches 42; Indels 36; Gaps 1;  
QY 1 ATGGCAAGATATGTTACTTCTCCCGGGTCTTGGCTGTATGCTGTGCTGATGGA 60  
Db 35 ATGGCAAGATGTTGTTTCTTCTCCCGGCTGTGCTGTATGCTGTGCTGATGGA 94  
QY 61 ATATTATGGACCGCTAGCTTCCAGAAAGCTCTGTGCAGATGATGATGTCTATCT 120  
Db 95 ATATTATGGACAGACTTGGTTCCAGAAAGCTGTGTGCAGATGATGATGTCTATCT 154  
QY 121 ATTTCTCTGGCTAGTGTCTCAGAGATTAATGCCCCGAGCTGTAGATTCATTACGTT 180  
Db 155 ATTTCTCTGGCCAGAGCTCAGAGATTAATGCTCCGAGCTGTAGATTCATTACGTT 214  
QY 181 AAAAAAGGCGCAGACATCTATGTGTACTCAAGCTGTGTAAGAAATGGAGCTGGAGAA 240  
Db 215 AAAAAAGGACACTGGATCTATGTTTACTCAAGCTGTGTTATGGCAATCAGTCGTG 269  
QY 241 TTTTGGGCTGGCAGTGTGTTATGGTATGGCCAGACAGATGGAGTCTGGGTATTTC 300  
Db 270 -----AGGATGAATGGGAACCGTGGTATTTC 298  
QY 301 CCCAGGAACCTGGTCAAGAAACAGCGCTGTGTACCAAGGAAGCTACCAAGGAAGTTCCAC 360  
Db 299 CCCAGCACTTGGTCCAGGAACAACATGTGTACCAAGAACCCACCAAGGAAGTTCTTACC 358  
QY 361 ACGGATATTGACTTCTTCTGGCAG 384  
Db 359 ACGGATATTGACTTTTCTTCTGGCAG 382

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 22:01:01 ; Search time 127.462 Seconds  
(without alignments)  
8132.484 Million cell updates/sec

Title: US-10-019-455A-4

Perfect score: 384

Sequence: 1 atggcaagaattgttact.....atattgactttttctgcgag 384

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1985.DAT:*
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8: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1987.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1988.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1989.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1990.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1991.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1992.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1994.DAT:*
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17: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1996.DAT:*
18: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1997.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	384	100.0	384	22	AAF59065
2	384	100.0	387	24	AAH17583
3	384	100.0	426	22	AAH26341
4	384	100.0	521	24	ABL95740
5	384	100.0	521	24	ABL88251
6	384	100.0	521	24	ABK33571
7	384	100.0	891	22	AAH98228
8	384	100.0	891	22	AAH26342

9	384	100.0	923	22	AAF59083	Human MLP nucleoti
10	384	100.0	1201	22	AAH26343	Human growth regul
11	330	85.9	330	22	AAF59079	Human MLP nucleoti
12	287	74.7	384	22	AAF59068	Mouse MLP nucleoti
13	287	74.7	947	22	AAF59084	Mouse MLP nucleoti
14	285.4	74.3	384	22	AAF59098	Rat MLP nucleotide
15	252.2	65.7	330	22	AAF59080	Mouse MLP nucleoti
16	249	64.8	330	22	AAF59099	Rat MLP nucleotide
17	217.4	56.6	307	22	AAF59093	Rat MLP nucleotide
18	193.8	50.5	261	22	AAF59092	Rat MLP nucleotide
19	64.8	16.9	433	22	AAH47783	Recombinant human
20	64.8	16.9	459	16	AAQ84050	Sequence encoding
c 21	64.8	16.9	459	22	AAI70083	Melanoma inhibitor
c 22	64.8	16.9	459	22	AD18732	Human antisense ol
c 23	63.8	16.6	555	23	ABV59229	Human prostate exp
c 24	63.2	16.5	581	16	AAQ84052	Sequence encoding
c 25	62.8	16.4	442	24	ABL63602	Breast cancer rela
c 26	62.8	16.4	442	24	ABL64012	Breast cancer rela
c 27	57.4	14.9	330	16	AAQ84061	Sequence encoding
c 28	54.2	14.1	305	16	AAQ84055	Amplified fragment
c 29	53.6	14.0	300	20	AAZ14828	Human gene express
c 30	53.6	14.0	429	22	AAZ22695	Human cDNA encodin
c 31	53.6	14.0	884	22	AAZ22459	Human cDNA encodin
c 32	53.6	14.0	1230	24	ABO79850	Human TANGO 130 pa
c 33	53.6	14.0	1263	21	AAZ51245	Human TANGO 130 CD
c 34	53.6	14.0	1263	24	ABQ79849	Human TANGO 130 po
c 35	53.6	14.0	4409	23	ABV21035	Human prostate exp
c 36	53.6	14.0	4409	23	ABV23751	Human prostate exp
c 37	53.6	14.0	4409	23	ABV26878	Human prostate exp
c 38	53.6	14.0	4409	23	ABV29625	Human prostate exp
c 39	53.6	14.0	5724	24	ABO79852	Human TANGO 130 po
c 40	53.6	14.0	8121	24	ABO79851	Human TANGO 130 po
c 41	52	13.5	417	22	AAH99775	Human protein enco
c 42	46	12.0	1060	22	AAF92140	Human PRO19670 cDN
c 43	46	12.0	1060	24	ABV74460	Human cDNA encodin
c 44	46	12.0	1060	24	ABL95738	Human angiogenesis
c 45	46	12.0	1060	24	ABL88249	Human PRO19670 cDN

#### ALIGNMENTS

#### RESULT 1

AAF59065

ID AAF59065 standard; DNA; 384 BP.

XX AAF59065;

AC AAF59065;

DT 23-APR-2001 (first entry)

DE Human MLP nucleotide sequence SEQ ID NO:4.

XX MLP; MTA; melanoma inhibitory activity; cancer; bone disease;

XX joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;

XX cardiant; gene therapy; secretory cell function regulator; promoter;

XX inhibitor; ds.

XX Homo sapiens.

OS Homo sapiens.

XX WO200102564-A1.

PN WO200102564-A1.

XX 11-JAN-2001.

PD 11-JAN-2001.

XX 29-JUN-2000; 2000WO-JP04278.

XX 30-JUN-1999; 99JP-0186718.

XX (TAKE ) TAKEDA CHEM IND LTD.

XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;

XX Tanaka H;

XX WPI; 2001-159271/16.









PR	22-JAN-2001;	2001US-0767609.	
PR	28-FEB-2001;	2001US-0796498.	
PR	28-FEB-2001;	2001WO-US06520.	
PR	01-MAR-2001;	2001WO-US06666.	
PR	09-MAR-2001;	2001US-0802706.	
PR	14-MAR-2001;	2001US-0806689.	
PR	22-MAR-2001;	2001US-0816744.	
PR	05-APR-2001;	2001US-0828366.	
PR	10-MAY-2001;	2001US-0854208.	
PR	10-MAY-2001;	2001US-0854280.	
PR	25-MAY-2001;	2001US-0866028.	
PR	25-MAY-2001;	2001US-0866034.	
PR	25-MAY-2001;	2001WO-US17092.	
PR	30-MAY-2001;	2001US-0870574.	
PR	30-MAY-2001;	2001WO-US17443.	
PR	01-JUN-2001;	2001WO-US17800.	
PR	20-JUN-2001;	2001WO-US19692.	
PR	28-JUN-2001;	2001WO-US00000.	
XX	(GETH ) GENENTECH INC.		
PA	(BAKE)/ BAKER K P.		
PA	(FERR)/ FERRARA N.		
PA	(GERR)/ GERRITSEN M E.		
PA	(GERR)/ GERRITSEN M E.		
PA	(GODD)/ GODDARD A.		
PA	(GODO)/ GODOWSKI P J.		
PA	(GURN)/ GURNEY A L.		
PA	(HILL)/ HILLAN K J.		
PA	(MARS)/ MARSTERS S A.		
PA	(PANJ)/ PAN J.		
PA	(PAON)/ PAONI N F.		
PA	(STEP)/ STEPHAN J F.		
PA	(WATA)/ WATANABE C K.		
PA	(WILL)/ WILLIAMS P M.		
PA	(WOOD)/ WOOD W I.		
XX			
PI	Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;		
PI	Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;		
PI	Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;		
XX			
XX	WPI; 2002-171999/22.		
DR	P-FSDB; ABB95602.		
XX			
PT	One hundred and eighty seven nucleic acids encoding PRO polypeptides,		
PT	useful in diagnosis and treatment of cardiovascular (e.g. myocardial		
PT	infarction), endothelial or angiogenic disorders in a mammal -		
XX			
PS	Claim 1; Fig 359; 567pp; English.		
XX			
CC	The present invention provides the protein and coding sequences of human		
CC	PRO proteins. These are useful for treating or diagnosing a		
CC	cardiovascular, endothelial or angiogenic disorder, including cardiac		
CC	hypertrophy, trauma, cancer, age-related macular degeneration,		
CC	atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,		
CC	angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour		
CC	angiogenesis (such as breast carcinoma and liver carcinoma) and wound		
CC	healing. The present sequence is a coding sequence of the invention.		
XX			
SQ	Sequence 521 BP; 167 A; 86 C; 131 G; 137 T; 0 other;		
	Query Match 100.0%; Score 384; DB 24; Length 521;		
	Best Local Similarity 100.0%; Pred. No. 1.1e-113;		
	Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 ATGCGAAGATATTGTTACTTTCTCCCGGGTCTGTGGCTGTATGCTGTGTCATGGA 60		
Db	38 ATGGCAAGATATTGTTACTTTCTCCCGGGTCTGTGGCTGTATGCTGTGTCATGGA 97		
QY	61 ATATTATGGACCGCTAGCTTCCAGAAAGCTCTGTGCAGATGATGATGTGTCTACT 120		
Db	98 ATATTATGGACCGCTAGCTTCCAGAAAGCTCTGTGCAGATGATGATGTGTCTACT 157		
QY	121 ATTTCTCTGGCTAGTGTCTCAAGAAGATTATATCCCGGGACTGTAGATTCAATACGTT 180		

Db	158 ATTTCTCTGGCTAGTGTCTCAAGAAGATTATATGCCCCGACTGTAGATTCAATACGTT 217		
QY	181 AAAAAAGGGCAGCAGATCTATGTGTACTCAAAAGTGTATAAAGAAATGAGCTGGAGAA 240		
Db	218 AAAAAAGGGCAGCAGATCTATGTGTACTCAAAAGTGTATAAAGAAATGAGCTGGAGAA 277		
QY	241 TTTTGGCTGGCAGTGTATTTATGTTGATGGCCAGGACGAGATGGAGTTCGTTATTTTC 300		
Db	278 TTTTGGCTGGCAGTGTATTTATGTTGATGGCCAGGACGAGATGGAGTTCGTTATTTTC 337		
QY	301 CCCAGGAACCTTGTCAAGGAACAGCGTGTGTACCCAGGAAGCTACCAAGGAAGTTCACC 360		
Db	338 CCCAGGAACCTTGTCAAGGAACAGCGTGTGTACCCAGGAAGCTACCAAGGAAGTTCACC 397		
CY	361 ACGGATATTGACTTCTTCTCGGAG 384		
Db	398 ACGGATATTGACTTCTTCTCGGAG 421		
RESULT 5			
ABL88251			
ID	ABL88251 standard; cDNA; 521 BP.		
XX			
AC	ABL88251;		
XX			
DT	16-MAY-2002 (first entry)		
XX			
DE	Human PRO9873 cDNA sequence SEQ ID NO:359.		
XX			
KW	Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;		
KW	vulnary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;		
KW	gene therapy; cardiovascular disorder; endothelial disorder; cancer;		
KW	angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;		
KW	age-related macular degeneration; arterial restenosis; angina;		
KW	rheumatoid arthritis; myocardial infarction; thrombophlebitis;		
KW	lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;		
KW	wound healing; chromosome mapping; gene mapping; gene; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200200690-A2.		
XX			
PD	03-JAN-2002.		
XX			
PF	20-JUN-2001; 2001WO-US19692.		
XX			
PR	23-JUN-2000; 2000US-213637P.		
PR	20-JUL-2000; 2000US-219556P.		
PR	25-JUL-2000; 2000US-220624P.		
PR	25-JUL-2000; 2000US-220664P.		
PR	28-JUL-2000; 2000WO-US20710.		
PR	02-AUG-2000; 2000US-222695P.		
PR	17-AUG-2000; 2000US-0643657.		
PR	23-AUG-2000; 2000WO-US23522.		
PR	24-AUG-2000; 2000WO-US23328.		
PR	07-SEP-2000; 2000US-230978P.		
PR	18-SEP-2000; 2000US-0664610.		
PR	18-SEP-2000; 2000US-0665350.		
PR	24-OCT-2000; 2000US-242922P.		
PR	08-NOV-2000; 2000US-0709238.		
PR	08-NOV-2000; 2000WO-US30952.		
PR	10-NOV-2000; 2000WO-US30873.		
PR	01-DEC-2000; 2000WO-US32678.		
PR	20-DEC-2000; 2000US-0747259.		
PR	20-DEC-2000; 2000WO-US34956.		
PR	22-JAN-2001; 2001US-0767609.		
PR	28-FEB-2001; 2001US-0796498.		
PR	28-FEB-2001; 2001WO-US06520.		
PR	01-MAR-2001; 2001WO-US06666.		
PR	09-MAR-2001; 2001US-0802706.		
PR	14-MAR-2001; 2001US-0806689.		
PR	22-MAR-2001; 2001US-0816744.		

[illegible]

CC fibroblast cells. The PRO polypeptide may also be used as molecular  
 CC weight markers and for tissue typing. The PRO nucleic acids have  
 CC applications in molecular biology, including use as hybridisation probes,  
 CC and in chromosome and gene mapping. ABK33536-ABK33657 represent human  
 CC PRO protein coding sequences of the invention.

XX Sequence 521 BP; 167 A; 86 C; 131 G; 137 T; 0 other;

Query Match 100.0%; Score 384; DB 24; Length 521;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-113;  
 Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCAAGAAATATTGTTACTTTCTCCCGGCTCTTGCGCTGATGCTGTCATGGA 60  
 DB 38 ATGGCAAGAAATATTGTTACTTTCTCCCGGCTCTTGCGCTGATGCTGTCATGGA 97  
 QY 61 ATATTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGATGCTTACT 120  
 DB 98 ATATTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGATGCTTACT 157  
 QY 121 ATTTCTCTGCTAGTCTCAAGAAGATTATATATGCCCCGAGCTGTAGATTCAATTAACGTT 180  
 DB 158 ATTTCTCTGCTAGTCTCAAGAAGATTATATATGCCCCGAGCTGTAGATTCAATTAACGTT 217  
 QY 181 AAAAAAGGGCAGCAGATCTATGTGATCTCAAGCTGTGTAAGAAATATGAGCTGGAGAA 240  
 DB 218 AAAAAAGGGCAGCAGATCTATGTGATCTCAAGCTGTGTAAGAAATATGAGCTGGAGAA 277  
 QY 241 TTTTGGGCTGGCAGTCTTTATGCTGATGCGCAGGACGAGATGGAGTCTGGGTTATTTC 300  
 DB 278 TTTTGGGCTGGCAGTCTTTATGCTGATGCGCAGGACGAGATGGAGTCTGGGTTATTTC 337  
 QY 301 CCCAGGAATTTGCTCAAGGAACAGCGTGTGTACCAAGGAGCTTACCAAGGAAGTTCCACC 360  
 DB 338 CCCAGGAATTTGCTCAAGGAACAGCGTGTGTACCAAGGAGCTTACCAAGGAAGTTCCACC 397  
 QY 361 ACGGATATTGACTTCTTCTGCGAG 384  
 DB 398 ACGGATATTGACTTCTTCTGCGAG 421

## RESULT 7

AAH98228  
 ID AAH98228 standard; cDNA; 891 BP.

AC AAH98228;  
 XX

DT 12-OCT-2001 (first entry)

XX Human EST-derived coding sequence SEQ ID NO: 85.

XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;  
 KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;  
 KW diagnostics; forensic test; gene mapping; genetic disorder;  
 KW biodiversity; gene therapy; nutrition; ss.

XX Homo sapiens.

XX WO200154477-A2.

XX 02-AUG-2001.

XX 25-JAN-2001; 2001WO-US02687.

XX 25-JAN-2000; 2000US-0491404.

XX 17-JUL-2000; 2000US-0617746.

XX 03-AUG-2000; 2000US-0631451.

XX 15-SEP-2000; 2000US-0663870.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;  
 PI Cao Y, Drmanac RA, Zhang J, Werthman T;

XX MPI; 2001-476164/51.  
 DR P-PSDB; AAM23569.

XX Isolated polypeptide for treatment of diseases, diagnostics, raising  
 PT antibodies and research use -

XX Claim 1; Page 236; 1275pp; English.

XX The present invention provides the protein and coding sequences of novel  
 CC proteins from a variety of organisms, including human, dog, cat, horse,  
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea  
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)  
 CC from the organism of interest. They can be used in diagnostics,  
 CC forensics, gene mapping, identification of mutations, to assess  
 CC biodiversity and for nutritional purposes. The present sequence is a cDNA  
 CC of the invention.

XX Sequence 891 BP; 272 A; 146 C; 214 G; 259 T; 0 other;

Query Match 100.0%; Score 384; DB 22; Length 891;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-113;  
 Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCAAGAAATATTGTTACTTTCTCCCGGCTCTTGCGCTGATGCTGTCATGGA 60  
 DB 19 ATGGCAAGAAATATTGTTACTTTCTCCCGGCTCTTGCGCTGATGCTGTCATGGA 78  
 QY 61 ATATTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGATGCTTACT 120  
 DB 79 ATATTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGATGCTTACT 138  
 QY 121 ATTTCTCTGCTAGTCTCAAGAAGATTATATATGCCCCGAGCTGTAGATTCAATTAACGTT 180  
 DB 139 ATTTCTCTGCTAGTCTCAAGAAGATTATATATGCCCCGAGCTGTAGATTCAATTAACGTT 198  
 QY 181 AAAAAAGGGCAGCAGATCTATGTGATCTCAAGCTGTGTAAGAAATATGAGCTGGAGAA 240  
 DB 199 AAAAAAGGGCAGCAGATCTATGTGATCTCAAGCTGTGTAAGAAATATGAGCTGGAGAA 258  
 QY 241 TTTTGGGCTGGCAGTCTTTATGCTGATGCGCAGGACGAGATGGAGTCTGGGTTATTTC 300  
 DB 259 TTTTGGGCTGGCAGTCTTTATGCTGATGCGCAGGACGAGATGGAGTCTGGGTTATTTC 318  
 QY 301 CCCAGGAATTTGCTCAAGGAACAGCGTGTGTACCAAGGAGCTTACCAAGGAAGTTCCACC 360  
 DB 319 CCCAGGAATTTGCTCAAGGAACAGCGTGTGTACCAAGGAGCTTACCAAGGAAGTTCCACC 378  
 QY 361 ACGGATATTGACTTCTTCTGCGAG 384  
 DB 379 ACGGATATTGACTTCTTCTGCGAG 402

## RESULT 8

AAH26342

ID AAH26342 standard; cDNA; 891 BP.

AC AAH26342;  
 XX

XX 02-OCT-2001 (first entry)

XX Human growth regulatory-like polypeptide partial cDNA clone.

XX Growth regulatory-like polypeptide; human; cartilage; melanoma;  
 KW neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;  
 KW ss.

XX Homo sapiens.

XX WO200155332-A2.

XX 02-AUG-2001.

```
PF 25-JAN-2001; 2001WO-US02455.
XX
XX
PR 25-JAN-2000; 2000US-0491404.
PR 02-MAY-2000; 2000US-0563786.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;
PI Drmanac RT;
XX
XX WPI; 2001-483233/52.
XX
XX Isolated human growth regulatory-like polypeptide useful for treating
PT e.g. Alzheimer's disease, cancer, autoimmune disorders, and nervous system
PT hyperproliferative disorders, coagulation disorders, and nervous system
PT disorders -
XX
XX Claim 1; Page 115; 119pp; English.
XX
XX The present sequence is that of a novel nucleic acid that was
CC assembled from human thymus cDNA library-derived Hyseq clone
CC identification number 16372272 (see AAH26341). A recursive
CC algorithm was used to extend the clone by pulling additional
CC sequences from different databases. A full-length sequence (see
CC AAH26343) encoding novel human growth regulatory-like polypeptide
CC (GRLP, see AAB82671) was subsequently obtained. Human GRLP
CC belongs to the same protein family as growth regulatory proteins,
CC growth factors, human melanoma derived growth regulatory protein
CC precursor (64% similarity and 45% identity over 111 amino acids)
CC or melanoma inhibitory activity, cattle cartilage-derived
CC retinoic acid sensitive protein (CD-RAP, 44% identity and 64%
CC similarity over 126 amino acids) and other retinoic acid-sensitive
CC proteins. GRLP polypeptides and polynucleotides of the invention
CC can be used in the prophylaxis, treatment (including gene therapy)
CC and diagnosis of disorders and diseases caused by, or involving,
CC cartilage development and maintenance, inhibition of melanoma cell
CC growth and tumours, including neuroectodermal tumours such as
CC gliomas. The polynucleotides can also be used to design probes
CC and primers, for chromosome and gene mapping, in the recombinant
CC production of protein, in the generation of antisense, ribozyme and
CC peptide-nucleic acid molecules, and to produce transgenic animals.
XX
XX Sequence 891 BP; 272 A; 146 C; 214 G; 259 T; 0 other;
XX
XX Query Match 100.0%; Score 384; DB 22; Length 891;
XX Best Local Similarity 100.0%; Pred. No. 1.4e-113;
XX Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCGAAGATATTGTTACTTTTCTCCCGGCTCTGCGCTGTATGCTGTGTCATGGA 60
DB 19 ATGCGAAGATATTGTTACTTTTCTCCCGGCTCTGCGCTGTATGCTGTGTCATGGA 78
QY 61 ATATTATGACCGCTCTAGCTTCCAGAAGCTCTGTGCAGATGATGCTGTCTACT 120
DB 79 ATATTATGACCGCTCTAGCTTCCAGAAGCTCTGTGCAGATGATGCTGTCTACT 138
QY 121 ATTTCTCTGGCTAGTGTCTCAAGAGATTATTAATCCCGGACTGTAGATTCATTAAAGTT 180
DB 139 ATTTCTCTGGCTAGTGTCTCAAGAGATTATTAATCCCGGACTGTAGATTCATTAAAGTT 198
QY 181 AAAAAAGGGCAGCAGATCTATGTGTCTCAAGAGCTGTGTAAAGAAATGGAGCTGGAGAA 240
DB 199 AAAAAAGGGCAGCAGATCTATGTGTCTCAAGAGCTGTGTAAAGAAATGGAGCTGGAGAA 258
QY 241 TTTTGGGCTGCAGTGTATGTTATGTTATGCGCAGACGAGATGGAGTCTGGGTATTTC 300
DB 259 TTTTGGGCTGCAGTGTATGTTATGTTATGCGCAGACGAGATGGAGTCTGGGTATTTC 318
QY 301 CCCAGGAACCTGGTCAAGACAGCGTGTGTACAGGAGCTACCAAGGAAGTTCCCAACC 360
DB 319 CCCAGGAACCTGGTCAAGACAGCGTGTGTGTACAGGAGCTACCAAGGAAGTTCCCAACC 378
QY 361 ACGGATATTGACTTCTTCTCTGGAG 384
```

```
DB 379 ACGGATATTGACTTCTTCTCTGGAG 402
|||
RESULT 9
AAF59083
ID AAF59083 standard; DNA; 923 BP.
XX
XX AAF59083;
XX
XX 23-APR-2001 (first entry)
XX
XX Human MLP nucleotide sequence SEQ ID NO:29.
XX
XX MLP; MTA; melanoma inhibitory activity; cancer; bone disease;
XX joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
XX cardiant; gene therapy; secretory cell function regulator; promoter;
XX inhibitor; ds.
XX
XX Homo sapiens.
XX
XX WO200102564-A1.
XX
XX 11-JAN-2001.
XX
XX 29-JUN-2000; 2000WO-JP04278.
XX
XX 30-JUN-1999; 99JP-0186718.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
XX Tanaka H;
XX WPI; 2001-159271/16.
XX
XX Safe, low-toxicity secretory cell function-regulatory protein and
XX encoded DNA, applicable as drugs, in diagnosis and development of
XX promoters and inhibitors for preventing or treating e.g. bone and joint
XX diseases -
XX
XX Example 1; Page 99-100; 111pp; Japanese.
XX
XX The present invention describes novel MLP proteins and their encoding
XX DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
XX activities, and can be used in gene therapy and as secretory cell
XX function regulators. The MLP proteins and DNAs can be used in drugs, in
XX the diagnosis and development of promoters and inhibitors for preventing
XX or treating bone and joint diseases as well as pathologic angiogenesis.
XX AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
XX in the exemplification of the present invention.
XX
XX Sequence 923 BP; 303 A; 147 C; 213 G; 260 T; 0 other;
XX
XX Query Match 100.0%; Score 384; DB 22; Length 923;
XX Best Local Similarity 100.0%; Pred. No. 1.5e-113;
XX Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCGAAGATATTGTTACTTTTCTCCCGGCTCTGCGCTGTATGCTGTGTCATGGA 60
DB 34 ATGCGAAGATATTGTTACTTTTCTCCCGGCTCTGCGCTGTATGCTGTGTCATGGA 93
QY 61 ATATTATGACCGCTCTAGCTTCCAGAAGCTCTGTGCAGATGATGCTGTCTACT 120
DB 94 ATATTATGACCGCTCTAGCTTCCAGAAGCTCTGTGCAGATGATGCTGTCTACT 153
QY 121 ATTTCTCTGGCTAGTGTCTCAAGAGATTATTAATCCCGGACTGTAGATTCATTAAAGTT 180
DB 154 ATTTCTCTGGCTAGTGTCTCAAGAGATTATTAATCCCGGACTGTAGATTCATTAAAGTT 213
QY 181 AAAAAAGGGCAGCAGATCTATGTGTCTCAAGAGCTGTGTAAAGAAATGGAGCTGGAGAA 240
DB 214 AAAAAAGGGCAGCAGATCTATGTGTCTCAAGAGCTGTGTAAAGAAATGGAGCTGGAGAA 273
```

QY 241 TTTTGGGTGGCAGTGTATGTTGATGGCCAGACAGATGGAGTCGTGGTTATTTTC 300  
Db 274 TTTTGGGTGGCAGTGTATGTTGATGGCCAGACAGATGGAGTCGTGGTTATTTTC 333  
QY 301 CCCAGGAACCTTGGTCAAGGAACAGCGTGTGTACCAAGGAAGCTTACCAAGGAAGTTCCACCC 360  
Db 334 CCCAGGAACCTTGGTCAAGGAACAGCGTGTGTACCAAGGAAGCTTACCAAGGAAGTTCCACCC 393  
QY 361 ACGGATATTGACTTCTTCTGCGAG 384  
Db 394 ACGGATATTGACTTCTTCTGCGAG 416

RESULT 10  
AAH26343  
ID AAH26343 standard; cDNA; 1201 BP.  
XX  
AC AAH26343;  
XX  
DT 02-OCT-2001 (first entry)  
XX  
DE Human growth regulatory-like polypeptide cDNA.  
XX  
KW Growth regulatory-like polypeptide; human; cartilage; melanoma;  
KW neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;  
KW ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 33..419  
FT /\*tag= a  
FT sig\_peptide 33..101  
FT /\*tag= b  
FT mat\_peptide 102..416  
FT /\*tag= c  
XX  
PN WO200155332-A2.  
XX  
PD 02-AUG-2001.  
XX  
PF 25-JAN-2001; 2001WO-US02455.  
XX  
PR 25-JAN-2000; 2000US-0491404.  
PR 02-MAY-2000; 2000US-0563786.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;  
PI Drmanac RT;  
XX  
DR WPI; 2001-483233/52.  
DR P-PSDB; AAB82671.  
XX  
PT Isolated human growth regulatory-like polypeptide useful for treating  
PT e.g. Alzheimer's disease, cancer, autoimmune disorders,  
PT hyperproliferative disorders, coagulation disorders, and nervous system  
PT disorders -  
XX  
PS Claim 1; Page 115-116; 119pp; English.  
XX  
CC The present sequence is that of a novel nucleic acid encoding  
CC human growth regulatory-like polypeptide (GRLP, see AAB82671).  
CC The sequence was assembled using human thymus cDNA library-derived  
CC Hyseq clone identification number 16372272 (see AAB26341) as seed,  
CC using software programs to pull additional sequences from Hyseq's  
CC proprietary database containing expressed sequence tag sequences,  
CC and by gel sequencing using primers to extend both 5' and 3' ends.  
CC The predicted protein has a mol.wt. of 14 kDa unglycosylated. GRLP  
CC belongs to the same protein family as growth regulatory proteins,  
CC growth factors, human melanoma derived growth regulatory protein  
CC precursor (64% similarity and 45% identity over 111 amino acids)

CC or melanoma inhibitory activity, cattle cartilage-derived  
CC retinoic acid sensitive protein (CD-RAP, 44% identity and 64%  
CC similarity over 126 amino acids) and other retinoic acid-sensitive  
CC proteins. GRIP polypeptides and polynucleotides of the invention  
CC can be used in the prophylaxis, treatment (including gene therapy)  
CC and diagnosis of disorders and diseases caused by, or involving,  
CC cartilage development and maintenance, inhibition of melanoma cell  
CC growth and tumours, including neuroectodermal tumours such as  
CC gliomas. The polynucleotides can also be used to design probes  
CC and primers, for chromosome and gene mapping, in the recombinant  
CC production of protein, in the generation of antisense, ribozyme and  
CC peptide-nucleic acid molecules, and to produce transgenic animals.  
CC They may also have cytokine and cell proliferation or  
CC differentiation activity, stem cell growth factor activity,  
CC haematopoiesis regulating activity, tissue growth activity,  
CC immunosuppressive or immunostimulant activity, activin/inhibin  
CC activity, chemotactic/chemokinetic activity, haemostatic and  
CC thrombolytic activity, use in cancer diagnosis and therapy,  
CC drug screening, receptor/ligand activity, antiinflammatory  
CC activity, and treatment of leukaemia, nervous system disorders,  
CC arthritis and inflammation.  
XX  
SQ Sequence 1201 BP; 357 A; 188 C; 275 G; 381 T; 0 other;  
Query Match 100.0%; Score 384; DB 22; Length 1201;  
Best Local Similarity 100.0%; Pred. No. 1.6e-113;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGGCAAGAAATATTGTTACTTTTCTCCCGGTCTTGTGGCTGTATGTGCTGTGATGGA 60  
Db 33 ATGGCAAGAAATATTGTTACTTTTCTCCCGGTCTTGTGGCTGTATGTGCTGTGATGGA 92  
QY 61 ATATTATGAGCCGTCTAGCTTCCAAAGAGCTCTGTGCAAGATGATGCTGTCTATCT 120  
Db 93 ATATTATGAGCCGTCTAGCTTCCAAAGAGCTCTGTGCAAGATGATGCTGTCTATCT 152  
QY 121 ATTTCTCTGGCTAGTGTCTCAAGAAGATTATAATGCCCGGACTGTAGATTCTTAACGTT 180  
Db 153 ATTTCTCTGGCTAGTGTCTCAAGAAGATTATAATGCCCGGACTGTAGATTCTTAACGTT 212  
QY 181 AAAAAAGGCGCAGCAGATCTATGTACTCAAGCTGGTAAAGAAAATGGAGCTGGAGAA 240  
Db 213 AAAAAAGGCGCAGCAGATCTATGTACTCAAGCTGGTAAAGAAAATGGAGCTGGAGAA 272  
QY 241 TTTTGGGCTGGCAGTGTATGCTGATGCGCCAGGACGAGATGGAGTCTGGGGTTATTTTC 300  
Db 273 TTTTGGGCTGGCAGTGTATGCTGATGCGCCAGGACGAGATGGAGTCTGGGGTTATTTTC 332  
QY 301 CCCAGGAACCTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTTCCACCC 360  
Db 333 CCCAGGAACCTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTTCCACCC 392  
QY 361 ACGGATATTGACTTCTTCTGCGAG 384  
Db 393 ACGGATATTGACTTCTTCTGCGAG 416  
RESULT 11  
AAF59079  
ID AAF59079 standard; DNA; 330 BP.  
XX  
AC AAF59079;  
XX  
DT 23-APR-2001 (first entry)  
XX  
DE Human MLP nucleotide sequence SEQ ID NO:23.  
XX  
KW MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
KW cardant; gene therapy; secretory cell function regulator; promoter;  
KW inhibitor; ds.  
XX  
OS Homo sapiens.

XX	WO200102564-A1.	XX	MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
PN		KW	joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
XX	11-JAN-2001.	KW	cardiant; gene therapy; secretory cell function regulator; promoter;
XX	29-JUN-2000; 2000WO-JP04278.	KW	inhibitor; ds.
XX	30-JUN-1999; 99JP-0186718.	OS	Mus musculus.
XX	(TAKE ) TAKEDA CHEM IND LTD.	XX	WO200102564-A1.
XX	Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;	XX	11-JAN-2001.
PI	Tanaka H;	XX	29-JUN-2000; 2000WO-JP04278.
XX	WPI; 2001-159271/16.	XX	30-JUN-1999; 99JP-0186718.
DR	P-PSDB; AAB69126.	XX	(TAKE ) TAKEDA CHEM IND LTD.
XX	Safe, low-toxicity secretory cell function-regulatory protein and	XX	Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
PT	encoded DNA, applicable as drugs, in diagnosis and development of	PI	Tanaka H;
PT	promoters and inhibitors for preventing or treating e.g. bone and joint	XX	WPI; 2001-159271/16.
PT	diseases -	DR	P-PSDB; AAB69125.
XX	Claim 8; Page 97; 111pp; Japanese.	XX	Safe, low-toxicity secretory cell function-regulatory protein and
XX	The present invention describes novel MLP proteins and their encoding	PT	encoded DNA, applicable as drugs, in diagnosis and development of
CC	DNAS. The MLP proteins and DNAs have antiinflammatory and cardiant	CC	promoters and inhibitors for preventing or treating e.g. bone and joint
CC	activities, and can be used in gene therapy and as secretory cell	PT	diseases -
CC	function regulators. The MLP proteins and DNAs can be used in drugs, in	XX	Claim 11; Page 93; 111pp; Japanese.
CC	the diagnosis and development of promoters and inhibitors for preventing	XX	The present invention describes novel MLP proteins and their encoding
CC	or treating bone and joint diseases as well as pathologic angiogenesis.	CC	DNAS. The MLP proteins and DNAs have antiinflammatory and cardiant
CC	AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used	CC	activities, and can be used in gene therapy and as secretory cell
CC	in the exemplification of the present invention.	CC	function regulators. The MLP proteins and DNAs can be used in drugs, in
XX	Sequence 330 BP; 91 A; 60 C; 91 G; 88 T; 0 other;	CC	the diagnosis and development of promoters and inhibitors for preventing
XX	Query Match 85.9%; Score 330; DB 22; Length 330;	CC	or treating bone and joint diseases as well as pathologic angiogenesis.
XX	Best Local Similarity 100.0%; Pred. No. 2.5e-96;	CC	AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
XX	Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CC	in the exemplification of the present invention.
QY	55 CATGGAATATTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGATGTC 114	XX	Sequence 384 BP; 98 A; 68 C; 111 G; 107 T; 0 other;
Db	1 CATGGAATATTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGATGTC 60	XX	Query Match 74.7%; Score 287; DB 22; Length 384;
QY	115 TATACTATTTCTGGCTAGTGTCTCAAGAGATTATATGCCCGGACTGTAGATTCA 174	XX	Best Local Similarity 84.3%; Pred. No. 2.1e-82;
Db	61 TATACTATTTCTGGCTAGTGTCTCAAGAGATTATATGCCCGGACTGTAGATTCA 120	XX	Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
QY	175 AACCTTAAAGAGGACGACATCTATGTACTCAAGCTGGTAAAGAAAATGGAGCT 234	QY	1 ATGCCAAGATATTGTTACTTTTCTCCCGGCTCTTGGCTGTATGTGTGTCATGGA 60
Db	121 AACGTTAAAGAGGACGACATCTATGTACTCAAGCTGGTAAAGAAAATGGAGCT 180	Db	1 ATGCCAAGGATATTGATTCTTTTGTGGGGGCTTTGGGTTCTATGTGCCGGGATGGT 60
QY	235 GGAGAAATTTGGCTGGCAGTGTATGATGATGATGATGATGATGATGATGATGAT 294	QY	61 ATATTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGATGATGATGAT 120
Db	181 GGAGAAATTTGGCTGGCAGTGTATGATGATGATGATGATGATGATGATGATGAT 240	Db	61 GTATTATGGATAAATTTCTTCTAAGAGTTGTGTGCGGATGAGGATGATGATGAT 120
QY	295 TATTTCCCGAGAACTTGGTCAAGGACAGCGTGTACCGAGAGCTACCAAGGAAGTT 354	QY	121 ATTTCTCTGGCTAGTGTCTCAAGAGATTATATGCCCGGACTGTAGATTCAATTA 180
Db	241 TATTTCCCGAGAACTTGGTCAAGGACAGCGTGTACCGAGAGCTACCAAGGAAGTT 300	Db	121 ATTTCTCTGGCAAGAGCAGAGATTACAAATGCCCGCAGACTGTAGTTTCATCATG 180
QY	355 CCCACACGGATATTGACTTCTTCTGCGAG 384	QY	181 AAAAAGAGGACGACAGATCTATGTACTCAAGCTGGTAAAGAAAATGGAGCTGAG 240
Db	301 CCCACACGGATATTGACTTCTTCTGCGAG 330	Db	181 AAGAAAGGACGACAGATCTATGTACTCAAGCTGGTAAAGAAAATGGAGCTGAG 240
RESULT 12		QY	241 TTTTGGCTGGCAGTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 300
AAF59068		Db	241 TTTTGGCTGGCAGTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 300
ID	AAF59068 standard; DNA; 384 BP.	QY	301 CCCAGGAATTTGGTCAAGGACAGCGTGTACCGAGAGCTACCAAGGAAGTTCC 360
XX	AAF59068;	Db	301 CCCAGGAATTTGGTCAAGGACAGCGTGTACCGAGAGCTACCAAGGAAGTTCC 360
XX	23-APR-2001 (first entry)	QY	361 ACGGATATTGACTTCTTCTGCGA 383
DT		Db	361 ACGGATATTGACTTCTTCTGCGA 383
XX	Mouse MLP nucleotide sequence SEQ ID NO:10.		

```
RESULT 13
ID AAF59084 standard; DNA; 947 BP.
XX
AC AAF59084;
XX
DT 23-APR-2001 (first entry)
XX
DE Mouse MLP nucleotide sequence SEQ ID NO:30.
XX
XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
XX joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
XX cardiant; gene therapy; secretory cell function regulator; promoter;
XX inhibitor; ds.
XX
OS Mus musculus.
XX
PN WO200102564-A1.
XX
PD 11-JAN-2001.
XX
XX 29-JUN-2000; 2000WO-JP04278.
XX
XX 30-JUN-1999; 99JP-0196718.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
XX Tanaka H;
XX WPI; 2001-159271/16.
XX
XX Safe, low-toxicity secretory cell function-regulatory protein and
XX encoded DNA, applicable as drugs, in diagnosis and development of
XX promoters and inhibitors for preventing or treating e.g. bone and joint
XX diseases -
XX
XX Example 2; Page 100-101; 111pp; Japanese.
XX
XX The present invention describes novel MLP proteins and their encoding
XX DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
XX activities, and can be used in gene therapy and as secretory cell
XX function regulators. The MLP proteins and DNAs can be used in drugs, in
XX the diagnosis and development of promoters and inhibitors for preventing
XX or treating bone and joint diseases as well as pathologic angiogenesis.
XX AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
XX in the exemplification of the present invention.
XX
XX Sequence 947 BP; 279 A; 158 C; 221 G; 289 T; 0 other;
XX
XX Query Match 74.7%; Score 287; DB 22; Length 947;
XX Best Local Similarity 84.3%; Pred. No. 3.2e-82;
XX Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
XX
QY 1 ATGGCAAGAATATTGTTACTTTCTCCCGGCTCTGTGGCTGTATGCTGTGATGGA 60
Dd |||||
Dd 11 ATGGCAAGGATATTGATTCTTTTGTCTGGGGCCCTTGTGGTCTATGTGCGGGCATG 70
QY |||||
QY 61 ATATTATGGACCGTCTAGCTTCCAAAGAGCTCTGTGCAGATGATGATGCTGTCTACT 120
Dd |||||
Dd 71 GTATTATATGATTAACCTTCTTCTAAGAGATTGTGTGGGATGAGGAGTGTCTACT 130
QY |||||
QY 121 ATTTCTCTGGCTAGTGTCTCAAGAAGATTATAATGCCCGGCTGTAGATTCATTACGTT 180
Dd |||||
Dd 131 ATTTCTCTGCAAGAGCAGCAGGAAGATTACAAATGCCCAGACTGTAGGTTCTATGTC 190
QY |||||
QY 181 AAAAAGGGCAGCAGATCTATGTGTACTCAAGCTGTAAAGAGCTGTAAGAAATGAGCTGAG 240
Dd |||||
Dd 191 AAGAAAGGGCAGCAGATCTATGTTTACTCAAAGCTGGTAAACAGAAACCGAGCTGGAG 250
QY |||||
QY 241 TTTTGGGCTGGCAGTGTGTTATGTTGATGGCCAGCAGATGGGAGTCGTGGGTTATTTC 300
|||

Db 251 TTTTGGGCTGGCAGTGTGTTATGTTGACCAACAGGATGAGATGGAAATTGTAGTTATTTC 310
QY 301 CCCAGAACTTGGTCAAGGAACAGCGTGTGTACCAAGAGCTACCAAGCAAGTTCCACC 360
Dd |||||
Dd 311 CCCAGCACTTGGTGAAGGAGCAGCGTGTATACCAAGAGGCCACCAAGAGATCCCAACC 370
QY 361 ACGGATATTGACTTCTTCTGCGA 383
Dd |||||
Dd 371 ACGGATATTGACTTCTTCTGTGA 393

RESULT 14
AAF59098
ID AAF59098 standard; DNA; 384 BP.
XX
AC AAF59098;
XX
DT 23-APR-2001 (first entry)
XX
DE Rat MLP nucleotide sequence SEQ ID NO:46.
XX
XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
XX joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
XX cardiant; gene therapy; secretory cell function regulator; promoter;
XX inhibitor; ds.
XX
OS Rattus sp.
XX
PN WO200102564-A1.
XX
PD 11-JAN-2001.
XX
XX 29-JUN-2000; 2000WO-JP04278.
XX
XX 30-JUN-1999; 99JP-0186718.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
XX Tanaka H;
XX WPI; 2001-159271/16.
XX
XX P-PSDB; AAB69130.
XX
XX Safe, low-toxicity secretory cell function-regulatory protein and
XX encoded DNA, applicable as drugs, in diagnosis and development of
XX promoters and inhibitors for preventing or treating e.g. bone and joint
XX diseases -
XX
XX Claim 13; Page 105-106; 111pp; Japanese.
XX
XX The present invention describes novel MLP proteins and their encoding
XX DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
XX activities, and can be used in gene therapy and as secretory cell
XX function regulators. The MLP proteins and DNAs can be used in drugs, in
XX the diagnosis and development of promoters and inhibitors for preventing
XX or treating bone and joint diseases as well as pathologic angiogenesis.
XX AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
XX in the exemplification of the present invention.
XX
XX Sequence 384 BP; 98 A; 72 C; 109 G; 105 T; 0 other;
XX
XX Query Match 74.3%; Score 285.4; DB 22; Length 384;
XX Best Local Similarity 84.1%; Pred. No. 6.9e-82;
XX Matches 322; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
XX
QY 1 ATGGCAAGAATATTGTTACTTTCTCCCGGCTCTGTGGCTGTATGCTGTGATGGA 60
Dd |||||
Dd 1 ATGGCAAGAATATTGATTCTTTTGTCTGGGGCCCTTGTGGCTCTCTGTGCGGGCATG 60
QY |||||
QY 61 ATATTATGGACCGTCTAGCTTCCAAAGAGCTCTGTGCAGATGATGATGCTGTCTACT 120
|||
```



Db 61 ATGTTTATGGATAAACTTCTTCTTAAGAAGTTGTGTGCAGATGAGAGTGTGTCTATACC 120  
 QY 121 ATTCTCTGGCTAGTCTCAAGAAGATTATAATGCCCGGACTGTAGATTCAATTAAAGTT 180  
 Db 121 ATTTCTCTGGCAAGACAGACAGAACTACATGCCCGGACTGTAGTTTCATCATGTC 180  
 QY 181 AAAAAGGGCAGCAGATCTATGTCTACTCAAAAGCTGTAAAGAAATGAGCTGGAGAA 240  
 Db 181 AAGAAGGGCAGCAGATCTATGTCTACTCAAAAGCTGTAAAGAAATGAGCTGGAGCA 240  
 QY 241 TTTTGGCTGCGAGTGTATGTGTGATGGCCAGCAGCAGATGGGAGTCGTGGGTATTTC 300  
 Db 241 TTCTGGCTGCGAGTGTATGTGTGATGGCCAGCAGCAGATGGGAGTGTGGGTATTTC 300  
 QY 301 CCCAGAACTTGGTCAAGGAAACAGCGTGTGTACAGGAAGCTACCAAGGAAAGTTCCCA 360  
 Db 301 CCCAGCAACTTGGTGTAGAGCAACGAGTGTACCAAGGAGGCCACCAAGGAGATTCCCA 360  
 QY 361 ACGGATATTGACTTCTTCTGCGA 383  
 Db 361 ACGGATATTGACTTCTTCTGCGA 383

## RESULT 15

AAF59080  
 ID AAF59080 standard; DNA; 330 BP.

AC AAF59080;

XX 23-APR-2001 (first entry)

XX Mouse MLP nucleotide sequence SEQ ID NO:25.

DE MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
 KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
 KW cardiant; gene therapy; secretory cell function regulator; promoter;  
 KW inhibitor; ds.

XX Mus musculus.

XX WO200102564-A1.

XX 11-JAN-2001.

XX 29-JUN-2000; 2000WO-JP04278.

XX 30-JUN-1999; 95JP-0186718.

XX (TAKE ) TAKEDA CHEM IND LTD.

XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
 PI Tanaka H;

XX WPI: 2001-159271/16.

DR P-PSDB; AAB69127.

PT Safe low-toxicity secretory cell function-regulatory protein and  
 PI encoded DNA, applicable as drugs, in diagnosis and development of  
 PT promoters and inhibitors for preventing or treating e.g. bone and joint  
 PT diseases -

XX Claim 10; Page 98; 111pp; Japanese.

XX The present invention describes novel MLP proteins and their encoding  
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
 CC activities, and can be used in gene therapy and as secretory cell  
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
 CC the diagnosis and development of promoters and inhibitors for preventing  
 CC or treating bone and joint diseases as well as pathologic angiogenesis.  
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
 CC in the exemplification of the present invention.

XX Sequence 330 BP; 91 A; 60 C; 92 G; 87 T; 0 other;

Query Match 65.7%; Score 252.2; DB 22; Length 330;  
 Best Local Similarity 85.4%; Pred. No. 3.4e-71;  
 Matches 281; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 55 CATGGAATATTTATGGACCGTCTAGCTTCCAGAAGCTCTGTGCAGATGATGAGTGTGTC 114  
 Db 1 CATGGTGTATTTATGGATAAACTTTCTTCTTAAGAAGTTGTGTGCGGATGAGAGTGTGTC 60  
 QY 115 TATACTATTTCTCTGGCTAGTGTCTCAAGAAGATTATAATGCCCGGACTGTAGATTCAATT 174  
 Db 61 TATACTATTTCTCTGGCAGAGACACAGGAAGATTCAATGCCCCCAGACTGTAGGTTTCATC 120  
 QY 175 AACGTTAAAAAGGGCAGCAGATCTATGTGTACTCAAGCTGTGTAAAGAAATGAGGCT 234  
 Db 121 GATGTCAAGAAAGGGCAGCAGATCTATGTGTACTCAAGCTGTGTAAAGAAATGAGGCT 180  
 QY 235 GGAGAAATTTTGGCTGGCAGTGTATTTATGGTGTATGTCAGGACGAGATGGGAGTCGTGGGT 294  
 Db 181 GGAGAGTTTGGCTGGCAGTGTATTTATGGTGTATGTCAGGACGAGATGGGAGTTGTAGGT 240  
 QY 295 TATTTCCCGCAGAACTTGGTCAAGAAACAGCGTGTGTACCCAGGAAGCTACCAAGGAAAGTT 354  
 Db 241 TATTTCCCGCAGCAACTTGGTGAAGGAGCAGCGTGTATACCCAGGAGGCCACCAAGGAGATC 300  
 QY 355 CCCACACCGGATATTGACTTCTTCTGCGA 383  
 Db 301 CCAACACCGGATATTGACTTCTTCTGCGA 329

Search completed: December 30, 2003, 02:14:31

Job time : 129.462 secs

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(without alignments)  
4172.254 Million cell updates/sec

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Perfect score: 384  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2244575 seqs, 1713117285 residues 4489150  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA.\*  
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17: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*  
18: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	384	100.0	426	15	US-10-216-038-1
2	384	100.0	521	13	US-10-216-163-71
3	384	100.0	521	13	US-10-218-765-71
4	384	100.0	521	13	US-10-219-063-71
5	384	100.0	521	13	US-10-219-066-71
6	384	100.0	521	13	US-10-219-067-71
7	384	100.0	521	13	US-10-219-068-71
8	384	100.0	521	13	US-10-219-069-71
9	384	100.0	521	13	US-10-219-073-71
10	384	100.0	521	13	US-10-219-475-71
11	384	100.0	521	13	US-10-219-480-71
12	384	100.0	521	13	US-10-219-483-71
13	384	100.0	521	13	US-10-219-525-71
14	384	100.0	521	13	US-10-219-526-71
15	384	100.0	521	13	US-10-219-530-71

16	384	100.0	521	13	US-10-219-531-71	Sequence 71, Appl
17	384	100.0	521	13	US-10-219-532-71	Sequence 71, Appl
18	384	100.0	521	13	US-10-219-533-71	Sequence 71, Appl
19	384	100.0	521	13	US-10-223-081-359	Sequence 359, App
20	384	100.0	521	13	US-10-230-437-71	Sequence 71, Appl
21	384	100.0	521	13	US-10-232-228-71	Sequence 71, Appl
22	384	100.0	521	13	US-10-223-082-359	Sequence 359, App
23	384	100.0	521	15	US-10-227-884-71	Sequence 71, Appl
24	384	100.0	521	15	US-10-230-163-71	Sequence 71, Appl
25	384	100.0	521	15	US-10-230-338-71	Sequence 71, Appl
26	384	100.0	521	15	US-10-218-631-71	Sequence 71, Appl
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38	384	100.0	521	15	US-10-219-479-71	Sequence 71, Appl
39	384	100.0	521	15	US-10-219-481-71	Sequence 71, Appl
40	384	100.0	521	15	US-10-230-260-71	Sequence 71, Appl
41	384	100.0	521	15	US-10-232-231-71	Sequence 71, Appl
42	384	100.0	521	15	US-10-232-233-71	Sequence 71, Appl
43	384	100.0	521	15	US-10-216-165-71	Sequence 71, Appl
44	384	100.0	521	15	US-10-218-956-71	Sequence 71, Appl
45	384	100.0	521	15	US-10-219-468-71	Sequence 71, Appl

ALIGNMENTS

RESULT 1  
US-10-216-038-1  
; Sequence 1, Application US/10216038  
; Publication No. US20030124573A1  
; GENERAL INFORMATION:  
; APPLICANT: Mize, Nancy K  
; APPLICANT: Boyle, Bryan J  
; APPLICANT: Ford, John E  
; APPLICANT: Arterburn, Matthew C  
; APPLICANT: Tang, Y Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Drmanac, Radoje T  
; APPLICANT: Song, Yong  
; APPLICANT: Sjastaad, Michael  
; TITLE OF INVENTION: Methods and Materials Relating to No. US20030124573A1 Growth R  
; TITLE OF INVENTION: Polypeptides and Polynucleotides  
; FILE REFERENCE: HYS-7CIP  
; CURRENT APPLICATION NUMBER: US/10/216,038  
; CURRENT FILING DATE: 2002-08-08  
; PRIOR APPLICATION NUMBER: US 09/563,786  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: US 09/491,404  
; PRIOR FILING DATE: 2000-01-25  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 1  
; LENGTH: 426  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (426)..(426)  
; OTHER INFORMATION: n = A, T, G, or C  
US-10-216-038-1

Query Match 100.0%; Score 384; DB 15; Length 426;  
Best Local Similarity 100.0%; Pred. No. 6.4e-118;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Tue Dec 30 10:20:46 2003

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DB 79 ATATTATGGACCGTCTAGCTTCCAAAGAGCTCTGTGCGAGATGAGTGTCTTACT 138
QY 121 ATTTCTCTGGCTAGTGTCTCAAGAAGATTATAATGCCCGGAGCTGTAGATTCAATTAACGTT 180
DB 139 ATTTCTCTGGCTAGTGTCTCAAGAAGATTATAATGCCCGGAGCTGTAGATTCAATTAACGTT 198
QY 181 AAAAAAGGCGAGAGATCTATGTGTACTCAAGAGCTGGTAAAAAGAAATGGAGCTGGAGAA 240
DB 199 AAAAAAGGCGAGAGATCTATGTGTACTCAAGAGCTGGTAAAAAGAAATGGAGCTGGAGAA 258
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US-10-216-163-71
; Sequence 71, Application US/10216163
; Publication No. US20030149239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin I.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C3
; CURRENT APPLICATION NUMBER: US/10/216,163
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
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; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
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; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-216-163-71

Query Match 100.0%; Score 384; DB 13; Length 521;
Best Local Similarity 100.0%; Pred. No. 7.1e-118;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3

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; Sequence 71, Application US/10218765
; Publication No. US20030187201A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin I.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C19
; CURRENT APPLICATION NUMBER: US/10/218,765
; PRIOR FILING DATE: 2002-08-12
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2 PRIOR APPLICATION NUMBER: 60/079294  
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4 PRIOR APPLICATION NUMBER: 60/079656  
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; PRIOR FILING DATE: 1999-07-20  
 ; PRIOR APPLICATION NUMBER: 60/145698 ✓  
 ; PRIOR FILING DATE: 1999-07-26  
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 ; PRIOR FILING DATE: 1999-07-28  
 ; PRIOR APPLICATION NUMBER: 60/146963 ✓  
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 ; PRIOR FILING DATE: 1999-12-07  
 ; PRIOR APPLICATION NUMBER: 60/169495 ✓  
 ; PRIOR FILING DATE: 1999-12-07  
 ; PRIOR APPLICATION NUMBER: 60/169835 ✓  
 ; PRIOR APPLICATION NUMBER: 60/169835

Query Match 100.0%; Score 384; DB 13; Length 521;  
 Best Local Similarity 100.0%; Pred. No. 7.le-118;  
 Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCGAAGATATTGTTACTTTTCTCCCGGCTCTGTCAGATGATGATGTCATGGA 60  
 DB 38 ATGCGAAGATATTGTTACTTTTCTCCCGGCTCTGTCAGATGATGATGTCATGGA 97  
 QY 61 ATATTTATGGACCGCTAGCTTCCAAAGAGCTCTGTCAGATGATGATGTCATGGA 120  
 DB 98 ATATTTATGGACCGCTAGCTTCCAAAGAGCTCTGTCAGATGATGATGTCATGGA 157  
 QY 121 ATTTCTCTGGCTAGTGTCTCAAGAGATTATATCCCGGCTCTGTCAGATGATGATGTCATGGA 180  
 DB 158 ATTTCTCTGGCTAGTGTCTCAAGAGATTATATCCCGGCTCTGTCAGATGATGATGTCATGGA 217  
 QY 181 AAAAAAGGCGACGAGATCTATGTTGATGGCGACGAGATGTCAGATGATGATGTCATGGA 240  
 DB 218 AAAAAAGGCGACGAGATCTATGTTGATGGCGACGAGATGTCAGATGATGATGTCATGGA 277  
 QY 241 TTTTGGGCTGGCAGTGTGTTATGTTGATGGCGACGAGATGTCAGATGATGATGTCATGGA 300  
 DB 278 TTTTGGGCTGGCAGTGTGTTATGTTGATGGCGACGAGATGTCAGATGATGATGTCATGGA 337  
 QY 301 CCCAGGAACCTTGGTCAAGGAACACCGTGTGTACCAAGAGCTACCAAGGAAGTTCCCAACC 360  
 DB 338 CCCAGGAACCTTGGTCAAGGAACACCGTGTGTACCAAGAGCTACCAAGGAAGTTCCCAACC 397  
 QY 361 ACGGATATTGACTTCTTCTCGGAG 384  
 DB 398 ACGGATATTGACTTCTTCTCGGAG 421

## RESULT 4

US-10-219-063-71  
 ; Sequence 71, Application US/10219063  
 ; Publication No. US20030187202A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Gerritsen, Mary  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stephan, Jean-Philippe F.  
 ; APPLICANT: Watanabe, Colin I.  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
 ; FILE REFERENCE: P3530PIC24  
 ; CURRENT APPLICATION NUMBER: US/10/219.063  
 ; CURRENT FILING DATE: 2002-08-13  
 ; PRIOR APPLICATION NUMBER: 10/1119,480  
 ; PRIOR FILING DATE: 2002-04-09  
 ; PRIOR APPLICATION NUMBER: 60/059113  
 ; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/062287  
 ; PRIOR FILING DATE: 1997-10-17  
 ; PRIOR APPLICATION NUMBER: 60/063549  
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 ; PRIOR FILING DATE: 1998-03-27  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 246  
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 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 US-10-219-063-71

Query Match 100.0%; Score 384; DB 13; Length 521;  
 Best Local Similarity 100.0%; Pred. No. 7.le-118;  
 Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCGAAGATATTGTTACTTTTCTCCCGGCTCTGTCAGATGATGATGTCATGGA 60  
 DB 38 ATGCGAAGATATTGTTACTTTTCTCCCGGCTCTGTCAGATGATGATGTCATGGA 97  
 QY 61 ATATTTATGGACCGCTAGCTTCCAAAGAGCTCTGTCAGATGATGATGTCATGGA 120  
 DB 98 ATATTTATGGACCGCTAGCTTCCAAAGAGCTCTGTCAGATGATGATGTCATGGA 157  
 QY 121 ATTTCTCTGGCTAGTGTCTCAAGAGATTATATCCCGGCTCTGTCAGATGATGATGTCATGGA 180  
 DB 158 ATTTCTCTGGCTAGTGTCTCAAGAGATTATATCCCGGCTCTGTCAGATGATGATGTCATGGA 217  
 QY 181 AAAAAAGGCGACGAGATCTATGTTGATGGCGACGAGATGTCAGATGATGATGTCATGGA 240  
 DB 218 AAAAAAGGCGACGAGATCTATGTTGATGGCGACGAGATGTCAGATGATGATGTCATGGA 277  
 QY 241 TTTTGGGCTGGCAGTGTGTTATGTTGATGGCGACGAGATGTCAGATGATGATGTCATGGA 300  
 DB 278 TTTTGGGCTGGCAGTGTGTTATGTTGATGGCGACGAGATGTCAGATGATGATGTCATGGA 337  
 QY 301 CCCAGGAACCTTGGTCAAGGAACACCGTGTGTACCAAGAGCTACCAAGGAAGTTCCCAACC 360  
 DB 338 CCCAGGAACCTTGGTCAAGGAACACCGTGTGTACCAAGAGCTACCAAGGAAGTTCCCAACC 397  
 QY 361 ACGGATATTGACTTCTTCTCGGAG 384  
 DB 398 ACGGATATTGACTTCTTCTCGGAG 421

## RESULT 5

US-10-219-066-71  
 ; Sequence 71, Application US/10219066  
 ; Publication No. US20030187203A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Gerritsen, Mary

APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3530P1C27  
CURRENT APPLICATION NUMBER: US/10/219,066  
CURRENT FILING DATE: 2002-08-13  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 246  
SEQ ID NO 71  
LENGTH: 521  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-219-066-71

Query Match 100.0%; Score 384; DB 13; Length 521;  
Best Local Similarity 100.0%; Pred. No. 7.1e-118;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGGCAAGATATTGTACTTTCTCCCGGGCTTGTGCTGTATGCTGTCATGGA 60  
Db 38 ATGGCAAGATATTGTACTTTCTCCCGGGCTTGTGCTGTATGCTGTCATGGA 97  
QY 61 ATATTTATGGACCGCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGTGTCTATCT 120  
Db 98 ATATTTATGGACCGCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGTGTCTATCT 157  
QY 121 ATTTCTCTGGCTAGTCTCAAGAGATTATATGCCCCGGGCTAGATTCATTACGTT 180  
Db 158 ATTTCTCTGGCTAGTCTCAAGAGATTATATGCCCCGGGCTAGATTCATTACGTT 217  
QY 181 AAAAAAGGCGCAGACATCTATGTGTACTCAAAGCTGTAAAGAAATGGAGCTGAGAA 240  
Db 218 AAAAAAGGCGCAGACATCTATGTGTACTCAAAGCTGTAAAGAAATGGAGCTGAGAA 277  
QY 241 TTTTGGGCTGGCAGTGTATGTTATGTTGTCAGGACGAGATGGAGTTCGTTATTTTC 300  
Db 278 TTTTGGGCTGGCAGTGTATGTTATGTTGTCAGGACGAGATGGAGTTCGTTATTTTC 337  
QY 301 CCCAGAACTTGGTCAAGCAAGCGTGTGTACCAAGAACTACCAAGAAAGTTCCACCC 360  
Db 338 CCCAGAACTTGGTCAAGCAAGCGTGTGTACCAAGAACTACCAAGAAAGTTCCACCC 397  
QY 361 ACGGATATTGACTTCTTCTGCGAG 384  
Db 398 ACGGATATTGACTTCTTCTGCGAG 421

RESULT 6  
US-10-219-067-71  
Sequence 71, Application US/10219067  
Publication No. US20030187204A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Desnoyers, Luc  
APPLICANT: Gerritsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3530P1C51  
CURRENT APPLICATION NUMBER: US/10/219,067  
CURRENT FILING DATE: 2002-08-14  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 246  
SEQ ID NO 71  
LENGTH: 521  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-219-067-71

Query Match 100.0%; Score 384; DB 13; Length 521;  
Best Local Similarity 100.0%; Pred. No. 7.1e-118;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGGCAAGATATTGTACTTTCTCCCGGGCTTGTGCTGTATGCTGTCATGGA 60  
Db 38 ATGGCAAGATATTGTACTTTCTCCCGGGCTTGTGCTGTATGCTGTCATGGA 97  
QY 61 ATATTTATGGACCGCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGTGTCTATCT 120  
Db 98 ATATTTATGGACCGCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGTGTCTATCT 157  
QY 121 ATTTCTCTGGCTAGTCTCAAGAGATTATATGCCCCGGGCTAGATTCATTACGTT 180  
Db 158 ATTTCTCTGGCTAGTCTCAAGAGATTATATGCCCCGGGCTAGATTCATTACGTT 217  
QY 181 AAAAAAGGCGCAGACATCTATGTGTACTCAAAGCTGTAAAGAAATGGAGCTGAGAA 240  
Db 218 AAAAAAGGCGCAGACATCTATGTGTACTCAAAGCTGTAAAGAAATGGAGCTGAGAA 277  
QY 241 TTTTGGGCTGGCAGTGTATGTTATGTTGTCAGGACGAGATGGAGTTCGTTATTTTC 300  
Db 278 TTTTGGGCTGGCAGTGTATGTTATGTTGTCAGGACGAGATGGAGTTCGTTATTTTC 337

QY	301	CC CAGGAAC TTGGT CAAGGAA CAGCGT GTGTAC CAGGAAG CTACCA AGGAAG TTCCACC	360
Db	338	CC CAGGAAC TTGGT CAAGGAA CAGCGT GTGTAC CAGGAAG CTACCA AGGAAG TTCCACC	397
QY	361	ACGGAT ATTGACT TCTTCTG CGAG	384
Db	398	ACGGAT ATTGACT TCTTCTG CGAG	421

RESULT 7  
US-10-219-068-71  
; Sequence 71, Application US/10219068  
; Publication No. US20030187205A1

Query Match 100.0%; Score 384; DB 13; Length 521;  
Best Local Similarity 100.0%; Pred. No. 7.1e-118;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

61	ATATTTATGACCGTCTAGCTTCCAGAGCTGTGTCAGATGATGAGTGTGTCTACT	120
Qy		
98	ATATTTATGACCGTCTAGCTTCCAGAGCTGTGTCAGATGATGAGTGTGTCTACT	157
Db		
121	ATTCTCTGGCTAGTCTCAAGAGATTATTAATGCCCGGCTCTAGATTCATTAACGTT	180
Qy		

Db	158	ATTCTCTGGCTAGTGCTCAAGAGATTATAATGCCCGAGCTGTAGATTTCATTAAACGTT	211
Qy	181	AAAAAGGCGCAGCAGATCTATGTCTATCAAAAGCTGTATAAGAAATAATGGAGCTGGAGAA	240
Db	218	AAAAAGGCGCAGCAGATCTATGTGTACTCAAGAGCTGTATAAGAAATAATGGAGCTGGAGAA	277
Qy	241	TTTTGGGCTGGCAGTGTATTGTCATGGCCACGACGAGATGGAGTCGTGGGTATTTC	300
Db	278	TTTTGGGCTGGCAGTGTATTGTCATGGCCACGACGAGATGGAGTCGTGGGTATTTC	337
Qy	301	CCACGAACTTGGTCAAGGAAACAGCGTGTGTACACGAGAACTACCAAGGAAAGTTCACAC	360
Db	338	CCACGAACTTGGTCAGGAAACAGCGTGTGTACCAAGGAACTACCAAGGAAAGTTCACAC	397
Qy	361	ACGGATATTGACTTCTTCTGCGAG	384
Db	398	ACGGATATTGACTTCTTCTGCGAG	421

RESULT 8  
US-10-219-069-71  
; Sequence 71, Application US/10219069  
; Publication NO. US20030187206A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

Query Match 100.0%; Score 384; DB 13; Length 521;  
Best Local Similarity 100.0%; Pred. No. 7.1e-118;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGCAAGAAATATTGTAATTTTCTCCCGGGTCTGTGGCTGTATGTGTGTCATGGA 60



Db 38 ATGGCAGATATTGTTCTTCTCCGGCTCTTGGCTGTATGCTGTGCATGGA 97  
QY 61 ATATTTATGACCGCTAGCTTCCAGAGCTCTGTGCAGATGATGCTGTCTATCT 120  
Db 98 ATATTTATGACCGCTAGCTTCCAGAGCTCTGTGCAGATGATGCTGTCTATCT 157  
QY 121 ATTTCTCGCTAGCTTCCAGAGCTTATATGCTCCCGGCTGTAGATTCATTAAAGTT 180  
Db 158 ATTTCTCGCTAGCTTCCAGAGCTTATATGCTCCCGGCTGTAGATTCATTAAAGTT 217  
QY 181 AAAAAAGGCGACAGATCTATGTACTCAAGCTGTTAAAGAAAAATGGAGCTGGAGAA 240  
Db 218 AAAAAAGGCGACAGATCTATGTACTCAAGCTGTTAAAGAAAAATGGAGCTGGAGAA 277  
QY 241 TTTTGGGCTGGCAGTGTATGTGATGCGCAGGACGATGGAGTCTGGGTATTTC 300  
Db 278 TTTTGGGCTGGCAGTGTATGTGATGCGCAGGACGATGGAGTCTGGGTATTTC 337  
QY 301 CCCAGGAATCTGCTCAAGGAACAGCGTGTGTACCGAGAGCTACCAAGAAAGTTCCACC 360  
Db 338 CCCAGGAATCTGCTCAAGGAACAGCGTGTGTACCGAGAGCTACCAAGAAAGTTCCACC 397  
QY 361 ACGGATATTGACTTCTTCTGCGAG 384  
Db 398 ACGGATATTGACTTCTTCTGCGAG 421

RESULT 9  
US-10-219-073-71  
; Sequence 71, Application US/10219073  
; Publication No. US20030187207A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3530PIC52  
; CURRENT APPLICATION NUMBER: US/10/219,073  
; PRIOR FILING DATE: 2002-08-14  
; PRIOR APPLICATION NUMBER: 10/119,480  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/069873  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 246  
; SEQ ID NO 71  
; LENGTH: 521

; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-219-073-71  
Query Match 100.0%; Score 384; DB 13; Length 521;  
Best Local Similarity 100.0%; Pred. No. 7.1e-118;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGGCAGATATTGTTCTTCTCCCGGCTCTTGGCTGTATGCTGTGCATGGA 60  
Db 38 ATGGCAGATATTGTTCTTCTTCTCCCGGCTCTTGGCTGTATGCTGTGCATGGA 97  
QY 61 ATATTTATGACCGCTAGCTTCCAGAGCTCTGTGCAGATGATGCTGTCTATCT 120  
Db 98 ATATTTATGACCGCTAGCTTCCAGAGCTCTGTGCAGATGATGCTGTCTATCT 157  
QY 121 ATTTCTCGCTAGCTTCCAGAGCTTATATGCTCCCGGCTGTAGATTCATTAAAGTT 180  
Db 158 ATTTCTCGCTAGCTTCCAGAGCTTATATGCTCCCGGCTGTAGATTCATTAAAGTT 217  
QY 181 AAAAAAGGCGACAGATCTATGTACTCAAGCTGTTAAAGAAAAATGGAGCTGGAGAA 240  
Db 218 AAAAAAGGCGACAGATCTATGTACTCAAGCTGTTAAAGAAAAATGGAGCTGGAGAA 277  
QY 241 TTTTGGGCTGGCAGTGTATGTGATGCGCAGGACGATGGAGTCTGGGTATTTC 300  
Db 278 TTTTGGGCTGGCAGTGTATGTGATGCGCAGGACGATGGAGTCTGGGTATTTC 337  
QY 301 CCCAGGAATCTGCTCAAGGAACAGCGTGTGTACCGAGAGCTACCAAGAAAGTTCCACC 360  
Db 338 CCCAGGAATCTGCTCAAGGAACAGCGTGTGTACCGAGAGCTACCAAGAAAGTTCCACC 397  
QY 361 ACGGATATTGACTTCTTCTGCGAG 384  
Db 398 ACGGATATTGACTTCTTCTGCGAG 421

RESULT 10  
US-10-219-475-71  
; Sequence 71, Application US/10219475  
; Publication No. US20030187208A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3530PIC49  
; CURRENT APPLICATION NUMBER: US/10/219,475  
; PRIOR FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: 10/119,480  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/069873  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294

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; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-475-71

Query Match      100.0%; Score 384; DB 13; Length 521;
Best Local Similarity 100.0%; Pred. No. 7.1e-118;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 ATGGCAAGATATTGTTACTTTTCTCCGGGCTCTTGCGCTGTATGCTGTGTCATGGA 60
DB  38 ATGGCAAGATATTGTTACTTTTCTCCGGGCTCTTGCGCTGTATGCTGTGTCATGGA 97

QY  61 ATATTATGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGATGCTGTATAT 120
DB  98 ATATTATGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGATGCTGTATAT 157

QY  121 ATTTCTGCGCTAGTCTCAAGAGATTATTAATGCCCGGACTGTAGATTCAATTAACGTT 180
DB  158 ATTTCTGCGCTAGTCTCAAGAGATTATTAATGCCCGGACTGTAGATTCAATTAACGTT 217

QY  181 AAAAAAGGCGACGAGATCTATGTCTCAAGCTGGTAAAGAAATGGAGCTGGAGAA 240
DB  218 AAAAAAGGCGACGAGATCTATGTCTCAAGCTGGTAAAGAAATGGAGCTGGAGAA 277

QY  241 TTTTGGGCTGCGAGTGTATGTTGATGCGCAGACAGATGGAGTCGCGGTTATTTC 300
DB  278 TTTTGGGCTGCGAGTGTATGTTGATGCGCAGACAGATGGAGTCGCGGTTATTTC 337

QY  301 CCCAGGAACTTGGTCAAGGACAGCGTGTGTACCAAGAGCTTACCAAGAGATTCCCAACC 360
DB  338 CCCAGGAACTTGGTCAAGGACAGCGTGTGTACCAAGAGCTTACCAAGAGATTCCCAACC 397

QY  361 ACGGATATTGACTTCTTCTGCGAG 384
DB  398 ACGGATATTGACTTCTTCTGCGAG 421

RESULT 11
US-10-219-480-71
; Sequence 71, Application US/10219480
; Publication No. US20030187209A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C38
; CURRENT APPLICATION NUMBER: US/10/219,480
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-480-71

Query Match      100.0%; Score 384; DB 13; Length 521;
Best Local Similarity 100.0%; Pred. No. 7.1e-118;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 ATGGCAAGATATTGTTACTTTTCTCCGGGCTCTTGCGCTGTATGCTGTGTCATGGA 60
DB  38 ATGGCAAGATATTGTTACTTTTCTCCGGGCTCTTGCGCTGTATGCTGTGTCATGGA 97

QY  61 ATATTATGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGATGCTGTATAT 120
DB  98 ATATTATGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGATGCTGTATAT 157

QY  121 ATTTCTGCGCTAGTCTCAAGAGATTATTAATGCCCGGACTGTAGATTCAATTAACGTT 180
DB  158 ATTTCTGCGCTAGTCTCAAGAGATTATTAATGCCCGGACTGTAGATTCAATTAACGTT 217

QY  181 AAAAAAGGCGACGAGATCTATGTCTCAAGCTGGTAAAGAAATGGAGCTGGAGAA 240
DB  218 AAAAAAGGCGACGAGATCTATGTCTCAAGCTGGTAAAGAAATGGAGCTGGAGAA 277

QY  241 TTTTGGGCTGCGAGTGTATGTTGATGCGCAGACAGATGGAGTCGCGGTTATTTC 300
DB  278 TTTTGGGCTGCGAGTGTATGTTGATGCGCAGACAGATGGAGTCGCGGTTATTTC 337

QY  301 CCCAGGAACTTGGTCAAGGACAGCGTGTGTACCAAGAGCTTACCAAGAGATTCCCAACC 360
DB  338 CCCAGGAACTTGGTCAAGGACAGCGTGTGTACCAAGAGCTTACCAAGAGATTCCCAACC 397

QY  361 ACGGATATTGACTTCTTCTGCGAG 384
DB  398 ACGGATATTGACTTCTTCTGCGAG 421

RESULT 12
US-10-219-483-71
; Sequence 71, Application US/10219483
; Publication No. US20030187210A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C38
; CURRENT APPLICATION NUMBER: US/10/219,480
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
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FILE REFERENCE: P3530P1C43  
CURRENT APPLICATION NUMBER: US/10/219,483  
CURRENT FILING DATE: 2002-08-13  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 246  
SEQ ID NO 71  
LENGTH: 521  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-219-483-71

Query Match 100.0%; Score 384; DB 13; Length 521;  
Best Local Similarity 100.0%; Pred. No. 7,1e-118;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGGCAAGAATATGTTACTTTTCTCCCGGGTCTTGCGCTGTATGCTGTGTCATGGA	60
Db	38	ATGGCAAGAATATGTTACTTTTCTCCCGGGTCTTGCGCTGTATGCTGTGTCATGGA	97
QY	61	ATATTATGACCGTCTAGCTTCCCAAGAGCTCTGTCAGATGATGAGTGTCTATCT	120
Db	98	ATATTATGACCGTCTAGCTTCCCAAGAGCTCTGTCAGATGATGAGTGTCTATCT	157
QY	121	ATTCTCTCGGTAGTGTCTCAAGAGATTAATGCTCCCGGACTGTAGATTCTTAACGTT	180
Db	158	ATTCTCTCGGTAGTGTCTCAAGAGATTAATGCTCCCGGACTGTAGATTCTTAACGTT	217
QY	181	AAAAAGGCGCAGAGATCTATGTGTACTCAAGCTGGTAAAGAAATGGAGCTGGAGAA	240
Db	218	AAAAAGGCGCAGAGATCTATGTGTACTCAAGCTGGTAAAGAAATGGAGCTGGAGAA	277
QY	241	TTTTGGCTGGCAGTGTATTATGTTATGTCGTCAGGACGAGATGGAGTCTGGTATTTC	300
Db	278	TTTTGGCTGGCAGTGTATTATGTTATGTCGTCAGGACGAGATGGAGTCTGGTATTTC	337
QY	301	CCAGGAATCTGGTCAAGGAACAGCGTGTGTACCCAGGAAGCTACCAAGGAAGTTCCACC	360
Db	338	CCAGGAATCTGGTCAAGGAACAGCGTGTGTACCCAGGAAGCTACCAAGGAAGTTCCACC	397
QY	361	ACGGATATTGACTTCTTCTCGGAG	384
Db	398	ACGGATATTGACTTCTTCTCGGAG	421

## RESULT 13

US-10-219-525-71  
Sequence 71, Application US/10219525  
Publication NO. US2003018721A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Desnoyers, Luc  
APPLICANT: Gerritsen, Mary  
APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
ACIDS  
FILE REFERENCE: P3530P1C29  
CURRENT APPLICATION NUMBER: US/10/219,525  
CURRENT FILING DATE: 2002-08-13  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 246  
SEQ ID NO 71  
LENGTH: 521  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-219-525-71

Query Match 100.0%; Score 384; DB 13; Length 521;  
Best Local Similarity 100.0%; Pred. No. 7,1e-118;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	38	ATGGCAAGAATATGTTACTTTTCTCCCGGGTCTTGCGCTGTATGCTGTGTCATGGA	97
QY	61	ATATTATGACCGTCTAGCTTCCCAAGAGCTCTGTCAGATGATGAGTGTCTATCT	120
Db	98	ATATTATGACCGTCTAGCTTCCCAAGAGCTCTGTCAGATGATGAGTGTCTATCT	157
QY	121	ATTCTCTCGGTAGTGTCTCAAGAGATTAATGCTCCCGGACTGTAGATTCTTAACGTT	180
Db	158	ATTCTCTCGGTAGTGTCTCAAGAGATTAATGCTCCCGGACTGTAGATTCTTAACGTT	217
QY	181	AAAAAGGCGCAGAGATCTATGTGTACTCAAGCTGGTAAAGAAATGGAGCTGGAGAA	240
Db	218	AAAAAGGCGCAGAGATCTATGTGTACTCAAGCTGGTAAAGAAATGGAGCTGGAGAA	277
QY	241	TTTTGGCTGGCAGTGTATTATGTTATGTCGTCAGGACGAGATGGAGTCTGGTATTTC	300
Db	278	TTTTGGCTGGCAGTGTATTATGTTATGTCGTCAGGACGAGATGGAGTCTGGTATTTC	337
QY	301	CCAGGAATCTGGTCAAGGAACAGCGTGTGTACCCAGGAAGCTACCAAGGAAGTTCCACC	360
Db	338	CCAGGAATCTGGTCAAGGAACAGCGTGTGTACCCAGGAAGCTACCAAGGAAGTTCCACC	397
QY	361	ACGGATATTGACTTCTTCTCGGAG	384
Db	398	ACGGATATTGACTTCTTCTCGGAG	421

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RESULT 14
US-10-219-526-71
; Sequence 71, Application US/10219526
; Publication No. US20030187212A1
; GENERAL INFORMATION:
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; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC41
; CURRENT APPLICATION NUMBER: US/10/219,526
; CURRENT FILING DATE: 2002-08-13
; PRIOR FILING DATE: 2002-04-09
; PRIOR FILING DATE: 1997-09-17
; PRIOR FILING DATE: 1997-10-17
; PRIOR FILING DATE: 1997-12-17
; PRIOR FILING DATE: 1998-03-20
; PRIOR FILING DATE: 1998-03-25
; PRIOR FILING DATE: 1998-03-26
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-526-71

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Best Local Similarity 100.0%; Pred. No. 7.1e-118;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 38 ATGCGAAGATATTGTTACTTTTCTCCCGGGTCTTGTGGCTGTATGCTGTGATGA 97

Qy 61 ATATTTATGACCGTCTAGCTTCCCAAGAGCTCTGTCAGATGATGAGTGTGTCTATCT 120
Db 98 ATATTTATGACCGTCTAGCTTCCCAAGAGCTCTGTCAGATGATGAGTGTGTCTATCT 157

Qy 121 ATTTCTCTGCTAGTGTCTCAAGAGATTATATGCCCCCGAGCTGTAGATTCAATTAAGTT 180
Db 158 ATTTCTCTGCTAGTGTCTCAAGAGATTATATGCCCCCGAGCTGTAGATTCAATTAAGTT 217

Qy 181 AAAAAAGGCGAGAGATCTATGTACTCAAGAGCTGTAAAGAGAAATGAGCTCGAGAA 240
Db 218 AAAAAAGGCGAGAGATCTATGTACTCAAGAGCTGTAAAGAGAAATGAGCTCGAGAA 277

Qy 241 TTTTGGGCTGGAGTGTATGTGTATGTCGACGAGATGGAGTGTGTTTATTTTC 300
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; Publication No. US20030187213A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC54
; CURRENT APPLICATION NUMBER: US/10/219,530
; CURRENT FILING DATE: 2002-08-14
; PRIOR FILING DATE: 2002-04-09
; PRIOR FILING DATE: 1997-09-17
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; PRIOR FILING DATE: 1997-12-17
; PRIOR FILING DATE: 1998-03-20
; PRIOR FILING DATE: 1998-03-25
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; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-530-71

Query Match      100.0%; Score 384; DB 13; Length 521;
Best Local Similarity 100.0%; Pred. No. 7.1e-118;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 38 ATGCGAAGATATTGTTACTTTTCTCCCGGGTCTTGTGGCTGTATGCTGTGATGA 97

Qy 61 ATATTTATGACCGTCTAGCTTCCCAAGAGCTCTGTCAGATGATGAGTGTGTCTATCT 120
Db 98 ATATTTATGACCGTCTAGCTTCCCAAGAGCTCTGTCAGATGATGAGTGTGTCTATCT 157

Qy 121 ATTTCTCTGCTAGTGTCTCAAGAGATTATATGCCCCCGAGCTGTAGATTCAATTAAGTT 180
Db 158 ATTTCTCTGCTAGTGTCTCAAGAGATTATATGCCCCCGAGCTGTAGATTCAATTAAGTT 217
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QY 301 CCCAGGAACCTTGGTCAAGGAACAGCGTGTGTACCAAGGAGCTACCAAGGAAGTTCCACC 360
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	DB ID	Description
1	384	100.0	384	US-10-019-455A-4
2	384	100.0	387	Sequence 4, Appli
3	384	100.0	387	Sequence 12, Appli
4	384	100.0	387	Sequence 12, Appli





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 Db 241 TTTTGGGCTGGAGTCTTTATGTCATGCGCAGACGAGATGGAGTCGTGGGTATTTC 300  
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 QY 301 CCAGGAACCTTGGTCAAGGAACAGCGTGTGTACAGGAAGCTACCAAGGAAGTTCCACCC 360  
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 Db 301 CCAGGAACCTTGGTCAAGGAACAGCGTGTGTACAGGAAGCTACCAAGGAAGTTCCACCC 360  
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 QY 361 ACGGATATTGACTTCTTCTGCGAG 384  
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## RESULT 3

PCT-US01-11797-12  
 ; Sequence 12, Application PC/TUS0111797  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SMITHKLINE BEECHAM CORPORATION  
 ; TITLE OF INVENTION: SMITHKLINE BEECHAM P.I.C.  
 ; FILE REFERENCE: GP50022  
 ; CURRENT APPLICATION NUMBER: PCT/US01/11797  
 ; CURRENT FILING DATE: 2001-04-11  
 ; PRIOR APPLICATION NUMBER: 60/196,603  
 ; PRIOR FILING DATE: 2000-04-13  
 ; PRIOR FILING DATE: 2000-04-13  
 ; PRIOR FILING DATE: 2000-04-13  
 ; NUMBER OF SEQ ID NOS: 48  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 12  
 ; LENGTH: 387  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 PCT-US01-11797-12

Query Match 100.0%; Score 384; DB 2; Length 387;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-107;  
 Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 ATGGCAAGAATATTTGTTACTTTCTCCCGGCTCTTGGTGTATGTCGTGTCATGGA 60  
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 Db 121 ATTTCTCTGGCTAGTCTCAAGAAATTAATGCCCCGGACTGTAGATTCAATTAACGTT 180  
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 Db 181 AAAAAAGGCGACAGATCTATGTACTCAAGCTGGTAAAGAAATGGAGCTGGAGAA 240  
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 QY 241 TTTTGGGCTGGAGTCTTTATGTCATGCGCAGACGAGATGGAGTCGTGGGTATTTC 300  
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 QY 301 CCAGGAACCTTGGTCAAGGAACAGCGTGTGTACAGGAAGCTACCAAGGAAGTTCCACCC 360  
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## RESULT 4

US-10-257-174-12  
 ; Sequence 12, Application US/10257174  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Agarwal, Pankaj

; APPLICANT: Murdoch, Paul R.  
 ; APPLICANT: Rizvi, Safia K.  
 ; APPLICANT: Smith, Randall F.  
 ; APPLICANT: Xiang, Zhaoying  
 ; TITLE OF INVENTION: NOVEL COMPOUNDS  
 ; FILE REFERENCE: GP50022  
 ; CURRENT APPLICATION NUMBER: US/10/257,174  
 ; CURRENT FILING DATE: 2002-10-10  
 ; PRIOR APPLICATION NUMBER: PCT/US01/11797  
 ; PRIOR FILING DATE: 2001-04-11  
 ; PRIOR APPLICATION NUMBER: 60/196,603  
 ; PRIOR FILING DATE: 2000-04-13  
 ; PRIOR APPLICATION NUMBER: 60/199,417  
 ; PRIOR FILING DATE: 2000-04-24  
 ; NUMBER OF SEQ ID NOS: 48  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 12  
 ; LENGTH: 387  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-257-174-12

Query Match 100.0%; Score 384; DB 49; Length 387;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-107;  
 Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCAAGAATATTTGTTACTTTCTCCCGGCTCTTGGTGTATGTCGTGTCATGGA 60  
 |||||  
 Db 1 ATGGCAAGAATATTTGTTACTTTCTCCCGGCTCTTGGTGTATGTCGTGTCATGGA 60  
 |||||  
 QY 61 ATATTATGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTATACT 120  
 |||||  
 Db 61 ATATTATGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTATACT 120  
 |||||  
 QY 121 ATTTCTCTGGCTAGTCTCAAGAAATTAATGCCCCGGACTGTAGATTCAATTAACGTT 180  
 |||||  
 Db 121 ATTTCTCTGGCTAGTCTCAAGAAATTAATGCCCCGGACTGTAGATTCAATTAACGTT 180  
 |||||  
 QY 181 AAAAAAGGCGACAGATCTATGTACTCAAGCTGGTAAAGAAATGGAGCTGGAGAA 240  
 |||||  
 Db 181 AAAAAAGGCGACAGATCTATGTACTCAAGCTGGTAAAGAAATGGAGCTGGAGAA 240  
 |||||  
 QY 241 TTTTGGGCTGGAGTCTTTATGTCATGCGCAGACGAGATGGAGTCGTGGGTATTTC 300  
 |||||  
 Db 241 TTTTGGGCTGGAGTCTTTATGTCATGCGCAGACGAGATGGAGTCGTGGGTATTTC 300  
 |||||  
 QY 301 CCAGGAACCTTGGTCAAGGAACAGCGTGTGTACAGGAAGCTACCAAGGAAGTTCCACCC 360  
 |||||  
 Db 301 CCAGGAACCTTGGTCAAGGAACAGCGTGTGTACAGGAAGCTACCAAGGAAGTTCCACCC 360  
 |||||  
 QY 361 ACGGATATTGACTTCTTCTGCGAG 384  
 |||||  
 Db 361 ACGGATATTGACTTCTTCTGCGAG 384  
 |||||

## RESULT 5

PCT-US01-02455-1  
 ; Sequence 1, Application PC/TUS0102455  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hyseq, Inc.  
 ; APPLICANT: Mize, Nancy K.  
 ; APPLICANT: Boyle, Bryan J.  
 ; APPLICANT: Ford, John E.  
 ; APPLICANT: Arterburn, Matthew C.  
 ; APPLICANT: Tang, Y Tom  
 ; APPLICANT: Liu, Chenghua  
 ; APPLICANT: Drmanac, Radoje T.  
 ; TITLE OF INVENTION: Methods and Materials Relating to Novel Growth Regulatory-like  
 ; Sequence 1, Application PC/TUS0102455  
 ; FILE REFERENCE: 21272-021 (HYS-7)  
 ; CURRENT APPLICATION NUMBER: PCT/US01/02455  
 ; CURRENT FILING DATE: 2001-01-25  
 ; PRIOR APPLICATION NUMBER: US 09/563,786

PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: US 09/491,404  
PRIOR FILING DATE: 2000-01-25  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 1  
LENGTH: 426  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)-(426)  
OTHER INFORMATION: n = A, T, G, or C  
PCT-US01-02455-1

Query Match 100.0%; Score 384; DB 1; Length 426;  
Best Local Similarity 100.0%; Pred. No. 1.2e-107;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGGCAAGAAATATTGTTACTTTTCTCCCGGGTCTTGTGGCTGTATGCTGTGCATGGA 60  
DB 19 ATGGCAAGAAATATTGTTACTTTTCTCCCGGGTCTTGTGGCTGTATGCTGTGCATGGA 78  
QY 61 ATATTTATGGACCGTCTAGCTTCCAGAGAGCTCTGTGCAGATGATGAGTGTCTATACT 120  
DB 79 ATATTTATGGACCGTCTAGCTTCCAGAGAGCTCTGTGCAGATGATGAGTGTCTATACT 138  
QY 121 ATTTCTCTGGCTAGTCTCAAGAGATTATAATGCCCGGACTGTAGATTCATTACGTT 180  
DB 139 ATTTCTCTGGCTAGTCTCAAGAGATTATAATGCCCGGACTGTAGATTCATTACGTT 198  
QY 181 AAAAAAGGCGCAGCAGATCTATGTACTCAAGAGCTGTAAAGAAATGGAGCTGGAGAA 240  
DB 199 AAAAAAGGCGCAGCAGATCTATGTACTCAAGAGCTGTAAAGAAATGGAGCTGGAGAA 258  
QY 241 TTTTGGGCTGCGAGTGTATGTTATGTTGATGGCCAGACAGATGGAGTCTGGGTTATTTTC 300  
DB 259 TTTTGGGCTGCGAGTGTATGTTATGTTGATGGCCAGACAGATGGAGTCTGGGTTATTTTC 318  
QY 301 CCCAGGAACCTTGGTCAAGAGAACAGCGTGTGTACAGAGAGCTACCAAGGAAGTTCCACC 360  
DB 319 CCCAGGAACCTTGGTCAAGAGAACAGCGTGTGTACAGAGAGCTACCAAGGAAGTTCCACC 378  
QY 361 ACGGATATGACTTCTTCTCGGAG 384  
DB 379 ACGGATATGACTTCTTCTCGGAG 402

RESULT 6  
PCT-US01-02455-1  
Sequence 1, Application PC/TUS0102455  
GENERAL INFORMATION:  
APPLICANT: Hyseq, Inc.  
APPLICANT: Mize, Nancy K  
APPLICANT: Boyle, Bryan J  
APPLICANT: Ford, John E  
APPLICANT: Arterburn, Matthew C  
APPLICANT: Tang, Y Tom  
APPLICANT: Liu, Chenghua  
APPLICANT: Drmanac, Radoje T  
TITLE OF INVENTION: Methods and Materials Relating to Novel Growth Regulatory-like  
FILE OF INVENTION: Polypeptides and Polynucleotides  
FILE REFERENCE: 21272-021 (HYS-7)  
CURRENT APPLICATION NUMBER: PCT/US01/02455  
CURRENT FILING DATE: 2001-01-25  
PRIOR APPLICATION NUMBER: US 09/563,786  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: US 09/491,404  
PRIOR FILING DATE: 2000-01-25  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 1  
LENGTH: 426

TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)-(426)  
OTHER INFORMATION: n = A, T, G, or C  
PCT-US01-02455-1

Query Match 100.0%; Score 384; DB 2; Length 426;  
Best Local Similarity 100.0%; Pred. No. 1.2e-107;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGGCAAGAAATATTGTTACTTTTCTCCCGGGTCTTGTGGCTGTATGCTGTGCATGGA 60  
DB 19 ATGGCAAGAAATATTGTTACTTTTCTCCCGGGTCTTGTGGCTGTATGCTGTGCATGGA 78  
QY 61 ATATTTATGGACCGTCTAGCTTCCAGAGAGCTCTGTGCAGATGATGAGTGTCTATACT 120  
DB 79 ATATTTATGGACCGTCTAGCTTCCAGAGAGCTCTGTGCAGATGATGAGTGTCTATACT 138  
QY 121 ATTTCTCTGGCTAGTCTCAAGAGATTATAATGCCCGGACTGTAGATTCATTACGTT 180  
DB 139 ATTTCTCTGGCTAGTCTCAAGAGATTATAATGCCCGGACTGTAGATTCATTACGTT 198  
QY 181 AAAAAAGGCGCAGCAGATCTATGTACTCAAGAGCTGTAAAGAAATGGAGCTGGAGAA 240  
DB 199 AAAAAAGGCGCAGCAGATCTATGTACTCAAGAGCTGTAAAGAAATGGAGCTGGAGAA 258  
QY 241 TTTTGGGCTGCGAGTGTATGTTATGTTGATGGCCAGACAGATGGAGTCTGGGTTATTTTC 300  
DB 259 TTTTGGGCTGCGAGTGTATGTTATGTTGATGGCCAGACAGATGGAGTCTGGGTTATTTTC 318  
QY 301 CCCAGGAACCTTGGTCAAGAGAACAGCGTGTGTACAGAGAGCTACCAAGGAAGTTCCACC 360  
DB 319 CCCAGGAACCTTGGTCAAGAGAACAGCGTGTGTACAGAGAGCTACCAAGGAAGTTCCACC 378  
QY 361 ACGGATATGACTTCTTCTCGGAG 384  
DB 379 ACGGATATGACTTCTTCTCGGAG 402

RESULT 7  
US-09-528-409-107188  
Sequence 107188, Application US/09528409  
GENERAL INFORMATION:  
APPLICANT: Drmanac, Radoje T.  
APPLICANT: Labat, Ivan  
APPLICANT: Stache-Crain, Birgit  
APPLICANT: Dickson, Mark  
APPLICANT: Jones, Lee W.  
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained  
FILE REFERENCE: 774  
CURRENT APPLICATION NUMBER: US/09/528,409  
CURRENT FILING DATE: 2000-03-17  
PRIOR APPLICATION NUMBER: 60/125,453  
PRIOR FILING DATE: 1999-03-19  
NUMBER OF SEQ ID NOS: 116231  
SOFTWARE: Hy-patent.pl Version 3.1  
SEQ ID NO 107188  
LENGTH: 426  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)-(426)  
OTHER INFORMATION: n = A, T, C or G  
US-09-528-409-107188

Query Match 100.0%; Score 384; DB 22; Length 426;  
Best Local Similarity 100.0%; Pred. No. 1.2e-107;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCAAGATATTGTTACTTTCTCCCGGCTCTGTGGCTGTATGCTGTGCTATGGA 60  
DB 19 ATGGCAAGATATTGTTACTTTCTCCCGGCTCTGTGGCTGTATGCTGTGCTATGGA 78  
QY 61 ATATTATGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGATGCTGTCTATCT 120  
DB 79 ATATTATGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGATGCTGTCTATCT 138  
QY 121 ATTTCTCTGGCTAGTCTCAAGAGATATTATATGCCCGGCTGTAGATTCATTAAAGTT 180  
DB 139 ATTTCTCTGGCTAGTCTCAAGAGATATTATATGCCCGGCTGTAGATTCATTAAAGTT 198  
QY 181 AAAAAAGGCGCAGCAGATCTATGTGTACTCAAAAGCTGTGTAAAGAAAATGGAGCTGGAGAA 240  
DB 199 AAAAAAGGCGCAGCAGATCTATGTGTACTCAAAAGCTGTGTAAAGAAAATGGAGCTGGAGAA 258  
QY 241 TTTTGGGCTGGCAGTGTATGTGTACTCAAAAGCTGTGTAAAGAAAATGGAGCTGGAGTTTC 300  
DB 259 TTTTGGGCTGGCAGTGTATGTGTACTCAAAAGCTGTGTAAAGAAAATGGAGCTGGAGTTTC 318  
QY 301 CCAGAACTTGGTCAAGAGATATTATATGCCCGGCTGTAGATTCATTAAAGTT 360  
DB 319 CCAGAACTTGGTCAAGAGATATTATATGCCCGGCTGTAGATTCATTAAAGTT 378  
QY 361 ACGGATATTGACTTCTTCTGCGAG 384  
DB 379 ACGGATATTGACTTCTTCTGCGAG 402

## RESULT 8

US-09-563-786A-1  
; Sequence 1, Application US/09563786A  
; GENERAL INFORMATION:  
; APPLICANT: Mize, Nancy K  
; APPLICANT: Boyle, Bryan J  
; APPLICANT: Ford, John E  
; APPLICANT: Arterburn, Matthew C  
; APPLICANT: Tang, Y Tom  
; APPLICANT: Liu, Chenchua  
; APPLICANT: Drmanac, Radoje T  
; TITLE OF INVENTION: Methods and Materials Relating to Novel Growth Regulatory-like  
; FILE REFERENCE: HYS-7  
; CURRENT APPLICATION NUMBER: US/09/563,786A  
; PRIOR FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 09/491,404  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 426  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(426)  
; OTHER INFORMATION: n = A, T, G, or C

Query Match 100.0%; Score 384; DB 25; Length 426;  
Best Local Similarity 100.0%; Pred. No. 1.2e-107;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCAAGATATTGTTACTTTCTCCCGGCTCTGTGGCTGTATGCTGTGCTATGGA 60  
DB 19 ATGGCAAGATATTGTTACTTTCTCCCGGCTCTGTGGCTGTATGCTGTGCTATGGA 78  
QY 61 ATATTATGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGATGCTGTCTATCT 120  
DB 79 ATATTATGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGATGCTGTCTATCT 138  
QY 121 ATTTCTCTGGCTAGTCTCAAGAGATATTATATGCCCGGCTGTAGATTCATTAAAGTT 180

DB 139 ATTTCTCTGGCTAGTCTCAAGAGATATTATATGCCCGGCTGTAGATTCATTAAAGTT 198  
QY 181 AAAAAAGGCGCAGCAGATCTATGTGTACTCAAAAGCTGTGTAAAGAAAATGGAGCTGGAGAA 240  
DB 199 AAAAAAGGCGCAGCAGATCTATGTGTACTCAAAAGCTGTGTAAAGAAAATGGAGCTGGAGAA 258  
QY 241 TTTTGGGCTGGCAGTGTATGTGTACTCAAAAGCTGTGTAAAGAAAATGGAGCTGGAGTTTC 300  
DB 259 TTTTGGGCTGGCAGTGTATGTGTACTCAAAAGCTGTGTAAAGAAAATGGAGCTGGAGTTTC 318  
QY 301 CCAGAACTTGGTCAAGAGATATTATATGCCCGGCTGTAGATTCATTAAAGTT 360  
DB 319 CCAGAACTTGGTCAAGAGATATTATATGCCCGGCTGTAGATTCATTAAAGTT 378  
QY 361 ACGGATATTGACTTCTTCTGCGAG 384  
DB 379 ACGGATATTGACTTCTTCTGCGAG 402

## RESULT 9

US-09-933-524-107188  
; Sequence 107188, Application US/09933524  
; GENERAL INFORMATION:  
; APPLICANT: Drmanac, Radoje T.  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Dickson, Mark  
; APPLICANT: Jones, Lee W.  
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained  
; FILE REFERENCE: From Various Libraries  
; CURRENT APPLICATION NUMBER: US/09/933,524  
; CURRENT FILING DATE: 2001-08-20  
; PRIOR APPLICATION NUMBER: 09/528,409  
; PRIOR FILING DATE: 2000-03-17  
; NUMBER OF SEQ ID NOS: 116231  
; SOFTWARE: HY-patent.pl Version 3.1  
; SEQ ID NO 107188  
; LENGTH: 426  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(426)  
; OTHER INFORMATION: n = A, T, C or G

Query Match 100.0%; Score 384; DB 39; Length 426;  
Best Local Similarity 100.0%; Pred. No. 1.2e-107;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCAAGATATTGTTACTTTCTCCCGGCTCTGTGGCTGTATGCTGTGCTATGGA 60  
DB 19 ATGGCAAGATATTGTTACTTTCTCCCGGCTCTGTGGCTGTATGCTGTGCTATGGA 78  
QY 61 ATATTATGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGATGCTGTCTATCT 120  
DB 79 ATATTATGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGATGCTGTCTATCT 138  
QY 121 ATTTCTCTGGCTAGTCTCAAGAGATATTATATGCCCGGCTGTAGATTCATTAAAGTT 180  
DB 139 ATTTCTCTGGCTAGTCTCAAGAGATATTATATGCCCGGCTGTAGATTCATTAAAGTT 198  
QY 181 AAAAAAGGCGCAGCAGATCTATGTGTACTCAAAAGCTGTGTAAAGAAAATGGAGCTGGAGAA 240  
DB 199 AAAAAAGGCGCAGCAGATCTATGTGTACTCAAAAGCTGTGTAAAGAAAATGGAGCTGGAGAA 258  
QY 241 TTTTGGGCTGGCAGTGTATGTGTACTCAAAAGCTGTGTAAAGAAAATGGAGCTGGAGTTTC 300  
DB 259 TTTTGGGCTGGCAGTGTATGTGTACTCAAAAGCTGTGTAAAGAAAATGGAGCTGGAGTTTC 318  
QY 301 CCAGAACTTGGTCAAGAGATATTATATGCCCGGCTGTAGATTCATTAAAGTT 360

Db 319 CCCAGGAATGGTCAAGAACAGCGTGTACACGAGAGCTACCAAGAGATTCCACACC 378  
Qy 361 ACGGATATTGACTTCTTCTGCGAG 384  
| | | | |  
Db 379 ACGGATATTGACTTCTTCTGCGAG 402

## RESULT 10

US-09-933-524A-107188  
; Sequence 107188, Application US/09933524A  
; GENERAL INFORMATION:  
; APPLICANT: Drmanac, Radoje T.  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Dickson, Mark  
; APPLICANT: Jones, Lee W.  
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained  
; FILE REFERENCE: From Various Libraries  
; CURRENT APPLICATION NUMBER: US/09/933,524A  
; PRIOR FILING DATE: 2001-08-20  
; PRIOR APPLICATION NUMBER: 09/528,409  
; PRIOR FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 116231  
; SOFTWARE: Hy-patent.pl Version 3.1  
; SEQ ID NO 107188  
; LENGTH: 426  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(426)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-933-524A-107188

Query Match 100.0%; Score 384; DB 39; Length 426;  
Best Local Similarity 100.0%; Pred. No. 1.2e-107;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGGCAAGAATATTGTTACTTTCTCCCGGGTCTTTGGCTGTATGCTGTGATGGA 60  
Db 19 ATGGCAAGAATATTGTTACTTTCTCCCGGGTCTTTGGCTGTATGCTGTGATGGA 78  
Qy 61 ATATTATGACCGTCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTATACT 120  
Db 79 ATATTATGACCGTCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTATACT 138  
Qy 121 ATTTCTCTGGCTAGTCTCAAGAAAGATTATATGCCCCGGACTGTAGATTCAATTAACGTT 180  
Db 139 ATTTCTCTGGCTAGTCTCAAGAAAGATTATATGCCCCGGACTGTAGATTCAATTAACGTT 198  
Qy 181 AAAAAAGGCGACAGATCTATGTACTCAAAAGCTGGTAAAGAAAATGGAGCTGGAGAA 240  
Db 199 AAAAAAGGCGACAGATCTATGTACTCAAAAGCTGGTAAAGAAAATGGAGCTGGAGAA 258  
Qy 241 TTTTGGGCTGGCAGTGTATGGTGTATGGCCAGGACGAGTCTGGGTATTTC 300  
Db 259 TTTTGGGCTGGCAGTGTATGGTGTATGGCCAGGACGAGTCTGGGTATTTC 318  
Qy 301 CCCAGGAATCTGTCAAGGAAACAGCGTGTATCCAGGAGAGCTACCAAGGAAGTTCCACACC 360  
Db 319 CCCAGGAATCTGTCAAGGAAACAGCGTGTATCCAGGAGAGCTACCAAGGAAGTTCCACACC 378  
Qy 361 ACGGATATTGACTTCTTCTGCGAG 384  
| | | | |  
Db 379 ACGGATATTGACTTCTTCTGCGAG 402

## RESULT 11

US-10-216-038-1  
; Sequence 1, Application US/10216038  
; GENERAL INFORMATION:  
; APPLICANT: Mize, Nancy K

; APPLICANT: Boyle, Bryan J  
; APPLICANT: Ford, John E  
; APPLICANT: Arterburn, Matthew C  
; APPLICANT: Tang, Y Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Drmanac, Radoje T  
; APPLICANT: Song, Yong  
; APPLICANT: Sjastad, Michael  
; TITLE OF INVENTION: Methods and Materials Relating to Novel Growth Regulatory-like  
; FILE REFERENCE: Polypeptides and Polynucleotides  
; CURRENT APPLICATION NUMBER: US/10/216,038  
; PRIOR FILING DATE: 2002-08-08  
; PRIOR APPLICATION NUMBER: US 09/563,786  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: US 09/491,404  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 426  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (426)...(426)  
; OTHER INFORMATION: n = A, T, G, or C  
US-10-216-038-1

Query Match 100.0%; Score 384; DB 48; Length 426;  
Best Local Similarity 100.0%; Pred. No. 1.2e-107;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGGCAAGAATATTGTTACTTTCTCCCGGGTCTTTGGCTGTATGCTGTGATGGA 60  
Db 19 ATGGCAAGAATATTGTTACTTTCTCCCGGGTCTTTGGCTGTATGCTGTGATGGA 78  
Qy 61 ATATTATGACCGTCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTATACT 120  
Db 79 ATATTATGACCGTCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTATACT 138  
Qy 121 ATTTCTCTGGCTAGTCTCAAGAAAGATTATATGCCCCGGACTGTAGATTCAATTAACGTT 180  
Db 139 ATTTCTCTGGCTAGTCTCAAGAAAGATTATATGCCCCGGACTGTAGATTCAATTAACGTT 198  
Qy 181 AAAAAAGGCGACAGATCTATGTACTCAAAAGCTGGTAAAGAAAATGGAGCTGGAGAA 240  
Db 199 AAAAAAGGCGACAGATCTATGTACTCAAAAGCTGGTAAAGAAAATGGAGCTGGAGAA 258  
Qy 241 TTTTGGGCTGGCAGTGTATGGTGTATGGCCAGGACGAGTCTGGGTATTTC 300  
Db 259 TTTTGGGCTGGCAGTGTATGGTGTATGGCCAGGACGAGTCTGGGTATTTC 318  
Qy 301 CCAGGAATCTGTCAAGGAAACAGCGTGTATCCAGGAGAGCTACCAAGGAAGTTCCACACC 360  
Db 319 CCAGGAATCTGTGTCAAGGAAACAGCGTGTATCCAGGAGAGCTACCAAGGAAGTTCCACACC 378  
Qy 361 ACGGATATTGACTTCTTCTGCGAG 384  
| | | | |  
Db 379 ACGGATATTGACTTCTTCTGCGAG 402

## RESULT 12

US-10-311-830-1  
; Sequence 1, Application US/10311830  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; APPLICANT: Mize, Nancy K  
; APPLICANT: Boyle, Bryan J  
; APPLICANT: Ford, John E  
; APPLICANT: Arterburn, Matthew C  
; APPLICANT: Tang, Y Tom  
; APPLICANT: Liu, Chenghua

APPLICANT: Drmanac, Radoje T  
TITLE OF INVENTION: Methods and Materials Relating to Novel Growth Regulatory-like  
TITLE OF INVENTION: Polypeptides and Polynucleotides  
FILE REFERENCE: 21272-021 (HVS-7)  
CURRENT APPLICATION NUMBER: US/10/311,830  
CURRENT FILING DATE: 2002-12-17  
PRIOR APPLICATION NUMBER: US 09/563,796  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: US 09/491,404  
PRIOR FILING DATE: 2000-01-25  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 1  
LENGTH: 426  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)-(426)  
OTHER INFORMATION: n = A, T, G, or C  
US-10-311-830-1

Query Match 100.0%; Score 384; DB 50; Length 426;  
Best Local Similarity 100.0%; Pred. No. 1.2e-107; Mismatches 0; Indels 0; Gaps 0;  
Matches 384; Conservative 0

Qy	1	ATGCAAGATATTTGTTACTTTTCCCTCCCGGTCTTTGGCTGTATGCTGTGCTGATGGA 60
Db	19	ATGCAAGATATTTGTTACTTTTCCCTCCCGGTCTTTGGCTGTATGCTGTGCTGATGGA 78
Qy	61	ATATTTATGACCGTCTAGCTTCCAGAGCTCTGCGAGATGATGCTGTCTACT 120
Db	79	ATATTTATGACCGTCTAGCTTCCAGAGCTCTGCGAGATGATGCTGTCTACT 138
Qy	121	ATTCTCTGCTGTGCTCAAGAGATTTATATGCCCGGCTGTAGATTCATTAACT 180
Db	139	ATTCTCTGCTGTGCTCAAGAGATTTATATGCCCGGCTGTAGATTCATTAACT 198
Qy	181	AAAAAGGACAGAGATCTATGCTCTCAAGCTGTAAAGAAATGGAGCTGGAGAA 240
Db	199	AAAAAGGACAGAGATCTATGCTCTCAAGCTGTAAAGAAATGGAGCTGGAGAA 258
Qy	241	TTTGGCTGGAGTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 300
Db	259	TTTGGCTGGAGTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 318
Qy	301	CCAGGAACTGCTCAAGACAGCTGTGTACCAAGAGCTACCAAGAGTCCACAC 360
Db	319	CCAGGAACTGCTCAAGACAGCTGTGTACCAAGAGCTACCAAGAGTCCACAC 378
Qy	361	ACGGATATTGACTTCTTCTCGAG 384
Db	379	ACGGATATTGACTTCTTCTCGAG 402

RESULT 13  
US-10-081-056-359  
Sequence 359, Application US/10081056  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
TITLE OF INVENTION: Ferrara, Napoleone  
FILE REFERENCE: Gerber, Hanspeter  
CURRENT APPLICATION NUMBER: Geritsen, Mary E.  
CURRENT FILING DATE: Goddard, Audrey  
PRIOR APPLICATION NUMBER: Godowski, Paul J.  
PRIOR FILING DATE: Gurney, Austin L.  
PRIOR APPLICATION NUMBER: Hillan, Kenneth J.  
PRIOR FILING DATE: Marsters, Scot A.  
PRIOR APPLICATION NUMBER: Pan, James  
PRIOR FILING DATE: Paoni, Nicholas F.  
PRIOR APPLICATION NUMBER: Stephan, Jean-Philippe F.  
PRIOR FILING DATE: Watanabe, Colin K.  
PRIOR APPLICATION NUMBER: Wood, William I.

APPLICANT: Williams, P. Mickey  
APPLICANT: Ye, Weilan  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND  
TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS  
FILE REFERENCE: P3235P1C1  
CURRENT APPLICATION NUMBER: US/10/081,056  
CURRENT FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: PCT/US01/21735  
PRIOR FILING DATE: 2001-07-09  
PRIOR APPLICATION NUMBER: US 60/219,556  
PRIOR FILING DATE: 2000-07-20  
PRIOR APPLICATION NUMBER: US 60/220,624  
PRIOR FILING DATE: 2000-07-25  
PRIOR APPLICATION NUMBER: US 60/220,664  
PRIOR FILING DATE: 2000-07-25  
PRIOR APPLICATION NUMBER: PCT/US00/20710  
PRIOR FILING DATE: 2000-07-28  
PRIOR APPLICATION NUMBER: US 60/222,695  
PRIOR FILING DATE: 2000-08-02  
PRIOR APPLICATION NUMBER: US 09/643,657  
PRIOR FILING DATE: 2000-08-17  
PRIOR APPLICATION NUMBER: PCT/US00/23522  
PRIOR FILING DATE: 2000-08-23  
PRIOR APPLICATION NUMBER: PCT/US00/23328  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: US 60/230,978  
PRIOR FILING DATE: 2000-09-07  
PRIOR APPLICATION NUMBER: US 60/000,000  
PRIOR FILING DATE: 2000-09-15  
PRIOR APPLICATION NUMBER: US 09/664,610  
PRIOR FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: US 09/665,350  
PRIOR FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: US 60/242,922  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 09/709,238  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: PCT/US00/30952  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: PCT/US00/30873  
PRIOR FILING DATE: 2000-11-10  
PRIOR APPLICATION NUMBER: PCT/US00/32678  
PRIOR FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: US 09/747,259  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/34956  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: US 09/767,609  
PRIOR FILING DATE: 2001-01-22  
PRIOR APPLICATION NUMBER: US 09/796,498  
PRIOR FILING DATE: 2001-02-28  
PRIOR APPLICATION NUMBER: PCT/US01/06520  
PRIOR FILING DATE: 2001-02-28  
PRIOR APPLICATION NUMBER: PCT/US01/06666  
PRIOR FILING DATE: 2001-03-01  
PRIOR APPLICATION NUMBER: US 09/802,706  
PRIOR FILING DATE: 2001-03-09  
PRIOR APPLICATION NUMBER: US 09/808,689  
PRIOR FILING DATE: 2001-03-14  
PRIOR APPLICATION NUMBER: US 09/816,744  
PRIOR FILING DATE: 2001-03-22  
PRIOR APPLICATION NUMBER: US 09/828,366  
PRIOR FILING DATE: 2001-04-05  
PRIOR APPLICATION NUMBER: US 09/854,208  
PRIOR FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: US 09/854,280  
PRIOR FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: US 09/866,028  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: US 09/866,034  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: PCT/US01/17092  
PRIOR FILING DATE: 2001-05-25

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; PRIOR APPLICATION NUMBER: US 09/870,574
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US01/17443
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/00000
; PRIOR FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 359
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homosapiens
; US-10-081-056-359

Query Match 100.0%; Score 384; DB 45; Length 521;
Best Local Similarity 100.0%; Pred. No. 1.3e-107;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCGAAGATATTTGTTACTTTTCTCCCGGGTCTTGTGGCTGTATGCTGTGATGCTGATGGA 60
Db 38 ATGCGAAGATATTTGTTACTTTTCTCCCGGGTCTTGTGGCTGTATGCTGTGATGCTGATGGA 97
Qy 61 ATATTTATGACCGTCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTTATACT 120
Db 98 ATATTTATGACCGTCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTTATACT 157
Qy 121 ATTTCTCTGCTAGTCTCAAGAGATTTATATGCCCCGGACTGTAGATTCATTAACTT 180
Db 158 ATTTCTCTGCTAGTCTCAAGAGATTTATATGCCCCGGACTGTAGATTCATTAACTT 217
Qy 181 AAAAAAGGCGAGCAGATCTATGTGTACTCAAGAGCTGTGTAAGAGAGAGAGAGAGAGAGAG 240
Db 218 AAAAAAGGCGAGCAGATCTATGTGTACTCAAGAGCTGTGTAAGAGAGAGAGAGAGAGAGAG 277
Qy 241 TTTTGGCTGGCAGTGTATGTATGCTGATGCCAGGAGAGATGCGAGTGTGGGTATTTC 300
Db 278 TTTTGGCTGGCAGTGTATGTATGCTGATGCCAGGAGAGATGCGAGTGTGGGTATTTC 337
Qy 301 CCCAGGAACCTTGTCAAGGAGCAGCTGTGTACTCAAGAGCTGTGTAAGAGAGAGAGAGAGAG 360
Db 338 CCCAGGAACCTTGTGTCAAGGAGCAGCTGTGTACTCAAGAGCTGTGTAAGAGAGAGAGAGAG 397
Qy 361 ACGGATATTGACTTCTTCTCGGAG 384
Db 398 ACGGATATTGACTTCTTCTCGGAG 421

RESULT 15
US-10-216-159A-71
; Sequence 71, Application US/10216159A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C6
; CURRENT APPLICATION NUMBER: US/10/216,159A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25

; PRIOR APPLICATION NUMBER: US 09/870,574
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US01/17443
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/00000
; PRIOR FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 359
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homosapiens
; US-10-081-056-359

Query Match 100.0%; Score 384; DB 45; Length 521;
Best Local Similarity 100.0%; Pred. No. 1.3e-107;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCGAAGATATTTGTTACTTTTCTCCCGGGTCTTGTGGCTGTATGCTGTGATGCTGATGGA 60
Db 38 ATGCGAAGATATTTGTTACTTTTCTCCCGGGTCTTGTGGCTGTATGCTGTGATGCTGATGGA 97
Qy 61 ATATTTATGACCGTCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTTATACT 120
Db 98 ATATTTATGACCGTCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTTATACT 157
Qy 121 ATTTCTCTGCTAGTCTCAAGAGATTTATATGCCCCGGACTGTAGATTCATTAACTT 180
Db 158 ATTTCTCTGCTAGTCTCAAGAGATTTATATGCCCCGGACTGTAGATTCATTAACTT 217
Qy 181 AAAAAAGGCGAGCAGATCTATGTGTACTCAAGAGCTGTGTAAGAGAGAGAGAGAGAGAGAG 240
Db 218 AAAAAAGGCGAGCAGATCTATGTGTACTCAAGAGCTGTGTAAGAGAGAGAGAGAGAGAGAG 277
Qy 241 TTTTGGCTGGCAGTGTATGTATGCTGATGCCAGGAGAGATGCGAGTGTGGGTATTTC 300
Db 278 TTTTGGCTGGCAGTGTATGTATGCTGATGCCAGGAGAGATGCGAGTGTGGGTATTTC 337
Qy 301 CCCAGGAACCTTGTCAAGGAGCAGCTGTGTACTCAAGAGCTGTGTAAGAGAGAGAGAGAGAG 360
Db 338 CCCAGGAACCTTGTGTCAAGGAGCAGCTGTGTACTCAAGAGCTGTGTAAGAGAGAGAGAGAG 397
Qy 361 ACGGATATTGACTTCTTCTCGGAG 384
Db 398 ACGGATATTGACTTCTTCTCGGAG 421

RESULT 14
US-10-119-480-71
; Sequence 71, Application US/10119480
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C1
; CURRENT APPLICATION NUMBER: US/10/119,480
; CURRENT FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 246
; PRIOR APPLICATION removed - See File Wrapper or Palm
; SEQ ID NO 71
; LENGTH: 521

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; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-216-159A-71

Query Match      100.0%; Score 384; DB 48; Length 521;
Best Local Similarity 100.0%; Pred. No. 1.3e-107;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCAAGATATGTTACTTTCTCCCGGGTCTTGTGGCTGTATGTCTGTGCATGGA 60
Db 38 ATGGCAAGATATGTTACTTTCTCCCGGGTCTTGTGGCTGTATGTCTGTGCATGGA 97
Qy 61 ATATTTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTTACT 120
Db 98 ATATTTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTTACT 157
Qy 121 ATTTCTCTGCTAGTCTCAAGAGATTTATATGCCCGGACTGTAGATTCAATTAACGTT 180
Db 158 ATTTCTCTGCTAGTCTCAAGAGATTTATATGCCCGGACTGTAGATTCAATTAACGTT 217
Qy 181 AAAAAAGGGCAGCAGATCTATGTGTACTCAAAAGCTGGTAAAAAGAAATGGAGCTGGAGAA 240
Db 218 AAAAAAGGGCAGCAGATCTATGTGTACTCAAAAGCTGGTAAAAAGAAATGGAGCTGGAGAA 277
Qy 241 TTTTGGCTGGCAGTGTATTTATGTGTATGGCCAGGACGAGATGGAGTCTGGGTTATTTC 300
Db 278 TTTTGGCTGGCAGTGTATTTATGTGTATGGCCAGGACGAGATGGAGTCTGGGTTATTTC 337
Qy 301 CCGAGAACTTGTCAAGGAACAGCGTGTATCCAGGAAGCTACCAAGGAAGTTCACCACC 360
Db 338 CCGAGAACTTGTCAAGGAACAGCGTGTATCCAGGAAGCTACCAAGGAAGTTCACCACC 397
Qy 361 ACGGATATTGACTTCTTCTCGGAG 384
Db 398 ACGGATATTGACTTCTTCTCGGAG 421

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Search completed: December 30, 2003, 09:01:32  
Job time : 1836.61 secs



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OM nucleic - nucleic search, using sw model

Run on: December 30, 2003, 01:34:27 ; Search time 31.014 Seconds  
(without alignments)  
5464.987 Million cell updates/sec

Title: US-10-019-455A-4

Perfect score: 384

Sequence: 1 atgggaagaattattgtact.....atattgactcttctgag 384

Scoring table: IDENTITY NUC

Gapop 10\_0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Watch 0%

Maximum Watch 100%

Listing first 45 summaries

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6: /cgn2\_6/prodata/2/ina/BACKFILES1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	64.8	16.9	459	1	US-08-578-649-1
2	63.2	16.5	581	1	US-08-578-649-4
3	57.4	14.9	330	1	US-08-578-649-18
4	54.2	14.1	305	1	US-08-578-649-8
5	40.4	10.5	596	1	US-08-578-649-24
6	40.4	10.5	3565	1	US-08-578-649-3
7	34	8.9	7218	1	US-08-232-463-14
8	33.6	8.8	1136	3	US-08-860-820-1
9	33.6	8.8	1929	3	US-09-359-161-4
10	33.6	8.8	2159	3	US-08-286-870A-7
11	32.8	8.5	6501	4	US-09-767-515-1
12	32.8	8.5	6501	4	US-09-767-515-2
13	32.2	8.4	202001	4	US-09-734-674-3
14	31.4	8.2	1944	4	US-09-252-991A-889
15	31.4	8.1	10357	4	US-08-961-527-191
16	31.2	8.1	4403765	3	US-09-103-840A-2
17	31.2	8.1	4411529	3	US-09-103-840A-1
18	30.8	8.0	1736	3	US-09-360-197-13
19	30.4	7.9	289	3	US-09-007-005-17
20	30.4	7.9	289	3	US-09-244-796-17
21	29.8	7.8	1830121	4	US-09-557-884-1
22	29.8	7.8	1830121	4	US-09-643-990A-1
23	29.6	7.7	1000	3	US-09-018-584A-38
24	29.6	7.7	319608	4	US-09-539-333D-1
25	29.6	7.7	319608	4	US-09-679-409-1
26	29.4	7.7	1497	4	US-09-220-132-94
27	29.4	7.7	2718	4	US-09-651-656-14

Sequence 14, Appli  
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Sequence 3486, Ap  
Sequence 161, App  
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Sequence 1171, Ap  
Sequence 3, Appli  
Sequence 10933, A  
Sequence 65, Appli  
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Sequence 116, App  
Sequence 94, Appl  
Sequence 2654, Ap  
Sequence 1103, Ap  
Sequence 4, Appli

## ALIGNMENTS

## RESULT 1

US-08-578-649-1  
; Sequence 1, Application US/08578649  
; Patent No. 5770366  
; GENERAL INFORMATION:  
; APPLICANT: Ulrich Bogdan  
; APPLICANT: Reinhard Buttner  
; APPLICANT: Brigitte Kaluza  
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felfe & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: Wordperfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/578,649  
; FILING DATE: 29-July-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE P 43 24 247.2  
; FILING DATE: 20-July-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Andrew L. Tiajolloff  
; REGISTRATION NUMBER: 31,575  
; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 688-9200  
; TELEFAX: (212) 838-3884  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 459 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 40..432  
; FEATURE:  
; NAME/KEY: sig\_peptide  
; LOCATION: 40..111  
; FEATURE:

NAME/KEY: mat\_peptide  
LOCATION: 112..432  
US-08-578-649-1

Query Match 16.9%; Score 64.8; DB 1; Length 459;  
Best Local Similarity 55.6%; Pred. No. 2.3e-11;  
Matches 170; Conservative 0; Mismatches 127; Indels 9; Gaps 2;  
QY 23 TCCTCCGGGCTCTGTGGCTGTATGTGCTGTGATGGAATATTTATGGACCCCTAGCTT 82  
Db 74 TCTTGTCTGTGCTCTTCGCGACCTGGTGTCAAGGGGTGGTCTATGCCCCAAGCTGGCTG 133  
QY 83 CCAAGAGCTCTGTGCGAGATGATGAGTGTCTATATCTATTTCTTGGCTAGTGTCTCAAG 142  
Db 134 ACCGAGCTGTGTGCGGACCAAGATGCGACACCTATCTCCATGGCTGTGGCCCTTC 193  
QY 143 AAGATTATAATGCCCGGACTGTAGATTCATTAAAGGTTAAAGGCGGAGCAGATCTATG 202  
Db 194 AGGACTACATGGCCCCCGGACTGGCGATTCCTGACCATTCACCGGGGCGAAGTGGTATG 253  
QY 203 TGTACTCAAGCTGTAAAGAAAATGGAGCTGGAGATTTTGGGCTGGCAGTGTATTG 262  
Db 254 TCTTCTCAAGCTG-----AAGGGCGTGGCGGCTCTTCGCGGAGCAGGTTTCAGG 307  
QY 263 GTGATGCGCAGGACGAGATGGAG---TCGTGGGTATTTCCTCCAGAACTTGGCTCAAG 319  
Db 308 GAGATTACTATGAGATCTGGCTGCTCGCTGGGCTATTTCCTCCAGTAGCATTTGCCGAG 367  
QY 320 AACAGC 325  
Db 368 AGGACC 373

## RESULT 2

US-08-578-649-4  
Sequence 4, Application US/08578649  
Patent No. 5770366  
GENERAL INFORMATION:  
APPLICANT: Ulrich Bogdan  
APPLICANT: Reinhard Buttnner  
APPLICANT: Brigitte Kaluza  
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/578,649  
FILING DATE: 29-July-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P 43 24 247.2  
FILING DATE: 20-July-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Andrew L. Flajoloff  
REGISTRATION NUMBER: 31,575  
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 581 base pairs  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 110..499  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 110..178  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 179..499  
US-08-578-649-4

Query Match 16.5%; Score 63.2; DB 1; Length 581;  
Best Local Similarity 54.3%; Pred. No. 8.3e-11;  
Matches 175; Conservative 0; Mismatches 138; Indels 9; Gaps 2;

QY 66 TATGGACCGCTTAGCTTCCAAAGAGCTCTGTGCGAGATGATGAGTGTCTATCTATTTC 125  
Db 184 TATGCCCAAGCTGCTGACTGGAAAGCTGTGTGCGGACGAGGAATGCGCCATCCTATCTC 243  
QY 126 TCTGGCTAGTGTCAAGAGATTATAATGCCCGGAGCTGTAGATTTCATTAAAGTTAAAA 185  
Db 244 CATGGCTGTGGCCCTCCAGACTACGTGGCCCTGTATGCGCGCTTCTTGACTATATAG 303  
QY 186 AGGCGACGAGATCTATGTGTACTCAAGAGCTGTGTAAGAAATGGAGCTGGAGAAATTTTG 245  
Db 304 GGCCAAAGTGGTGTATGTCTCTTCCAAAGTTG-----AAGGGCGCTGGCGGCTTTTCTG 357  
QY 246 GGCTGGCAGTGTATTGGTGTATGCGGAGGACGAGATGGGAG---TCGTGGGTATTTCCTC 302  
Db 358 GGGAGGCGAGTGTTCAGGAGGTTACTATGGAGACCTTGGCAGCCGCTGGGCTATTTCCTC 417  
QY 303 CAGGAACCTTGTCAAGGACAGCGTGTGTACAGGAGCTGTGTACAGGAGCTTACCAAGAAAGTTCCCAACAC 362  
Db 418 CAGTAGCATTTGTCGGGAGGACCTGAACTCGAAACCTGGCCAAATTTGATATGAAGACCGA 477  
QY 363 GGATATTGACTTCTTCTGCGAG 384  
Db 478 TCAATGGGATTTCTACTGCCAG 499

## RESULT 3

US-08-578-649-18  
Sequence 18, Application US/08578649  
Patent No. 5770366  
GENERAL INFORMATION:  
APPLICANT: Ulrich Bogdan  
APPLICANT: Reinhard Buttnner  
APPLICANT: Brigitte Kaluza  
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/578,649  
FILING DATE: 29-July-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P 43 24 247.2  
FILING DATE: 20-July-1993  
ATTORNEY/AGENT INFORMATION:

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RESULT 5
US-08-578-649-24
; Sequence 24, Application US/08578649
; Patent No. 5770366
; GENERAL INFORMATION:
; APPLICANT: Ulrich Bogdan
; APPLICANT: Reinhard Butner
; APPLICANT: Brigitte Kaluza
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/578,649
; FILING DATE: 29-July-1994

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NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Alexandria Road, Suite 500  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22131-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,463  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA: 435  
APPLICATION NUMBER: US/07/935,313  
FILING DATE:  
APPLICATION NUMBER: EP 91 114 300.6  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)836-9300  
TELEFAX: (703)683-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7218 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: pTZ9pt-F15  
US-08-232-463-14

[illegible]

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RESULT 8
US-08-860-820-1
; Sequence 1, Application US/08860820
; Patent No. 6245967
; GENERAL INFORMATION:
; APPLICANT: Sonnewald, Uwe
; APPLICANT: Kossmann, Jens
; APPLICANT: Bowien, Eotro
; TITLE OF INVENTION: PROCESS AND DNA MOLECULES FOR INCREASING
; TITLE OF INVENTION: THE PHOTOSYNTHESIS RATE IN PLANTS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:

```

ADDRESSEE: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/860,820  
FILING DATE: 04-SEP-1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 19502053.7  
FILING DATE: 13-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley, James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: AGREVO-7  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-596-9000  
TELEFAX: 212-596-9090  
INFORMATION FOR SEQ ID NO: 1:  
LENGTH: 1136 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 30..1121  
US-08-860-820-1

	Query March	8.8%;	Score 33.6;	DB 3;	Length 1136;
	Best Local Similarity	56.2%;	Pred. No. 0.42;		
	Matches 63;	Conservative 0;	Mismatches 49;	Indels 0;	Gaps 0;
Qy	226	AATGGAGCTGGAGAAATTTGGCTGGCGAGTGTTTTATGCTATGTCGCCAGGACGAGATCGGA	285		
Db	204	AATCAAGCCGAGAAAGCAGGGCGCGTCAAGCTGCAGGGCGAAATCCAGCAGCAAGCTGGAC	263		
Qy	286	GTCTGTGGTGTATTTTCCCGAGAACTTGGTCAAGGAACAGCGTGTGTACCGG	337		
Db	264	GTGCTGAGCAATACCACTTCTCGCGGTCAACGAGTGGGCGCGGTACCTGG	315		

RESULT 9  
US-09-359-161-4/c  
; Sequence 4, Application US/09359161A  
; Patent No. 6342656  
; GENERAL INFORMATION:  
; APPLICANT: Bradford, Kent J.  
; APPLICANT: Dahal, Peetambar  
; APPLICANT: Yang, Hong  
; APPLICANT: Cooley, Michael  
; APPLICANT: Downie, Bruce  
; APPLICANT: Gee, Oliver  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Regulation of Source-Sink Relationships and Responses  
; TITLE OF INVENTION: To Stress Conditions in Plants  
; FILE REFERENCE: 023070-095900US  
; CURRENT APPLICATION NUMBER: US/09/359,161A  
; CURRENT FILING DATE: 1999-07-21  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 1929



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; TITLE OF INVENTION: Amino Acid Analogues
; FILE REFERENCE: 30431.6US01
; CURRENT APPLICATION NUMBER: US/09/767,515
; CURRENT FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/207,627
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 6501
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pOE15-W305F
US-09-767-515-2

Query Match      8.5%; Score 32.8; DB 4; Length 6501;
Best Local Similarity 54.0%; Pred. No. 1.8;
Matches 67; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 234 TGAGAAATTTGGCTGGCAGTGTATGATGATGCCAGGAGAGATGGAGTGTGGG 293
DB 2259 TGGTGAAGCGTGGGAAAGCGTGAATTTGGTAAAGCGGTGCGGAAATCATGGCGTGC 2318
QY 294 TTATTTCCCGAGAACTTGTCAAGGAACAGCGTGTGTACAGGAAGCTACCAAGGAAGT 353
DB 2319 TGAITGGCTAACCGTATGTGATGAAACAGGCTCCGTGGTGGTGGCGAAACAGGAAG 2378
QY 354 TCCC 357
DB 2379 CCGC 2382

RESULT 13
US-09-734-674-3
; Sequence 3, Application US/09734674
; Patent No. 6498022
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; FILE REFERENCE: CL001018
; CURRENT APPLICATION NUMBER: US/09/734, 674
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 202001
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(202001)
; OTHER INFORMATION: n = A, T, C or G
US-09-734-674-3

Query Match      8.4%; Score 32.2; DB 4; Length 202001;
Best Local Similarity 49.7%; Pred. No. 15;
Matches 82; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 119 CTAATTTCTGGCTAGTGTCTCAAGAAATTAATGCCCCGAGTGTAGATCAATTAACG 178
DB 183409 CTTAAGCTCAGGAGAGAGTGAAGCGAGAGCTGAGTGGTCCGTGAATCATTAGCAAGTCT 183468
QY 179 TTAAGAAAGCGCAGCAGATCTATGTGTACTCAAAAGCTGTGTAAAGAAATGGAGCTGGAG 238
DB 183469 GAAAGTCAAGCCATGGTATGATGAATCTTCCAGGAGAAAGAAACAGAGATGAG 183528
QY 239 AATTTGGCTGGCAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATG 283
DB 183529 AGTCAGGAATCCCAATGTTGAGGGGGCAATAATAAGGAAGAGATTG 183573
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## RESULT 14

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US-09-252-991A-889/c
; Sequence 889, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 889
; LENGTH: 1944
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-889
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Query Match      8.2%; Score 31.4; DB 4; Length 1944;
Best Local Similarity 51.8%; Pred. No. 2.8;
Matches 71; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
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QY 235 GGAGAAATTTGGGCTGGCAGTGTATGATGATGCCAGGAGAGATGGAGTGTGGGT 294
DB 420 GGGGTAGTGTAGATGGCGCAATTTGAACACCATGGCCAGGCCGAGATCGGATCAT 361
QY 295 TATTTCCCGAGAACTTGGTCAAGGAACAGCGTGTGTACCAAGAAAGCTACCAAGGAAGTT 354
DB 360 CGTTGGCCGGAAGCTTCCGCCAGGTCCATGATCTTCAGCGTGTGATCCGAGGGCGAT 301
QY 355 CCCACCGCGATATGA 371
DB 300 CGGACCTGGCGGTGA 284
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## RESULT 15

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US-08-961-527-191/c
; Sequence 191, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
```



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; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 191:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10357 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-191

Query Match      8.1%; Score 31.2; DB 4; Length 10357;
Best Local Similarity 55.6%; Pred.No. 7.4;
Matches 60; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

Qy      48  TGGTGTGCTATGGAATATTATGACCGCTAGCTTCCAAGAAGCTCTGTGCAGATGATGA 107
Db      1592  TGGTGACCAAGAGGTTGGACGGTCTTGCTGAACACATTCACITTTTGAAGATTT 1533

Qy      108  GTGTGTCTATCTATTCTCTGGCTAGTGTCAAGAAGATTATAATGC 155
Db      1532  GGGTGTCTCTGCAATTGAAGTGGGTATTCCTTTTCAGACCCCTGTTGC 1485
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Search completed: December 30, 2003, 06:10:38  
Job time : 41.014 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: December 29, 2003, 22:08:26 ; Search time 1216 Seconds  
(without alignments)  
12918.830 Million cell updates/sec

Title: US-10-019-455A-10  
Perfect score: 384  
Sequence: 1 atggcaaggatattgattct.....attatgactttctgtgaa 384

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl.\*  
1: gb\_ba.\*  
2: gb\_htg.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*  
15: em\_ba.\*  
16: em\_fun.\*  
17: em\_hum.\*  
18: em\_in.\*  
19: em\_mu.\*  
20: em\_om.\*  
21: em\_or.\*  
22: em\_ov.\*  
23: em\_pat.\*  
24: em\_ph.\*  
25: em\_pl.\*  
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29: em\_vi.\*  
30: em\_htg\_hum.\*  
31: em\_htg\_inv.\*  
32: em\_htg\_other.\*  
33: em\_htg\_mus.\*  
34: em\_htg\_pln.\*  
35: em\_htg\_rod.\*  
36: em\_htg\_mam.\*  
37: em\_htg\_vrt.\*  
38: em\_sy.\*  
39: em\_htgo\_hum.\*  
40: em\_htgo\_mus.\*  
41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	384	100.0	384	6	BD010805	BD010805 Novel pol
2	384	100.0	384	6	BD093106	BD093106 Novel pol
3	384	100.0	929	10	AF243504	AF243504 Mus muscu
4	384	100.0	947	6	BD010821	BD010821 Novel pol
5	384	100.0	947	6	BD093122	BD093122 Novel pol
6	384	100.0	958	10	MMU243539	AU243939 Mus muscu
7	384	100.0	1054	10	AF233333	AF233333 Mus muscu
8	344	89.6	384	6	BD010835	BD010835 Novel pol
9	344	89.6	384	6	BD093136	BD093136 Novel pol
10	330	85.9	330	6	BD010817	BD010817 Novel pol
11	330	85.9	330	6	BD093118	BD093118 Novel pol
12	294.8	76.8	330	6	BD010836	BD010836 Novel pol
13	294.8	76.8	330	6	BD093137	BD093137 Novel pol
14	287	74.7	384	6	BD010802	BD010802 Novel pol
15	287	74.7	384	6	BD093103	BD093103 Novel pol
16	287	74.7	521	6	AX358818	AX358818 Sequence
17	287	74.7	521	6	AX362311	AX362311 Sequence
18	287	74.7	521	6	AX454774	AX454774 Sequence
19	287	74.7	521	6	AX491252	AX491252 Sequence
20	287	74.7	846	9	AF233261	AF233261 Homo sapi
21	287	74.7	865	9	AF243505	AF243505 Homo sapi
22	287	74.7	923	6	BD010820	BD010820 Novel pol
23	287	74.7	923	6	BD093121	BD093121 Novel pol
24	287	74.7	1422	9	HSA242552	AJ242552 Homo sapi
25	267.8	69.7	307	6	BD010830	BD010830 Novel pol
26	267.8	69.7	307	6	BD093131	BD093131 Novel pol
27	252.2	65.7	330	6	BD010816	BD010816 Novel pol
28	252.2	65.7	330	6	BD093117	BD093117 Novel pol
29	233.8	60.9	261	6	BD010829	BD010829 Novel pol
30	233.8	60.9	261	6	BD093130	BD093130 Novel pol
31	178	46.4	484	5	AF233518	AF233518 Gallus ga
32	142.4	37.1	144765	2	EX510362	EX510362 Mus muscu
33	135.6	35.3	466	5	AF233519	AF233519 Rana cate
34	126	32.8	215581	2	AC106161	AC106161 Rattus no
35	114.8	29.9	232	9	HSA252325	AJ252325 Homo sapi
36	114.8	29.9	121151	9	HS705D16	AL034428 Human DNA
37	81.8	21.3	259	9	HSA252326	AJ252326 Homo sapi
38	76.4	19.9	358	9	HSA252324	AJ252324 Homo sapi
39	68.6	17.9	545	10	MMU67884	U67884 Rattus norv
40	66.2	17.2	580	10	MMU1A	X94322 M.musculus
41	66.2	17.2	581	6	A42945	A42945 Sequence 4
42	66.2	17.2	581	6	AX016788	AX016788 Sequence
43	60.2	15.7	396	9	BT007044	BT007044 Homo sapi
44	60.2	15.7	396	12	BT007775	BT007775 Synthetic
45	60.2	15.7	433	6	AX253435	AX253435 Sequence

ALIGNMENTS

RESULT 1  
BD010805  
LOCUS BD010805 384 bp DNA linear PAT 31-JAN-2002  
DEFINITION Novel polypeptide and DNA thereof.  
ACCESSION BD010805  
VERSION BD010805.1 GI:18639178  
KEYWORDS JP 2001069994-A/6.  
SOURCE Mus sp.  
ORGANISM Mus sp.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 384)  
AUTHORS Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y.,  
Yoshimura,K. and Tanaka,H.  
TITLE Novel polypeptide and DNA thereof

JOURNAL Patent: JP 2001069994-A 6 21-MAR-2001;  
TAKEDA CHEMICAL INDUSTRIES LTD  
COMMENT OS Mus sp. (mouse)  
PN JP 2001069994-A/6  
PD 21-MAR-2001  
PF 29-JUN-2000 JP 2000195911  
PR  
PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI  
SHINICHI MOGI,  
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA  
PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC  
A61P19/08,  
PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC  
G01N33/53//  
PC C12P21/08, C12N15/00, A61K37/02, C12N5/00  
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FT source 1..384  
FT /organism="Mus sp. (mouse)".  
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/db\_xref="taxon:10095"  
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Best Local Similarity 100.0%; Pred. No. 1.8e-106;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGGCAAGGATATTCATCTTTGCTGGGGCCCTTGTGTTCTATGTGCGGGCATGGT 60  
Db 1 ATGGCAAGGATATTCATCTTTGCTGGGGCCCTTGTGTTCTATGTGCGGGCATGGT 60  
QY 61 GTATTATGGAATAAATTCTTCTTAAGAAGTTGTGCGGATGAGGAGTGTTCTATACT 120  
Db 61 GTATTATGGAATAAATTCTTCTTAAGAAGTTGTGCGGATGAGGAGTGTTCTATACT 120  
QY 121 ATTTCTCTGGCAAGACAGAGATTCATCTTCTTAAGAAGTTGTGCGGATGAGGAGTGTTCTATACT 180  
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QY 181 AAGAAAGGCGACAGATCTATGTTTACTTCCAAAGCTGGTAAACAGAAAACGGAGCTGGAGAG 240  
Db 181 AAGAAAGGCGACAGATCTATGTTTACTTCCAAAGCTGGTAAACAGAAAACGGAGCTGGAGAG 240  
QY 241 TTTTGGGCTGGCAGTGTTTATGGTGACCAACAGGATGAGATGGGAATTTAGGTTATTTC 300  
Db 241 TTTTGGGCTGGCAGTGTTTATGGTGACCAACAGGATGAGATGGGAATTTAGGTTATTTC 300  
QY 301 CCCAGCACTTGGTGAAGGACAGCGTGTATACCAAGGAGGCCACCAAGGAGATCCCAACC 360  
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QY 361 ACGGATATTGACTTCTCTGTGAA 384  
Db 361 ACGGATATTGACTTCTCTGTGAA 384  
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DEFINITION BD093106  
ACCESSION BD093106.1 GI:22638694  
VERSION BD093106.1  
KEYWORDS WO 0102564-A/6.  
SOURCE Mus sp.  
ORGANISM Mus sp.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 384)  
AUTHORS Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,

Yoshimura, K. and Tanaka, H.  
Novel polypeptide and its DNA  
Patent: WO 0102564-A 6 11-JAN-2001;  
TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO  
OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,  
HIDEYUKI TANAKA  
COMMENT OS Mus sp. (mouse)  
PN WO 0102564-A/6  
PD 11-JUN-2001  
PF 29-JUN-2000 WO 2000JP004278  
PF 30-JUN-1999 JP 99P 186718  
PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI  
MOGI,  
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA  
PC C12N15/12, C12N5/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC  
A61K38/17,  
PC A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7088// (C12P21/  
PC 02, C12R1:19)  
CC  
FH Key Location/Qualifiers.  
FEATURES  
source 1..384  
Location/Qualifiers  
/organism="Mus sp."  
/mol\_type="genomic DNA"  
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BASE COUNT 98 a 68 c 111 g 107 t  
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Query Match 100.0%; Score 384; DB 6; Length 384;  
Best Local Similarity 100.0%; Pred. No. 1.8e-106;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGGCAAGGATATTCATCTTTGCTGGGGCCCTTGTGTTCTATGTGCGGGCATGGT 60  
Db 1 ATGGCAAGGATATTCATCTTTGCTGGGGCCCTTGTGTTCTATGTGCGGGCATGGT 60  
QY 61 GTATTATGGAATAAATTCTTCTTAAGAAGTTGTGCGGATGAGGAGTGTTCTATACT 120  
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Db 121 ATTTCTCTGGCAAGACAGAGATTCATCTTCTTAAGAAGTTGTGCGGATGAGGAGTGTTCTATACT 180  
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Db 181 AAGAAAGGCGACAGATCTATGTTTACTTCCAAAGCTGGTAAACAGAAAACGGAGCTGGAGAG 240  
QY 241 TTTTGGGCTGGCAGTGTTTATGGTGACCAACAGGATGAGATGGGAATTTAGGTTATTTC 300  
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QY 301 CCCAGCACTTGGTGAAGGACAGCGTGTATACCAAGGAGGCCACCAAGGAGATCCCAACC 360  
Db 301 CCCAGCACTTGGTGAAGGACAGCGTGTATACCAAGGAGGCCACCAAGGAGATCCCAACC 360  
QY 361 ACGGATATTGACTTCTCTGTGAA 384  
Db 361 ACGGATATTGACTTCTCTGTGAA 384  
RESULT 3  
AF243504  
LOCUS Mus musculus fibrocyte-derived protein (Fdp) mRNA ROD 26-DEC-2000  
DEFINITION AF243504  
ACCESSION AF243504  
VERSION AF243504.1 GI:11991841  
KEYWORDS Mus musculus (house mouse)  
SOURCE Mus musculus  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 929)  
AUTHORS Cohen-Salmon,M., Frenz,D., Liu,W., Verpy,E., Voegelings,S. and Petit,C.  
TITLE Fdp, a new fibrocyte-derived protein related to MIA/CD-RAP, has an in vitro effect on the early differentiation of the inner ear mesenchyme  
JOURNAL J. Biol. Chem. 275 (51), 40036-40041 (2000)  
MEDLINE 20568254  
PUBMED 10998416  
REFERENCE 2 (bases 1 to 929)  
AUTHORS Cohen-Salmon,M., Frenz,D., Verpy,E., Voegelings,S. and Petit,C.  
TITLE Direct Submission  
JOURNAL Submitted (09-MAR-2000) Biotechnologies, Institut Pasteur, 25 rue du Dr. Roux, Paris 75015, France  
FEATURES  
source location/Qualifiers  
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BASE COUNT 260 a 156 c 220 g 293 t  
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Best Local Similarity 100.0%; Pred. No. 2e-106;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGCCAAGGATATTGATCTTTTGGGGCCCTTGGTCTTATGTGCGGGCATGGT 60  
Db 9 ATGCCAAGGATATTGATCTTTTGGGGCCCTTGGTCTTATGTGCGGGCATGGT 68  
Qy 61 GTATTTATGGATAAATCTTCTTAAGAAGTTGTGCGGATGAGGTGCTTACT 120  
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Qy 181 AAGAAAGGCGACAGATCTATGTTTACTCCAAAGCTGGTAACAGAAACGGAGCTGGAGAG 240  
Db 189 AAGAAAGGCGACAGATCTATGTTTACTCCAAAGCTGGTAACAGAAACGGAGCTGGAGAG 248  
Qy 241 TTTTGGGCTGCGAGTGTATGTTGTCACCAAGGATGAGATGGAATGTAGGTTATTTTC 300  
Db 249 TTTTGGGCTGCGAGTGTATGTTGTCACCAAGGATGAGATGGAATGTAGGTTATTTTC 308  
Qy 301 CCCAGCAACTTGGTGAAGGACGCGGTGTATACAGAGGCGCAACCAAGGATCCCCAAC 360  
Db 309 CCCAGCAACTTGGTGAAGGACGCGGTGTATACAGAGGCGCAACCAAGGATCCCCAAC 368  
Qy 361 ACGGATATTGACTTCTCTGTGAA 384  
Db 369 ACGGATATTGACTTCTCTGTGAA 392

REFERENCE 4  
BD010821  
LOCUS BD010821 947 bp DNA linear PAT 31-JAN-2002  
DEFINITION Novel polypeptide and DNA thereof.  
ACCESSION BD010821

VERSION BD010821.1 GI:18639194  
KEYWORDS JP 2001069994-A/22.  
SOURCE Mus sp.  
ORGANISM Mus sp.  
REFERENCE 1 (bases 1 to 947)  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y., Yoshimura,K. and Tanaka,H.  
TITLE Novel polypeptide and DNA thereof  
JOURNAL Patent: JP 2001069994-A 22 21-MAR-2001;  
TAKEDA CHEMICAL INDUSTRIES LTD  
COMMENT OS Mus sp. (mouse)  
PN JP 2001069994-A/22  
PD 21-MAR-2001  
PF 29-JUN-2000 JP 2000195911  
PR PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI SHINICHI MOGI.  
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA  
PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC A61F19/08,  
PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC G01N33/53//  
PC C12P21/08, C12N15/00, A61K37/02, C12N5/00  
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FT source 1..947  
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Query Match 100.0%; Score 384; DB 6; Length 947;  
Best Local Similarity 100.0%; Pred. No. 2e-106;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGCCAAGGATATTGATCTTTTGGGGCCCTTGGTCTTATGTGCGGGCATGGT 60  
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Qy 61 GTATTTATGGATAAATCTTCTTAAGAAGTTGTGCGGATGAGGTGCTTACT 120  
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Db 131 ATTTCTCTGGCAAGACAGAGAGATTACAATGCCCAGACTGTAGGTTTCATGATGC 190  
Qy 181 AAGAAAGGCGACAGATCTATGTTTACTCCAAAGCTGGTAACAGAAACGGAGCTGGAGAG 240  
Db 191 AAGAAAGGCGACAGATCTATGTTTACTCCAAAGCTGGTAACAGAAACGGAGCTGGAGAG 250  
Qy 241 TTTTGGGCTGCGAGTGTATGTTGTCACCAAGGATGAGATGGAATGTAGGTTATTTTC 300  
Db 251 TTTTGGGCTGCGAGTGTATGTTGTCACCAAGGATGAGATGGAATGTAGGTTATTTTC 310  
Qy 301 CCCAGCAACTTGGTGAAGGACGCGGTGTATACAGAGGCGCAACCAAGGATCCCCAAC 360  
Db 311 CCCAGCAACTTGGTGAAGGACGCGGTGTATACAGAGGCGCAACCAAGGATCCCCAAC 370  
Qy 361 ACGGATATTGACTTCTCTGTGAA 384  
Db 371 ACGGATATTGACTTCTCTGTGAA 394

RESULT 5  
BD093122 947 bp DNA linear PAT 27-AUG-2002  
LOCUS BD093122

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DEFINITION Novel polypeptide and its DNA.
ACCESSION BD093122
VERSION BD093122.1 GI:22638710
KEYWORDS WO 0102564-A/22.
SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
JOURNAL Yoshimura, K. and Tanaka, H.
PATENT: WO 0102564-A/22 11-JAN-2001;
TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO
OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,
HIDYUKI TANAKA
COMMENT OS Mus sp. (mouse)
PN WO 0102564-A/22
PD 11-JAN-2001
PF 29-JUN-2000 WO 2000JP004278
PR 30-JUN-1999 JP 99P 186718
PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
MOGI,
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/12, C12N5/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC
A61K38/17,
PC A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7088// (C12P21/
PC 02, C12R1:19)
CC
FH Key Location/Qualifiers.
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Best Local Similarity 100.0%; Pred. No. 2e-106;
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QY 1 ATGGCAAGGATATGATCTTTTGTGGGGCCCTGTGGTCTATGTCGGCGCATGCT 60
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Db |||
QY 61 GTATTTATGGATAAACTTTCTTAAGAAAGTTGTGTGGGATGAGGAGTGTCTATCT 120
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QY 71 GTATTTATGGATAAACTTTCTTAAGAAAGTTGTGTGGGATGAGGAGTGTCTATCT 130
Db |||
QY 121 ATTTCTCTGGCAGACAGCAGGAGATTACAATGCCCGCAGCTGTAGGTTTCATGATGC 180
Db |||
QY 131 ATTTCTCTGGCAGACAGCAGGAGATTACAATGCCCGCAGCTGTAGGTTTCATGATGC 190
Db |||
QY 181 AAGAAAGGCGCAGCATCTATGTTTACTCCAGCTGGTAAACAGAAAACGAGCTGGAGAG 240
Db |||
QY 191 AAGAAAGGCGCAGCATCTATGTTTACTCCAGCTGGTAAACAGAAAACGAGCTGGAGAG 250
Db |||
QY 241 TTTTGGGCTGGCAGTGTATGTTGATGACCAACGAGATGAGATGGAAATGTAGTTATTTTC 300
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QY 251 TTTTGGGCTGGCAGTGTATGTTGATGACCAACGAGATGAGATGGAAATGTAGTTATTTTC 310
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QY 301 CCCAGCAACTTGGTGAAGAGCAGCGTGTATACCGAGGGCCACCAAGAGATCCCAACC 360
Db |||
QY 311 CCCAGCAACTTGGTGAAGAGCAGCGTGTATACCGAGGGCCACCAAGAGATCCCAACC 370
Db |||
QY 361 ACGGATATTGACTTCTTCTGTGAA 384
Db |||
QY 371 ACGGATATTGACTTCTTCTGTGAA 394
Db |||
RESULT 6
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MMU243939 958 bp mRNA linear ROD 29-JAN-2001
LOCUS Mus musculus mRNA for melanoma inhibitory activity-like protein
DEFINITION (Mial gene).
ACCESSION AJ243939
VERSION AJ243939.1 GI:12619174
KEYWORDS melanoma inhibitory activity-like protein; Mial gene.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE Rendtorff, N.D., Frodin, M., Attie-Bitach, T., Vekemans, M. and
JOURNAL Tommerup, N.
PATENT: Identification and characterization of an inner ear-expressed human
OGI, melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent
HIDYUKI TANAKA polymorphism that abolishes translation
COMMENT Genomics 71 (1), 40-52 (2001)
PC 21100875
PD 11161796
PF 2 (bases 1 to 958)
PR Rendtorff, N.D.
PI Direct Submission
PC Submitted (20-JUL-1999) Rendtorff N.D., Department of Medical
Genetics, Institute of Medical Biochemistry and Genetics,
Blegdamsvej 3, 2200 Copenhagen N, DENMARK
PC Related sequence: AJ242552.
CC
FH Key Location/Qualifiers.
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BASE COUNT 1. 958
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 2e-106;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGCAAGGATATGATCTTTTGTGGGGCCCTGTGGTCTATGTCGGCGCATGCT 60
Db |||
QY 24 ATGGCAAGGATATGATCTTTTGTGGGGCCCTGTGGTCTATGTCGGCGCATGCT 83
Db |||
QY 61 GTATTTATGGATAAACTTTCTTAAGAAAGTTGTGTGGGATGAGGAGTGTCTATCT 120
Db |||
QY 84 GTATTTATGGATAAACTTTCTTAAGAAAGTTGTGTGGGATGAGGAGTGTCTATCT 143
Db |||
QY 121 ATTTCTCTGGCAGACAGCAGGAGATTACAATGCCCGCAGCTGTAGGTTTCATGATGC 180
Db |||
QY 144 ATTTCTCTGGCAGACAGCAGGAGATTACAATGCCCGCAGCTGTAGGTTTCATGATGC 203
Db |||
QY 181 AAGAAAGGCGCAGCATCTATGTTTACTCCAGCTGGTAAACAGAAAACGAGCTGGAGAG 240
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Db      204 AAGAAAGGCGCAGCAGATCTATGTTTACTCCAGCTGGTAACAGAAAACGAGCTGGAGG 263
Qy      241 TTTTGGGCTGGCAGTGTATGCTGACACACAGGATGAGATGGGAATTGTAGGTATTTC 300
Db      264 TTTTGGGCTGGCAGTGTATGCTGACACACAGGATGAGATGGGAATTGTAGGTATTTC 323
Qy      301 CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACACAGGAGGCCACCAAGAGATCCCAACC 360
Db      324 CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACACAGGAGGCCACCAAGAGATCCCAACC 383
Qy      361 ACGGATATTGACTTCTCTCTGTGAA 384
Db      384 ACGGATATTGACTTCTCTCTGTGAA 407

RESULT 7
AF233333      1054 bp  mRNA  linear  ROD 06-JUL-2000
LOCUS      Mus musculus otoraplin mRNA, complete cds.
DEFINITION      AF233333
ACCESSION      AF233333.1 GI:8927429
VERSION      Mus musculus (house mouse)
SOURCE      Mus musculus
ORGANISM      Mus musculus
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1054)
Robertson,N.G., Heller,S., Lin,J.S., Resendes,B.L., Weremowicz,S.,
Denis,C.S., Bell,A.M., Hudspeth,A.J. and Morton,C.C.
TITLE      A novel conserved cochlear gene, OTOR: identification, expression
JOURNAL      analysis, and chromosomal mapping
MEDLINE      Genomics 66 (3), 242-248 (2000)
20334619
PUBMED      10873378
2 (bases 1 to 1054)
Robertson,N.G., Heller,S., Lin,J.S., Resendes,B.L., Weremowicz,S.,
Denis,C.S., Bell,A.M., Hudspeth,A.J. and Morton,C.C.
AUTHORS      Direct Submission
TITLE      Submitted (10-FEB-2000) Pathology, Brigham and Women's Hospital, 75
JOURNAL      Francis Street, Boston, MA 02115, USA
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BASE COUNT      296 a 183 c 265 g 310 t
ORIGIN

Query Match      100.0%; Score 384; DB 10; Length 1054;
Best Local Similarity 100.0%; Pred. No. 2e-106;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ATGCAAGGATATTGATTCTTTCTTGGGGCCCTTGTGTTCTATGTCGGGCGCATGGT 60
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Qy      61 GTATTTATGATAAATCTTCTTAAGAGTTGTGCGGATGAGGAGTGTCCTACT 120
Db      78 GTATTTATGATAAATCTTCTTCTTAAGAGTTGTGCGGATGAGGAGTGTCCTACT 137
Qy      121 ATTTCTCTGGCAAGCAGCAGAGATTACAAATGCCCCAGACTGTAGTTCATCGATGC 180
Db      138 ATTTCTCTGGCAAGCAGCAGAGATTACAAATGCCCCAGACTGTAGTTCATCGATGC 197

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Qy      181 AAGAAAGGCGCAGCAGATCTATGTTTACTCCAGCTGGTAACAGAAAACGAGCTGGAGG 240
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Qy      241 TTTTGGGCTGGCAGTGTATGCTGACACACAGGATGAGATGGGAATTGTAGGTATTTC 300
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Qy      301 CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACACAGGAGGCCACCAAGAGATCCCAACC 360
Db      318 CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACACAGGAGGCCACCAAGAGATCCCAACC 377
Qy      361 ACGGATATTGACTTCTCTCTGTGAA 384
Db      378 ACGGATATTGACTTCTCTCTGTGAA 401

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RESULT 8
BD010835      384 bp  DNA  linear  PAT 31-JAN-2002
LOCUS      Novel polypeptide and DNA thereof.
DEFINITION      BD010835
ACCESSION      BD010835
VERSION      BD010835.1 GI:18639208
KEYWORDS      JP 2001069994-A/36.
SOURCE      Rattus sp.
ORGANISM      Rattus sp.
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 384)
Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y.,
Yoshimura,K. and Tanaka,H.
TITLE      Novel polypeptide and DNA thereof
JOURNAL      Patent: JP 2001069994-A 36 21-MAR-2001;
COMMENT      TAKEDA CHEMICAL INDUSTRIES LTD
OS      Rattus sp. (rat)
PN      JP 2001069994-A/36
PD      21-MAR-2001
PF      29-JUN-2000 JP 2000195911
PR      YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI
SHINICHI MOGI,
PI      YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC      C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P9/00,A61P19/02, PC
A61P19/08,
PC      C07K14/47,C07K16/18,C12N1/21,C12N5/10,G01N33/15,G01N33/50, PC
G01N33/53//
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FH      Key      Location/Qualifiers
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Query Match      89.6%; Score 344; DB 6; Length 384;
Best Local Similarity 93.5%; Pred. No. 3.3e-94;
Matches 359; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Qy      1 ATGCAAGGATATTGATTCTTTCTTGGGGCCCTTGTGTTCTATGTCGGGCGCATGGT 60
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 Db 361 ACGGATATTGACTTCTTCTGTGAA 384

RESULT 9  
 LOCUS BD093136 384 bp DNA linear PAT 27-AUG-2002  
 DEFINITION Novel polypeptide and its DNA.  
 ACCESSION BD093136  
 VERSION BD093136.1 GI:22638724  
 KEYWORDS WO 0102564-A/36.  
 SOURCE Rattus sp.  
 ORGANISM Rattus sp.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE  
 AUTHORS Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y.,  
 Yoshimura,K. and Tanaka,H.  
 TITLE Novel polypeptide and its DNA  
 JOURNAL Patent: WO 0102564-A 36 11-JAN-2001;  
 TAKEDA CHEMICAL INDUSTRIES LTD,YASUAKI ITO,KAZUNORI NISHI, KAZUHIRO  
 OGI, SHOICHI OKUBO, SHINICHI MOGI,YUKO NOGUCHI,KOJI YOSHIMURA,  
 HIDEYUKI TANAKA

COMMENT  
 OS Rattus sp. (rat)  
 PN WO 0102564-A/36  
 PD 11-JAN-2001  
 PF 29-JUN-2000 WO 2000P004278  
 PR 30-JUN-1999 JP 99P 186718  
 PI YASUAKI ITO,KAZUNORI NISHI,KAZUHIRO OGI,SHOICHI OKUBO,SHINICHI

PI MOGI,  
 PI YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA  
 PC C12N15/12,C12N5/10,C12P21/02,C07K14/47,C07K16/18,A61K45/00, PC  
 A61K38/17,  
 PC A61K39/395,A61K49/16,A61P19/02,A61P19/08,A61K31/7088/(C12P21/  
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PH Key Location/Qualifiers.

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Query Match 89.6%; Score 344; DB 6; Length 384;  
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 Matches 359; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1 ATGCGAAGGATATTGATCTTTTCTGCTGGGGGCTTGCTGTTCTATGTCGGGGCATGTT 60  
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QY 61 GTATTTATGGATAAACTTTCTTCTTAAGAAGTTGTGTGCGGATGAGGAGTGTGCTATACT 120

Db 61 ATGTTTATGGATAAACTTTCTTCTTAAGAAGTTGTGTGCGGATGAGGAGTGTGCTATACT 120  
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 Db 121 ATTTCTCTGGCAGAGCAGAGGATTACAATGCCCGCAGACTGTAGGTTTCATCAATGTC 180  
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 Db 361 ACGGATATTGACTTCTTCTGTGAA 384

RESULT 10

LOCUS BD010817 330 bp DNA linear PAT 31-JAN-2002  
 DEFINITION Novel polypeptide and DNA thereof.  
 ACCESSION BD010817  
 VERSION BD010817.1 GI:18639190  
 KEYWORDS JP 2001069994-A/18.  
 SOURCE Mus sp.  
 ORGANISM Mus sp.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y.,  
 Yoshimura,K. and Tanaka,H.  
 TITLE Novel polypeptide and DNA thereof  
 JOURNAL Patent: JP 2001069994-A 18 21-MAR-2001;  
 TAKEDA CHEMICAL INDUSTRIES LTD

COMMENT  
 OS Mus sp. (mouse)  
 PN JP 2001069994-A/18  
 PD 21-MAR-2001  
 PF 29-JUN-2000 JP 2000195911  
 PR  
 PI YASUAKI ITO,KAZUNORI NISHI,KAZUHIRO OGI,SHOICHI OKUBO, PI  
 SHINICHI MOGI,  
 PI YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA  
 PC C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P9/00,A61P19/02, PC  
 A61P19/08,  
 PC C07K14/47,C07K16/18,C12N1/21,C12N5/10,G01N33/50, PC  
 G01N33/53//  
 PC C12P21/08,C12N15/00,A61K37/02,C12N5/00  
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PH Key Location/Qualifiers  
 FT source 1. .330  
 FT /organism="Mus sp. (mouse)"/

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BASE COUNT 91 a 60 c 92 g 87 t

ORIGIN

Query Match 85.9%; Score 330; DB 6; Length 330;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-90;  
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 CATGGTGTATTTATGATAAACTTTCTTCTTAAGAAGTTGTGTGCGGATGAGGAGTGTGTC 114

Db 1 CATGGTGTATTTATGATAAACTTTCTTCTTAAGAAGTTGTGTGCGGATGAGGAGTGTGTC 60



Qy 115 TATACTATTTCTCTGGCAAGACACAGGAAGATTACAATGCCAGAGCTGTAGGTTTCATC 174  
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 Qy 175 GATGTCAGAAAGGCGCAGCATCTATGTTTACTCCAAAGCTGGTAAACAGAAAACCGAGCT 234  
 Db 121 GATGTCAGAAAGGCGCAGCATCTATGTTTACTCCAAAGCTGGTAAACAGAAAACCGAGCT 180  
 Qy 235 GGAGAGTTTTGGGCTGGCAGTGTATGTTAGTGACCAACAGGATGAGATGGGAATTTAGGT 294  
 Db 181 GGAGAGTTTTGGGCTGGCAGTGTATGTTAGTGACCAACAGGATGAGATGGGAATTTAGGT 240  
 Qy 295 TATTTCCCGCAGCACTTGGTGAAGCAGCGTGTATACCAAGGCGCCACCAAGGAGATC 354  
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 Qy 355 CCAACCGGATATTGACTTCTCTGTGAA 384  
 Db 301 CCAACCGGATATTGACTTCTCTGTGAA 330

RESULT 11  
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 LOCUS Novel polypeptide and its DNA. linear PAT 27-AUG-2002  
 DEFINITION  
 ACCESSION BD093118  
 VERSION BD093118.1 GI:22638706  
 KEYWORDS WO 0102564-A/18.  
 SOURCE Mus sp.  
 ORGANISM Mus sp.  
 REFERENCE 1 (bases 1 to 330)  
 AUTHORS Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y., Yoshimura, K. and Tanaka, H.  
 TITLE Novel polypeptide and its DNA  
 JOURNAL Patent: WO 0102564-A 18 11-JAN-2001;  
 TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA  
 COMMENT OS Mus sp. (mouse)  
 PN WO 0102564-A/18  
 PD 11-JAN-2001  
 PF 29-JUN-2000 WO 2000JP004278  
 PR 30-JUN-1999 JP 99P 186718  
 PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI MOGI,

PI MOGI,  
 PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA  
 PC C12N15/12, C12N5/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC A61K38/17,  
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 Db 301 CCAACCGGATATTGACTTCTCTGTGAA 330

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 LOCUS Novel polypeptide and DNA thereof. linear PAT 31-JAN-2002  
 DEFINITION  
 ACCESSION BD010836  
 VERSION BD010836.1 GI:18639209  
 KEYWORDS JP 2001069994-A/37.  
 SOURCE Rattus sp.  
 ORGANISM Rattus sp.  
 REFERENCE 1 (bases 1 to 330)  
 AUTHORS Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y., Yoshimura, K. and Tanaka, H.  
 TITLE Novel polypeptide and DNA thereof  
 JOURNAL Patent: JP 2001069994-A 37 21-MAR-2001;  
 TAKEDA CHEMICAL INDUSTRIES LTD  
 COMMENT OS Rattus sp. (rat)  
 PN JP 2001069994-A/37  
 PD 21-MAR-2001  
 PF 29-JUN-2000 JP 2000195911  
 PR YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI SHINICHI MOGI,  
 PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA  
 PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC A61P19/08,  
 PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC G01N33/53//  
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Qy 235 GGAGAGTTTTGGGCTGGCAGTGTATGTTGATGACACCAAGGATGAGATGGGAATTTAGGT 294

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Qy 355 CCAACACCGATATTGACTTCTTCTGTGAA 384

Db 301 CCAACACCGATATTGACTTCTTCTGTGAA 330

RESULT 13

BD093137

LOCUS

DEFINITION Novel polypeptide and its DNA.

ACCESSION BD093137

VERSION BD093137.1 GI:22638725

KEYWORDS WO 0102564-A/37.

SOURCE Rattus sp.

ORGANISM Rattus sp.

REFERENCE 1 (bases 1 to 330)

AUTHORS Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y., Yoshimura,K. and Tanaka,H.

TITLE Novel polypeptide and its DNA

JOURNAL Patent: WO 0102564-A 37 11-JAN-2001;

TAKEDA CHEMICAL INDUSTRIES LTD.YASUAKI ITO,KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI MOGI,YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA

COMMENT OS Rattus sp. (rat)

PN WO 0102564-A/37

PD 11-JAN-2001

PF 29-JUN-2000 WO 2000JP004278

PR 30-JUN-1999 JP 99P 186718

PI YASUAKI ITO,KAZUNORI NISHI,KAZUHIRO OGI,SHOICHI OKUBO,SHINICHI MOGI, YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA

FEATURES

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Best Local Similarity 93.3%; Pred. No. 4e-79;

Matches 308; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Qy 55 CATGGTGATTATGGATTAACCTTTCTTCTAAGAGTGTGTGCGGATGAGAGTGTGTC 114

Db 1 CATGGCATGTTTATGGATTAACCTTTCTTCTAAGAGTGTGTGCGGATGAGAGTGTGTC 60

Qy 115 TATACATTTCTCTGGCAAGACACAGGAAGATTACAAATGCCCGGAGCTGTAGGTTTCATC 174

Db 61 TATACCAATTTCTCTGGCAAGACACAGGAAGACTACAAATGCCCGGAGCTGTAGGTTTCATC 120

Qy 175 GATGTCAGAAAGGCGCAGACATCTATGTTTACTCCAAAGCTGGTAAACAGAAAAACGGAGCT 234

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Qy 235 GGAGAGTTTTGGGCTGGCAGTGTATGTTGATGACACCAAGGATGAGATGGGAATTTAGGT 294

Db 181 GGGGCAATTTCTGGGCTGGCAGTGTATGTTGATGACACCAAGGATGAGATGGGAATTTAGGT 240

Qy 295 TATTTCCCAAGCAACTTGGTGAAGCAGCAGCTGTATACCAAGGAGGCCACCAAGGAGATC 354

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Qy 355 CCAACACCGATATTGACTTCTTCTGTGAA 384

Db 301 CCAACACCGATATTGACTTCTTCTGTGAA 330

RESULT 14

BD010802

LOCUS

DEFINITION Novel polypeptide and DNA thereof.

ACCESSION BD010802

VERSION BD010802.1 GI:18639175

KEYWORDS JP 2001069994-A/3.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 384)

AUTHORS Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y., Yoshimura,K. and Tanaka,H.

TITLE Novel polypeptide and DNA thereof

JOURNAL Patent: JP 2001069994-A 3 21-MAR-2001;

TAKEDA CHEMICAL INDUSTRIES LTD

COMMENT OS Homo sapiens (human)

PN JP 2001069994-A/3

PD 21-MAR-2001

PP 29-JUN-2000 JP 2000195911

PR YASUAKI ITO,KAZUNORI NISHI,KAZUHIRO OGI,SHOICHI OKUBO, PI SHINICHI MOGI, YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA

PC C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P9/00,A61P19/02, PC A61P19/08,

PC C07K14/47,C07K16/18,C12N1/21,C12N5/10,G01N33/15,G01N33/50, PC G01N33/53//

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PH Key Location/Qualifiers

FT source 1..384

FT /organism="Homo sapiens (human)"

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Best Local Similarity 84.3%; Pred. No. 9.9e-77;

Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

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## RESULT 15

BD093103 384 bp DNA linear PAT 27-AUG-2002  
 Novel polypeptide and its DNA.

BD093103  
 BD093103  
 BD093103.1 GI:22638691

VERSION  
 WO 0102564-A/3.

KEYWORDS  
 SOURCE

ORGANISM  
 Homo sapiens (human)

REFERENCE  
 AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 384)

Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y.,  
 Yoshimura,K. and Tanaka,H.

Novel polypeptide and its DNA

Patent: WO 0102564-A 3 11-JAN-2001;

TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO

OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,  
 HIDEYUKI TANAKA

OS Homo sapiens (human)

PN WO 0102564-A/3

PD 11-JAN-2001

PF 29-JUN-2000 WO 2000JP004278

PR 30-JUN-1999 JP 99P 186718

PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI

PI MOGI,

PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA

PC C12N15/12, C12N5/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC

A61K38/17,

PC A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7088, (C12P21/

02, C12R1:119)

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CC

FH Key Location/Qualifiers.

FEATURES

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/db\_xref="taxon:9606"

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Best Local Similarity 84.3%; Pred. No. 9.9e-77;

Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

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Search completed: December 30, 2003, 04:07:57

Job time : 1217 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 30, 2003, 01:02:37 ; Search time 1278.03 Seconds  
(without alignments)  
7302.593 Million cell updates/sec

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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 20  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: em\_esthum.\*  
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4: em\_estnu.\*  
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6: em\_estpl.\*  
7: em\_estro.\*  
8: em\_hic.\*  
9: gb\_estl.\*  
10: gb\_est2.\*  
11: gb\_hic.\*  
12: gb\_est3.\*  
13: gb\_est4.\*  
14: gb\_est5.\*  
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23: em\_gss\_mus.\*  
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29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	384	100.0	514	13	BQ568498
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5	384	100.0	560	13	BQ569741
6	384	100.0	608	13	BQ564944
7	384	100.0	630	13	BQ568471
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9	382.4	99.6	474	13	BQ565637
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11	366.2	95.4	409	13	BQ566932
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13	340.4	88.6	365	13	BY232622
14	300	78.1	604	13	BQ567343
15	260	67.7	280	13	BQ568785
16	244	63.5	485	13	BQ565179
17	204	53.1	588	13	BQ566776
18	196	51.0	795	13	BU748241
19	184.2	48.0	527	10	BE236443
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23	142.2	37.0	178	13	BQ567219
24	140.4	36.6	186	13	BQ564457
25	137.6	35.8	678	10	BB647928
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29	107	27.9	646	13	BQ563767
30	101.8	26.5	338	9	AW021345
31	99.2	25.8	1201	13	EX418941
32	98.8	25.7	978	13	EX444840
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LOCUS	g1143b10.y1	Mouse Organ of Corti cDNA	pBluescript	Mus musculus cDNA
DEFINITION	Clone g1143b10 5', mRNA sequence.			
ACCESSION	BQ570035			
VERSION	BQ570035.1	GI:21473352		
KEYWORDS	EST.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus; Kachar, B.			
REFERENCE	1 (bases 1 to 398)			
AUTHORS	EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing			
TITLE	Unpublished			
JOURNAL	Contact: Kachar, B.			
COMMENT	Structural Cell Biology National Institute of Deafness and other Communication Disorders 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA Tel: 301-402-1599 Fax: 301-402-1765 Email: kacharbeniddc.nih.gov Plate: 143 row: b column: 10 Seq primer: M13RPI reverse primer (ABI). Location/Qualifiers			
FEATURES				



epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's EXassist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

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DB      367  ACGGATATTGACTTCTTCTCTGAA 390

RESULT 3
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DEFINITION BQ568498 514 bp mRNA linear EST 19-JUN-2002
clone g1109c02.Y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
BQ568498
VERSION BQ568498.1 GI:21471815
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Kachar, B.
EST analysis of gene expression in the mouse Organ of Corti at the
onset of hearing
Unpublished
Contact: Kachar, B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: Kacharbenidded.nih.gov
Plate: 109 row: c column: 02
Seq primer: M13RP1 reverse primer (ABI).
FEATURES
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
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/clone_lib="Mouse Organ of Corti cDNA pBluescript"
/notes="Organ: Organ of Corti; Vector: pBluescript; The
organ of Corti (OC) was fine dissected from a total of 386
OC as follows: 102 samples from post-natal (P) day 5; 72
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
14 from P12 and 24 from P13. After killing animals by
cervical dislocation followed by decapitation, the bulla
was removed and opened in Leibowitz medium. The bony
capsule of the cochlea was chipped away, stria vascularis
and spiral ligament were removed and the sensory
epithelium was carefully dissected out of the modiolus.
Total RNA was extracted using the micro Fasttrack kit
(catalog # K1593-02; Invitrogen, Carlsbad, CA), according
to manufacturer's instructions. Reverse transcription and
library construction were carried out with the Uni-Zap XR
vector kit (catalog # 237211, Stratagene) and Uni-Zap XR
Gigapack III Gold Cloning kit (catalog # 237612), both
from Stratagene (La Jolla, CA, USA), according to
manufacturer's instructions. Briefly: 1.5 ug mRNA was
reverse transcribed using a hybrid oligo(dT) linker-primer
that contains an Xho I site. First strand synthesis was
primed with the linker-primer and transcribed using
Moloney murine leukemia virus reverse transcriptase
(MMLV-RT) and 5-methyl dCTP. The second strand was
synthesized with DNA polymerase and RNase H. Complementary
DNA was blunt ended with Pfu DNA polymerase, ligated with
EcoR I adapters in the presence of ligase and digested
with Xho I. The cDNA was sequentially size fractionated
with Xho I. The cDNA was sequentially size fractionated

```

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BASE COUNT 147 a 85 c 143 g 139 t  
ORIGIN

Query Match 100.0%; Score 384; DB 13; Length 514;

Best Local Similarity 100.0%; Pred. NO. 4.1e-106;

Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 241 TTTTGGGCTGGCAGTGTATTGATGACCCAGGATGAGATGGGAATTCAGTTATTTTC 300
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RESULT 4

BQ564134

LOCUS

DEFINITION

g11d01.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA

clone g11d01 5', mRNA sequence.

ACCESSION

BQ564134

VERSION

BQ564134.1 GI:21467451

KEYWORDS

BQ564134 534 bp mRNA linear EST 19-JUN-2002

# SOURCE

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 534)

# REFERENCE

## AUTHORS

## TITLE

EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing

# JOURNAL

## COMMENT

Contact: Kachar B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kacharbenidcd.nih.gov

Plate: 11 row: d column: 01

Seq primer: M13Rpl reverse primer (ABI).

Location/Qualifiers

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/sex="male and female"

/dev\_stage="Post natal day 5 to 13"

/clone\_lib="Mouse Organ of Corti cDNA pBluescript"

/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMuV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on XLI Blue MRF<sup>+</sup> cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTATGACC) and 25<sup>th</sup>

# FEATURES

## source



strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 155 a 87 c 148 g 144 t  
ORIGIN

Query Match 100.0%; Score 384; DB 13; Length 534;

Best Local Similarity 100.0%; Pred. No. 4.2e-106; Indels 0; Gaps 0;  
Matches 384; Conservative 0; Mismatches 0;

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Db 303 CCAGCAACTTGTGTAAGGACGACGCTGTATACAGAGAGCCACCAAGGAGATCCCAACC 362
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Qy 361 ACGGATATTGACTTCTTCTGTGAA 384
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Db 363 ACGGATATTGACTTCTTCTGTGAA 386
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## RESULT 5

BQ569741

LOCUS

DEFINITION BQ569741 560 bp mRNA linear EST 19-JUN-2002  
Clone g1135f01.1 Mouse Organ of Corti cDNA pbluescript Mus musculus cDNA

ACCESSION BQ569741

VERSION BQ569741.1 GI:21473058

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 560)

REFERENCE

AUTHORS

TITLE EST analysis of gene expression in the mouse Organ of Corti at the  
onset of hearing

JOURNAL

COMMENT

Contact: Kachar, B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA

Tel: 301-402-1599

Fax: 301-402-1765

Email: kachar@nidcd.nih.gov

Plate: 135 row: f column: 01

Seq primer: M13RPI reverse primer (ABI).

## FEATURES

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Organ of Corti (OC) was fine dissected from a total of 386  
OC as follows: 102 samples from post-natal (P) day 5; 72  
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;  
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cervical dislocation followed by decapitation, the bulla  
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synthesized with DNA polymerase and RNase H. Complementary  
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Concert96(TM) plasmid purification kit (Invitrogen,  
Carlsbad, CA) as instructed by the manufacturer. ESTs from  
the 5' end of the cDNA clones were generated with the  
universal M13 reverse primer (CAGGAACAGCTATGACC) and 25x  
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Biosystems, Foster City, CA). Sequencing reactions were  
performed on MJ Tetrad thermal cyclers (MJ Research,  
Waltham, MA), and analyzed on 3700 automated capillary  
sequencers using POP5 polymer (Applied Biosystems, Foster  
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as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10;  
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genes are present in GenBank and have known function; 23%  
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ORIGIN

Query Match 100.0%; Score 384; DB 13; Length 560;

Best Local Similarity 100.0%; Pred. No. 4.3e-106;

Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGCAAGGATATTGATTTCTTTCTTGGGGCCTTGTTCTATGTTGCGGCATGGT 60  
Dbb  
6 ATGCAAGGATATTGATTTCTTTCTTGGGGCCTTGTTCTATGTTGCGGCATGGT 65  
Qy 61 GTATTATGATTAACCTTTCTTAAGAGTTGTCGGATAGGAGTGTCATACT 120  
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RESULT 6  
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DEFINITION clone gi27909 5', mRNA sequence.

ACCESSION BQ564944  
VERSION BQ564944.1 GI:21468261  
KEYWORDS EST.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 608)  
Kachar,B.  
EST analysis of gene expression in the mouse Organ of Corti at the  
onset of hearing  
Unpublished  
Contact: Kachar,B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4243 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kachar@nidcd.nih.gov  
Plate: 27 row: g column: 09  
Seq primer: M13RPI reverse primer (ABI).

Location/Qualifiers  
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organ of Corti (OC) was fine dissected from a total of 386  
OC as follows: 102 samples from post-natal (P) day 5; 72  
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;  
14 from P12 and 24 from P13. After killing animals by  
cervical dislocation followed by decapitation, the bulla  
was removed and opened in Leibowitz medium. The bony  
capsule of the cochlea was chipped away, stria vascularis

FEATURES  
source  
1 ATGCAAGGATATTGATTTCTTTCTTGGGGCCTTGTTCTATGTTGCGGCATGGT 60  
Dbb 6 ATGCAAGGATATTGATTTCTTTCTTGGGGCCTTGTTCTATGTTGCGGCATGGT 72  
Qy 61 GTATTATGATTAACCTTTCTTAAGAGTTGTCGGATAGGAGTGTCATACT 120  
Dbb 66 GTATTATGATTAACCTTTCTTAAGAGTTGTCGGATAGGAGTGTCATACT 132  
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Qy 181 AAGAAAGGCGACAGATATTTCTTCACCTGCTGTAACAGAAACGGAGCTGGAGAG 240  
Dbb 186 AAGAAAGGCGACAGATATTTCTTCACCTGCTGTAACAGAAACGGAGCTGGAGAG 252  
Qy 241 TTTTGGGCTGCAGTGTATTTGTTGACCAACAGATAGATGGGAATTTAGTTATTTC 300

and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMuLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's Exsist 11223 was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concer96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 169 a 107 c 166 g 166 t  
ORIGIN  
Query Match 100.0%; Score 384; DB 13; Length 608;  
Best Local Similarity 100.0%; Pred. No. 4.5e-106;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGCAAGGATATTGATTTCTTTCTTGGGGCCTTGTTCTATGTTGCGGCATGGT 60  
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Db      313 CCCAGCAACTTGGTGAAGGAGCAGCGGTGTATACAGAGGCCACCAAGGAGATCCCAACC 372
QY      361 ACGGATATTGACTTCTCTCTGAA 384
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Db      373 ACGGATATTGACTTCTCTGAA 396
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RESULT 7
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DEFINITION gi108g04.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
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VERSION   BQ568471.1 GI:21471788
KEYWORDS EST.
SOURCE   Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 630)
AUTHORS Kachar,B.
TITLE   EST analysis of gene expression in the mouse Organ of Corti at the
onset of hearing
JOURNAL Unpublished
COMMENT Contact: Kachar,B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: kachar@nidcd.nih.gov
Plate: 108 row: g column: 04
Seq primer: M13Rpl reverse primer (ABI).

FEATURES
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/clone_lib="Mouse Organ of Corti cDNA pBluescript"
/notes="Organ: Organ of Corti; Vector: pBluescript; The
organ of Corti (OC) was fine dissected from a total of 386
OC as follows: 102 samples from post-natal (P) day 5; 72
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
14 from P12 and 24 from P13. After killing animals by
cervical dislocation followed by decapitation, the bulla
was removed and opened in Leibowitz medium. The bony
capsule of the cochlea was chipped away, stria vascularis
and spiral ligament were removed and the sensory
epithelium was carefully dissected out of the modiolus.
Total RNA was extracted using the micro Fasttrack kit
(catalog # K1593-02; Invitrogen, Carlsbad, CA), according
to manufacturer's instructions. Reverse transcription and
library construction were carried out with the Uni-Zap XR
vector kit (catalog # 237211, Stratagene) and Uni-Zap XR
Gigapack III Gold Cloning kit (catalog # 237612), both
from Stratagene (La Jolla, CA, USA), according to
manufacturer's instructions. Briefly: 1.5 ug mRNA was
reverse transcribed using a hybrid oligo(dT) linker-primer
that contains an xho I site. First strand synthesis was
primed with the linker- primer and transcribed using
Moloney murine leukemia virus reverse transcriptase
(MMLV-RT) and 5-methyl dCTP. The second strand was
synthesized with DNA polymerase and RNase H. Complementary
DNA was blunt ended with Pfu DNA polymerase, ligated with
EcoR I adapters in the presence of ligase and digested

```

```

with Xho I. The cDNA was sequentially size fractionated
over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden)
and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA)
columns to enrich for cDNAs greater than 400bp and 1000 bp
, respectively. The cDNA was then directionally ligated to
the Uni-ZAP XR vector, which had been predigested with
EcoR I and Xho I. The phagemid was packaged with Gigapak
III Gold and, upon titration on XL1 Blue MRF' cells, the
yield of the phage library was estimated to be 11,100,000
recombinants. Stratagene's ExAssist Interference
resistance helper phage (catalogue # 211203) was adopted
to rescue plasmid DNA from the phages. Upon plating of the
rescued library, individual cDNA clones were selected and
grown in 96-well, 2 ml growth plate. Plasmid DNA was
purified from 200 ul of saturated culture with the
Concert96(TM) plasmid purification kit (Invitrogen,
Carlsbad, CA) as instructed by the manufacturer. ESTs from
the 5' end of the cDNA clones were generated with the
universal M13 reverse primer (CAGGAACAGCTATGACC) and 25%
strength BigDye terminator sequencing chemistry (Applied
Biosystems, Foster City, CA). Sequencing reactions were
performed on MJ Tetrad thermal cyclers (MJ Research,
Walham, MA), and analyzed on 3700 automated capillary
sequencers using POP5 polymer (Applied Biosystems, Foster
City, CA). The frequency distribution of the library is
as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10;
1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of
genes are present in GenBank and have know function; 23%
have hits in GenBank, but do not have assigned function;
12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT      178 a      111 c      167 g      174 t
ORIGIN
Query Match      100.0%; Score 384; DB 13; Length 630;
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Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 ATGCGAAGGATATTGATTTCTTTGCTGGGGGCTTGTCTTCTATCTGCGGGCATGGT 60
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Db      73 GTATTTATGATAAACTTTCTTCTTAAGAAGTTGTGCGGATGAGGAGTGTCTATACT 132
QY      121 ATTTCTCGCAGAGACACAGAGATTAACAATGCCCCAGACTTAGGTTTCATCGATGTC 180
Db      133 ATTTCTCGCAGAGACACAGAGATTAACAATGCCCCAGACTTAGGTTTCATCGATGTC 192
QY      181 AAGAAAGGCGCAGAGATCTATGTTTACTCCAAAGCTGTACAGAAACGGAGCTGGAGAG 240
Db      193 AAGAAAGGCGCAGAGATCTATGTTTACTCCAAAGCTGTGTAAACAAACGGAGCTGGAGAG 252
QY      241 TTTTGGCTGCGCAGTGTATTATGTTGACCAACAGATGAGATGGGAATTTAGGTTTATTC 300
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Db      373 ACGGATATTGACTTCTCTGAA 396
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RESULT 8
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DEFINITION BB611549 RIKEN full-length enriched, 13 days embryo head Mus
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ACCESSION BB611549
VERSION   BB611549.1 GI:15393547

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/clone lib="Mouse Organ of Corti cDNA pBluescript"  
/note="Organ: Organ of Corti; vector: pBluescript; The  
organ of Corti (OC) was fine dissected from a total of 386  
OC as follows: 102 samples from post-natal (P) day 5; 72  
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;  
14 from P12 and 24 from P13. After killing animals by  
cervical dislocation followed by decapitation, the bulla  
was removed and opened in Leibowitz medium. The bony  
capsule of the cochlea was chipped away, stria vascularis  
and spiral ligament were removed and the sensory  
epithelium was carefully dissected out of the modiolus.  
Total RNA was extracted using the Micro Fasttrack kit  
(catalog # K1593-02; Invitrogen, Carlsbad, CA), according  
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vector kit (catalog # 237211, Stratagene) and Uni-Zap XR  
Gigapack III Gold Cloning kit (catalog # 237612), both  
from Stratagene (La Jolla, CA, USA), according to  
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that contains an Xho I site. First strand synthesis was  
primed with the linker- primer and transcribed using  
Moloney murine leukemia virus reverse transcriptase  
(MMLV-RT) and 5-methyl dCTP. The second strand was  
synthesized with DNA polymerase and RNase H. Complementary  
DNA was blunt ended with pfu DNA polymerase, ligated with  
EcoR I adapters in the presence of ligase and digested  
with Xho I. The cDNA was sequentially size fractionated  
over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden)  
and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA)  
columns to enrich for cDNAs greater than 400bp and 1000 bp  
, respectively. The cDNA was then directionally ligated to  
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III Gold and, upon titration on Xli Blue MRF<sup>+</sup> cells, the  
yield of the phage library was estimated to be 11,100,000  
recombinants. Stratagene's ExAssist Interference  
resistance helper phage (catalogue # 211203) was adopted  
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rescued library, individual cDNA clones were selected and  
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purified from 200 ul of saturated culture with the  
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Carlsbad, CA) as instructed by the manufacturer. ESTs from  
the 5' end of the cDNA clones were generated with the  
universal M13 reverse primer (CAGGAACAGTATGACC) and 25x  
strength BigDye terminator sequencing chemistry (Applied  
Biosystems, Foster City, CA). Sequencing reactions were  
performed on MJ Tetrad thermal cyclers (MJ Research,  
Waltham, MA), and analyzed on 3700 automated capillary  
sequencers using POP5 polymer (Applied Biosystems, Foster  
City, CA). The frequency distribution of the library is  
as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10;  
1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of  
genes are present in GenBank and have known function; 23%  
have hits in GenBank, but do not have assigned function;  
12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 145 a 78 c 131 g 120 t  
ORIGIN

Query Match 99.6%; Score 382.4; DB 13; Length 474;  
Best Local Similarity 99.7%; Pred. No. 1.2e-105;  
Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCAAGGATATGATCTTTTCCTGGGGGCTTGTGTTCTATGTCGGGATCGT 60  
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Dd 74 GTATTTATGATAAATCTTCTTAAGAGTTGTCGGGATGAGGATGTCGTATCT 133  
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Dd 194 AGAAAGGGCAGCAGAGATCTATGTTTACTCCAGCTGGTAAACAGAAACGGAGCTGGAGAG 253  
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Dd 254 TTTTGGCTGGCAGCTGTTTATGGTGACCCAGGATGAGATGGAAATTTAGGTATTTC 313  
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Dd 314 CCAGCAACTTGGTGAAGGAGCAGCGTGTATACAGGAGCCACCAAGGAGATCCCAACC 373  
QY 361 ACGGATATTGACTTCTTCTGTGAA 384  
Dd 374 ACGGATATTGACTTCTTCTGTGAA 397

RESULT 10  
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LOCUS  
DEFINITION BQ563768 684 bp mRNA linear EST 19-JUN-2002  
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ACCESSION BQ563768  
VERSION BQ563768.1 GI:21466749  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Kachar, B.  
1 (bases 1 to 684)  
REFERENCE  
AUTHORS EST analysis of gene expression in the mouse Organ of Corti at the  
TITLE onset of hearing  
JOURNAL Unpublished  
COMMENT Contact: Kachar, B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kacharbenidd.nih.gov  
Plate: 06 row: c column: 09  
Seq primer: M13RPI reverse primer (ABI).  
FEATURES  
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/note="Organ: Organ of Corti; vector: pBluescript; The  
organ of Corti (OC) was fine dissected from a total of 386  
OC as follows: 102 samples from post-natal (P) day 5; 72  
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;  
14 from P12 and 24 from P13. After killing animals by  
cervical dislocation followed by decapitation, the bulla  
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epithelium was carefully dissected out of the modiolus.  
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194 a 120 c 178 g 192 t

Query Match 99.6%; Score 382.4; DB 13; Length 684;  
Best Local Similarity 99.7%; Pred. No. 1.5e-105;  
Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGCAAGGATATTCATTCTTTGCTTGGGGCCCTTGTGGTTCTATGTCCGGGATGGT 60  
DB 13 ATGGCAGGATATTCATTCTTTGCTTGGGGCCCTTGTGGTTCTATGTCCGGGATGGT 72

QY 61 GTATTATGGATAAATCTTTCTTCTAAGAAAGTTGTGGGGATGAGGAGTGTCTATACT 120  
DB 73 GTATTATGGATAAATCTTTCTTCTAAGAAAGTTGTGGGGATGAGGAGTGTCTATACT 132

QY 121 ATTTCTCTGGCAAGACAGACAGAAATTAATGCTCCAGACTGTAGGTTTCATCGATGTC 180  
DB 133 ATTTCTCTGGCAAGACAGACAGAAATTAATGCTCCAGACTGTAGGTTTCATCGATGTC 192

QY 181 AAGAAGGGCAGCAGATCTATGTTTCTCAAGCTGGTAAACAGAAAACGGAGCTGGAGAG 240  
DB 193 AAGAAGGGCAGCAGATCTATGTTTCTCAAGCTGGTAAACAGAAAACGGAGCTGGAGAG 252

QY 241 TTTTGGGCTGGCAGTGTATTGTTGACACACAGAGATGAGATGGGAATTTAGTTATTTC 300  
DB 253 TTTTGGGCTGGCAGTGTATTGTTGACACACAGAGATGAGATGGGAATTTAGTTATTTC 312

QY 301 CCACGAACTTGGTGAAGAGCAGCGTGTATACCGAGGGCCCAACGAGAGATCCCAACC 360  
DB 313 CCACGAACTTGGTGAAGAGCAGCGTGTATACCGAGGGCCCAACGAGAGATCCCAACC 372

QY 361 ACGGATATTGACTTCTTCTGTGAA 384  
DB 373 ACGGATATTGACTTCTTCTGTGAA 396

RESULT 11  
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ACCESSION BQ566932  
VERSION BQ566932.1 GI:21470249  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM  
REFERENCE  
AUTHORS Kachar,B.  
TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing  
JOURNAL Unpublished  
COMMENT Contact: Kachar,B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kacharbenid@nih.gov  
Plate: 73 row: 9 column: 09  
Seq primer: M13RP1 reverse primer (ABI).  
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/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMuLV-Rt) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on XL1 Blue MRF<sup>+</sup> cells, the yield of the phage library was estimated to be 11,100,000

BQ566932 409 bp mRNA linear EST 19-JUN-2002  
gi73g09.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone gi73g09 5', mRNA sequence.  
ACCESSION BQ566932  
VERSION BQ566932.1 GI:21470249  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM  
REFERENCE  
AUTHORS Kachar,B.  
TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing  
JOURNAL Unpublished  
COMMENT Contact: Kachar,B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kacharbenid@nih.gov  
Plate: 73 row: 9 column: 09  
Seq primer: M13RP1 reverse primer (ABI).  
Location/Qualifiers  
1. 409  
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/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMuLV-Rt) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on XL1 Blue MRF<sup>+</sup> cells, the yield of the phage library was estimated to be 11,100,000



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BASE COUNT	102 a	75 c	121 g	111 t
ORIGIN				
Query Match	95.4%	Score 366.2;	DB 13;	Length 409;
Best Local Similarity	99.0%;	Pred. No. 9.9e-101;		
Matches 379;	Conservative 0;	Mismatches 3;	Indels 1;	Gaps 1;
Qy	1 ATGCAAGGATATTGATTCTTTTCTGGGGCCCTTGGTTCATGTCGGGCATGGT 60			
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RESULT 12  
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ACCESSION BQ565411  
VERSION BQ565411.1 GI:21468728  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 490)  
Kachar,B.  
EST Analysis of gene expression in the mouse Organ of Corti at the onset of hearing

JOURNAL COMMENT

Unpublished

Contact: Kachar, B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kachar@nidcd.nih.gov  
Plate: 37 row: b column: 12  
Seq primer: M13RP1 reverse primer (ABI).  
Location/Qualifiers

FEATURES

source

1. 490  
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/sex="male and female"  
/dev stage="Post natal day 5 to 13"  
/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fastscript kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on Xli Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGTATGACC) and 25¢ strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of





```

QY 181 AAGAAAGGCGAGAGATCTATGTTTACTCCAGCTGGTAACAGAAACGAGCTGGAGAG 240
    |||||
Db 204 AAGAAAGGCGAGAGATCTATGTTTACTCCAGCTGGTAACAGAAACGAGCTGGAGAG 263
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QY 241 TTTTGGGCTGGCAGTGTGTTATGGTGACACAGAGATGAGATGGAAATTGTAGGTTATTTTC 300
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Db 264 TTTTGGGCTGGCAGTGTGTTATGGTGACACAGAGATGAGATGGAAATTGTAGGTTATTTTC 323
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QY 301 CCCAGCAACTGGTGAAGGAGCAGCGTGTATACAGAGAGGCC 342
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Db 324 CCCAGCAACTGGTGAAGGAGCAGCGTGTATACAGAGAGGCC 365
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RESULT 14
BQ567343
LOCUS
DEFINITION g188d08.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
clone gi88d08 5', mRNA sequence.

```

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ACCESSION BQ567343
VERSION BQ567343.1 GI:21470660
KEYWORDS EST.
SOURCE Mus musculus (house mouse)

```

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ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 604)

```

```

REFERENCE Kachar,B.
AUTHORS EST analysis of gene expression in the mouse Organ of Corti at the
TITLE onset of hearing
JOURNAL Unpublished
COMMENT Contact: Kachar,B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: kachar@nidcd.nih.gov
Plate: 88 row: d column: 08
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
1..604
/organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
/db_xref="taxon:10090"
/clone="g188d08"
/sex="male and female"
/dev_stages="Post natal day 5 to 13"
/clone_lib="Mouse Organ of Corti cDNA pBluescript"
/organ="Organ of Corti; Vector: pBluescript; The
organ of Corti (OC) was fine dissected from a total of 386
OC as follows: 102 samples from post-natal (P) day 5; 72
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
14 from P12 and 24 from P13. After killing animals by
cervical dislocation followed by decapitation, the bulla
was removed and opened in Leibowitz medium. The bony
capsule of the cochlea was chipped away, stria vascularis
and spiral ligament were removed and the sensory
epithelium was carefully dissected out of the modiolus.
Total RNA was extracted using the micro Fasttrack kit
(catalog # K1593-02; Invitrogen, Carlsbad, CA), according
to manufacturer's instructions. Reverse transcription and
library construction were carried out with the Uni-Zap XR
vector kit (catalog # 237211, Stratagene) and Uni-Zap XR
Gigapack III Gold Cloning kit (catalog # 237612), both
from Stratagene (La Jolla, CA, USA), according to
manufacturer's instructions. Briefly: 1.5 ug mRNA was
reverse transcribed using a hybrid oligo(dT) linker-primer
that contains an Xho I site. First strand synthesis was
primed with the linker- primer and transcribed using
Moloney murine leukemia virus reverse transcriptase
(MMLV-RT) and 5-methyl dCTP. The second strand was

```

```

BASE COUNT 178 a 108 c 152 g 166 t
ORIGIN
Query Match 78.1%; Score 300; DB 13; Length 604;
Best Local Similarity 100.0%; Pred. No. 2.1e-80;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 145 GATTACAAATGCCCAGACTGTAGGTTTCATCGATGTCAAGAAAGGCGACAGATCTATGTT 204
    |||||
Db 61 GATTACAAATGCCCAGACTGTAGGTTTCATCGATGTCAAGAAAGGCGACAGATCTATGTT 120
    |||||
QY 205 TACTCCAAAGCTGGTAACAGAAACGGAGCTGGAGAGTTTTCGGCTGGCAGTGTATTATGCT 264
    |||||
Db 121 TACTCCAAAGCTGGTAACAGAAACGGAGCTGGAGAGTTTTCGGCTGGCAGTGTATTATGCT 180
    |||||
QY 265 GACCACAGGATGAGATGGGAATTGTAGGTTATTTCCACAGAACTTGGTGAAGAGCAG 324
    |||||
Db 181 GACCACAGGATGAGATGGGAATTGTAGGTTATTTCCACAGAACTTGGTGAAGAGCAG 240
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QY 325 CGTGTATACCAAGAGGCCCAACAGAGATCCCAACCGGATATTGACTTCTCTGTGAA 384
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Db 241 CGTGTATACCAAGAGGCCCAACAGAGATCCCAACCGGATATTGACTTCTCTGTGAA 300
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RESULT 15
BQ568785
LOCUS
DEFINITION gill4f04.y2 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
clone gill4f04 5', mRNA sequence.

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ACCESSION BQ568785
VERSION BQ568785.1 GI:21472102
KEYWORDS EST.
SOURCE Mus musculus (house mouse)

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ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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BQ568785 280 bp mRNA linear EST 19-JUN-2002
gill4f04.y2 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
clone gill4f04 5', mRNA sequence.

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ACCESSION BQ568785
VERSION BQ568785.1 GI:21472102
KEYWORDS EST.
SOURCE Mus musculus (house mouse)

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ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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Tue Dec 30 10:20:36 2003

REFERENCE 1 (bases 1 to 280)  
 AUTHORS Kachar, B.  
 TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing  
 JOURNAL Unpublished  
 COMMENT Contact: Kachar, B.  
 Structural Cell Biology  
 National Institute of Deafness and other Communication Disorders  
 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
 Tel: 301-402-1599  
 Fax: 301-402-1785  
 Email: kachar@nidcd.nih.gov  
 Plate: 114 row: F column: 04  
 Seq primer: M13RP1 reverse primer (ABI).  
 Location/Qualifiers  
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 /organism="Mus musculus"  
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 /clone="gill14f04"  
 /sex="male and female"  
 /dev\_stage="Post natal day 5 to 13"  
 /clone\_lib="Mouse Organ of Corti cDNA pBluescript"  
 /note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack Kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on Xli Blue MRF<sup>+</sup> cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACACCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary

sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT	72 a	44 c	85 g	79 t
ORIGIN				
Query Match	67.7%	Score 260;	DB 13;	Length 280;
Best Local Similarity	100.0%	Pred. No. 2.2e-68;		
Matches 260;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	ATGCAAGGATATTGATTCCTTTTCCTTGGGGCCCTTGTGTTCTATGTCGGGCGCATGGT	60	
Db	21	ATGCAAGGATATTGATTCCTTTTCCTTGGGGCCCTTGTGTTCTATGTCGGGCGCATGGT	80	
Qy	61	GTATTTATGGATAAATCTTCTTCTAAGAAGTTGTGCGGATGAGGAGTGTGTCTATACT	120	
Db	81	GTATTTATGGATAAATCTTCTTCTAAGAAGTTGTGCGGATGAGGAGTGTGTCTATACT	140	
Qy	121	ATTTCTCTGGCAAGACACAGCAAGATTACAAATGCCCAGACTGTAGGTTTCATCGATGTC	180	
Db	141	ATTTCTCTGGCAAGACACAGCAAGATTACAAATGCCCAGACTGTAGGTTTCATCGATGTC	200	
Qy	181	AAGAAAGGGCAGCAGATCTATGTTTACTCCAAAGCTGTAAACAGAAACGGAGCTGGAGAG	240	
Db	201	AAGAAAGGGCAGCAGATCTATGTTTACTCCAAAGCTGTAAACAGAAACGGAGCTGGAGAG	260	
Qy	241	TTTTGGGCTGGCAGTGTGTTTA	260	
Db	261	TTTTGGGCTGGCAGTGTGTTTA	280	

Search completed: December 30, 2003, 06:07:15  
 Job time : 1280.36 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 22:01:01 ; Search time 127,462 Seconds  
(without alignments)  
8132.484 Million cell updates/sec

Title: US-10-019-455A-10  
Perfect score: 384  
Sequence: 1 atggcaaggatattgattct.....atattgactttctgtgaa 384

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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25: /SIDSI1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	384	100.0	384	22	Mouse MLP nucleoti
2	384	100.0	947	22	Mouse MLP nucleoti
3	344	89.6	384	22	Rat MLP nucleotide
4	330	85.9	330	22	Mouse MLP nucleoti
5	294.8	76.8	330	22	Rat MLP nucleotide
6	287	74.7	384	22	Human MLP nucleoti
7	287	74.7	387	24	DNA encoding novel
8	287	74.7	426	22	Human growth regul

9	287	74.7	521	24	ABL95740	Human angiogenesis
10	287	74.7	521	24	ABL88251	Human PRO9873 cDNA
11	287	74.7	521	24	ABK33571	cDNA encoding huma
12	287	74.7	891	22	AAH98228	Human EST-derived
13	287	74.7	891	22	AAH26342	Human growth regul
14	287	74.7	923	22	AAF59083	Human MLP nucleoti
15	287	74.7	1201	22	AAH26343	Human growth regul
16	267.8	69.7	307	22	AAF59093	Rat MLP nucleotide
17	252.2	65.7	330	22	AAF59079	Human MLP nucleoti
18	233.8	60.9	261	22	AAF59092	Rat MLP nucleotide
19	66.2	17.2	581	16	AAQ84052	Sequence encoding
20	60.2	15.7	433	22	AAH47783	Recombinant human
21	60.2	15.7	459	16	AAQ84050	Sequence encoding
22	60.2	15.7	459	22	AAI70083	Melanoma inhibitor
23	60.2	15.7	459	22	ABD18732	Human antisenase ol
24	60.2	15.7	555	23	ABV59229	Human prostate exp
25	58.6	15.3	442	24	ABL63602	Breast cancer rela
26	58.6	15.3	442	24	ABU64012	Breast cancer rela
27	55.2	14.4	330	16	AAQ84061	Sequence encoding
28	52.6	13.7	305	16	AAQ84055	Amplified fragment
29	47.2	12.3	300	20	AAZ14828	Human gene express
30	47.2	12.3	417	22	AAH99775	Human protein enco
31	47.2	12.3	429	22	AAH22695	Human cDNA encodin
32	47.2	12.3	884	22	AAH22459	Human cDNA encodin
33	47.2	12.3	1060	22	AAF92140	Human PRO19670 cDN
34	47.2	12.3	1060	24	ABH74460	Human cDNA encodin
35	47.2	12.3	1060	24	ABL95738	Human angiogenesis
36	47.2	12.3	1060	24	ABL88249	Human PRO19670 cDN
37	47.2	12.3	1060	25	ACA57963	Human PRO19670 cDN
38	47.2	12.3	1060	25	ACA58892	cDNA encoding huma
39	47.2	12.3	1060	25	ACA60445	Novel human secret
40	47.2	12.3	1060	25	ACA63455	cDNA encoding huma
41	47.2	12.3	1060	25	ABX98433	Human cDNA encodin
42	47.2	12.3	1060	25	ABX98935	Novel human secret
43	47.2	12.3	1060	25	ACA05980	Human secreted/tra
44	47.2	12.3	1060	25	ABX98024	Human PRO polynucl
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ALIGNMENTS

RESULT 1

AAF59068  
ID AAF59068 standard; DNA; 384 BP.

XX AAF59068;

AC AAF59068;

DT 23-APR-2001 (first entry)

XX Mouse MLP nucleotide sequence SEQ ID NO:10.

DE MLP; MTA; melanoma inhibitory activity; cancer; bone disease;  
KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
KW cardiant; gene therapy; secretory cell function regulator; promoter;  
KW inhibitor; ds.

OS Mus musculus.

XX WO200102564-A1.

PN 11-JAN-2001.

PD 29-JUN-2000; 2000WO-JP04278.

PF 30-JUN-1999; 99JP-0186718.

XX (TAKE ) TAKEDA CHEM IND LTD.

XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;

PI Tanaka H;

XX WPI; 2001-159271/16.

DR P-PSDB; AAB69125.  
XX Safe, low-toxicity secretory cell function-regulatory protein and  
PT encoded DNA, applicable as drugs, in diagnosis and development of  
PT promoters and inhibitors for preventing or treating e.g. bone and joint  
PT diseases -  
XX  
XX Claim 11; Page 93; 111pp; Japanese.  
XX  
XX The present invention describes novel MLP proteins and their encoding  
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
CC activities, and can be used in gene therapy and as secretory cell  
CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
CC the diagnosis and development of promoters and inhibitors for preventing  
CC or treating bone and joint diseases as well as pathologic angiogenesis.  
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
CC in the exemplification of the present invention.  
XX  
XX Sequence 384 BP; 98 A; 68 C; 111 G; 107 T; 0 other;  
SQ  
Query Match 100.0%; Score 384; DB 22; Length 384;  
Best Local Similarity 100.0%; Pred. No. 1.6e-113;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 ATGGCAAGGATATTGATCTTTTGGTGGGGCCCTTGTGCTTCTATGTCGGGCAATGGT 60  
QY 61 GTATTTATCGATAAATCTTCTTAAGAAGTTGTGCGGATGAGAGTGTCTATACT 120  
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Db 121 ATTTCTCTGGCAAGACACAGGAAGATTCAATGCCCCAGACTGTAGTTTCATCGATGC 180  
QY 181 AAGAAAGGCGAGCAGATCTATGTTTCTCAAGCTGTAAACAGAAACCGAGCTGGAGAG 240  
Db 181 AAGAAAGGCGAGCAGATCTATGTTTCTCAAGCTGTAAACAGAAACCGAGCTGGAGAG 240  
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QY 301 CCAGCAACTTGTGAAGAGCAGCGTGTATACAGAGAGGCCACCAAGGAGATCCCAACC 360  
Db 301 CCAGCAACTTGTGAAGAGCAGCGTGTATACAGAGAGGCCACCAAGGAGATCCCAACC 360  
QY 361 ACGGATATTGACTTCTTCTGTGAA 384  
Db 361 ACGGATATTGACTTCTTCTGTGAA 384  
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XX  
AC AAF59084;  
XX  
XX 23-APR-2001 (first entry)  
XX Mouse MLP nucleotide sequence SEQ ID NO:30.  
XX  
XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
KW cardiant; gene therapy; secretory cell function regulator; promoter;  
KW inhibitor; ds.  
XX  
XX Mus musculus.  
XX  
XX WO200102564-A1.  
XX  
XX 11-JAN-2001.  
PD

XX 29-JUN-2000; 2000WO-JP04278.  
PF  
XX 30-JUN-1999; 99JP-0186718.  
PR  
XX (TAKE ) TAKEDA CHEM IND LTD.  
PA  
XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
PI Tanaka H;  
PI  
XX WPI; 2001-159271/16.  
DR  
XX Safe, low-toxicity secretory cell function-regulatory protein and  
PT encoded DNA, applicable as drugs, in diagnosis and development of  
PT promoters and inhibitors for preventing or treating e.g. bone and joint  
PT diseases -  
PT  
XX Example 2; Page 100-101; 111pp; Japanese.  
PS  
XX The present invention describes novel MLP proteins and their encoding  
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
CC activities, and can be used in gene therapy and as secretory cell  
CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
CC the diagnosis and development of promoters and inhibitors for preventing  
CC or treating bone and joint diseases as well as pathologic angiogenesis.  
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
CC in the exemplification of the present invention.  
XX  
XX Sequence 947 BP; 279 A; 158 C; 221 G; 289 T; 0 other;  
SQ  
Query Match 100.0%; Score 384; DB 22; Length 947;  
Best Local Similarity 100.0%; Pred. No. 2.4e-113;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGGCAAGGATATTGATCTTTTGGTGGGGCCCTTGTGCTTCTATGTCGGGCAATGGT 60  
Db 11 ATGGCAAGGATATTGATCTTTTGGTGGGGCCCTTGTGCTTCTATGTCGGGCAATGGT 70  
QY 61 GTATTTATCGATAAATCTTCTTAAGAAGTTGTGCGGATGAGAGTGTCTATACT 120  
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QY 121 ATTTCTCTGGCAAGACACAGGAAGATTCAATGCCCCAGACTGTAGTTTCATCGATGC 180  
Db 131 ATTTCTCTGGCAAGACACAGGAAGATTCAATGCCCCAGACTGTAGTTTCATCGATGC 190  
QY 181 AAGAAAGGCGAGCAGATCTATGTTTCTCAAGCTGTAAACAGAAACCGAGCTGGAGAG 240  
Db 191 AAGAAAGGCGAGCAGATCTATGTTTCTCAAGCTGTAAACAGAAACCGAGCTGGAGAG 250  
QY 241 TTTTGGGCTGGCAGTGTATGTTGACCCAGGATGAGATGGGAATTGTAGTTATTTC 300  
Db 251 TTTTGGGCTGGCAGTGTATGTTGACCCAGGATGAGATGGGAATTGTAGTTATTTC 310  
QY 301 CCAGCAACTTGTGAAGAGCAGCGTGTATACAGAGAGGCCACCAAGGAGATCCCAACC 360  
Db 311 CCAGCAACTTGTGAAGAGCAGCGTGTATACAGAGAGGCCACCAAGGAGATCCCAACC 370  
QY 361 ACGGATATTGACTTCTTCTGTGAA 384  
Db 371 ACGGATATTGACTTCTTCTGTGAA 394  
RESULT 3  
AAF59098  
ID AAF59098 standard; DNA; 384 BP.  
XX  
AC AAF59098;  
XX  
XX 23-APR-2001 (first entry)  
XX  
XX Rat MLP nucleotide sequence SEQ ID NO:46.  
XX  
XX

KW MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
 KW Joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
 KW cardiant; gene therapy; secretory cell function regulator; promoter;  
 KW inhibitor; ds.  
 XX  
 OS Rattus sp.  
 XX  
 PN WO200102564-A1.  
 XX  
 XX 11-JAN-2001.  
 XX  
 XX 29-JUN-2000; 2000WO-JP04278.  
 XX  
 XX 30-JUN-1999; 99JP-0186718.  
 XX  
 XX (TAKE ) TAKEDA CHEM IND LTD.  
 XX  
 XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
 PI Tanaka H;  
 XX  
 DR WPI; 2001-159271/16.  
 XX  
 DR P-PSDB; AAB69130.  
 XX  
 XX Safe, low-toxicity secretory cell function-regulatory protein and  
 PT encoded DNA, applicable as drugs, in diagnosis and development of  
 PT promoters and inhibitors for preventing or treating e.g. bone and joint  
 PT diseases -  
 XX  
 XX Claim 13; Page 105-106; 11lpp; Japanese.  
 XX  
 XX The present invention describes novel MLP proteins and their encoding  
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
 CC activities, and can be used in gene therapy and as secretory cell  
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
 CC the diagnosis and development of promoters and inhibitors for preventing  
 CC or treating bone and joint diseases as well as pathologic angiogenesis.  
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
 CC in the exemplification of the present invention.  
 XX  
 XX Sequence 384 BP; 98 A; 72 C; 109 G; 105 T; 0 other;  
 SQ  
 Query Match 89.6%; Score 344; DB 22; Length 384;  
 Best Local Similarity 93.5%; Pred. No. 1.3e-100;  
 Matches 359; Conservative 0; Mismatches 25; Indels 0; Gaps 0;  
 QY 1 ATGGCAAGATATGATCTTTCTTGGGGGCTTGTGTTCTATGTCGCGGCGATGGT 60  
 DB 1 ATGGCAAGATATGATCTTTCTTGGGGGCTTGTGTTCTATGTCGCGGCGATGGC 60  
 QY 61 GTATTATGGATAAACTTTCTTCTAAGAAGTTGTGCGGATGAGGAGTGTGTCTATCT 120  
 DB 61 ATGTTATGGATAAACTTTCTTCTAAGAAGTTGTGCGAGTGGAGAGTGTGTCTATCT 120  
 QY 121 ATTTCTTGGCAAGACAGACAGGAAGTAACTAATGCCCGGCTTGTGTTCTATGTCGATGTC 180  
 DB 121 ATTTCTTGGCAAGACAGACAGGAAGTAACTAATGCCCGGCTTGTGTTCTATGTCGATGTC 180  
 QY 181 AAGAAAGGCGAGAGTCTATGTTTCTTCAAGCTGTTAAGAAACGAGGAGTGGAGAG 240  
 DB 181 AAGAAAGGCGAGAGTCTATGTTTCTTCAAGCTGTTAAGAAATGGAGTGGGGCA 240  
 QY 241 TTTTGGGCTGGCAGTGTATGTTGTTGACACAGGATGAGATGGAAATGTAGGTTATTTTC 300  
 DB 241 TTCTGGGCTGGCAGTGTATGTTGTTGACACAGGATGAGATGGAAATGTGGTTATTTTC 300  
 QY 301 CCAGCAACTTGGTGAAGGAGCGGTGTATACAGAGGCGCCACAGGAGATCCCAACC 360  
 DB 301 CCAGCAACTTGGTGAAGGAGCGGTGTATACAGAGGCGCCACAGGAGATTCACACC 360  
 QY 361 ACGGATATTCAGTCTTCTCTGGA 384  
 DB 361 ACGGATATTCAGTCTTCTCTGGA 384

RESULT 4  
 AAF59080  
 ID AAF59080 standard; DNA; 330 BP.  
 XX  
 AC AAF59080;  
 XX  
 DT 23-APR-2001 (first entry)  
 XX  
 DE Mouse MLP nucleotide sequence SEQ ID NO:25.  
 XX  
 KW MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
 KW Joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
 KW cardiant; gene therapy; secretory cell function regulator; promoter;  
 KW inhibitor; ds.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO200102564-A1.  
 XX  
 XX 11-JAN-2001.  
 XX  
 XX 29-JUN-2000; 2000WO-JP04278.  
 XX  
 XX 30-JUN-1999; 99JP-0186718.  
 XX  
 XX (TAKE ) TAKEDA CHEM IND LTD.  
 XX  
 XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
 PI Tanaka H;  
 XX  
 DR WPI; 2001-159271/16.  
 XX  
 DR P-PSDB; AAB69127.  
 XX  
 PT Safe, low-toxicity secretory cell function-regulatory protein and  
 PT encoded DNA, applicable as drugs, in diagnosis and development of  
 PT promoters and inhibitors for preventing or treating e.g. bone and joint  
 PT diseases -  
 XX  
 XX Claim 10; Page 98; 11lpp; Japanese.  
 XX  
 XX The present invention describes novel MLP proteins and their encoding  
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
 CC activities, and can be used in gene therapy and as secretory cell  
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
 CC the diagnosis and development of promoters and inhibitors for preventing  
 CC or treating bone and joint diseases as well as pathologic angiogenesis.  
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
 CC in the exemplification of the present invention.  
 XX  
 XX Sequence 330 BP; 91 A; 60 C; 92 G; 87 T; 0 other;  
 SQ  
 Query Match 85.9%; Score 330; DB 22; Length 330;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-96;  
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 55 CATGGTGTTATTTATGGATTAACCTTTCTTCTAAGAAGTTGTGCGGATGAGGAGTGTGTC 114  
 DB 1 CATGGTGTTATTTATGGATAAACCTTTCTTCTAAGAAGTTGTGCGGATGAGGAGTGTGTC 60  
 QY 115 TATATCTATTTCTCTGGCAAGACAGACAGGAAGATTACAATGCCCGAGCTGTAGTTTCATC 174  
 DB 61 TATATCTATTTCTCTGGCAAGACAGACAGGAAGATTACAATGCCCGAGCTGTAGTTTCATC 120  
 QY 175 GATGTCAGAAAGGCGAGAGTCTATGTTTCTTCCAGCTGTTAAGAAACGAGGCT 234  
 DB 121 GATGTCAGAAAGGCGAGAGTCTATGTTTCTTCCAGCTGTTAAGAAACGAGGCT 180  
 QY 235 GGAGAGTTTGGGCTGGCAGTGTATGTTGTTGACACAGGATGAGATGGAAATGTAGGT 294  
 DB 181 GGAGAGTTTGGGCTGGCAGTGTATGTTGTTGACACAGGATGAGATGGAAATGTAGGT 240  
 QY 295 TATTTCCCGAGCAACTTGGTGAAGGAGCAGCGTGTATACCAGGAGGCCACCGAGGATC 354

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```
Db 241 TATTTCCCGAGCACTTGGTGAAGGAGCAGCGTGTATACAGGAGGCCACAGGAGATC 300
|||
QY 355 CCAACACGGATATTGACTTCTTCTGTGAA 384
|||
Db 301 CCAACACGGATATTGACTTCTTCTGTGAA 330
|||

RESULT 5
AAF59099
ID AAF59099 standard; DNA; 330 BP.
XX AC AAF59099;
XX DT 23-APR-2001 (first entry)
XX DE Rat MLP nucleotide sequence SEQ ID NO:48.
XX KW MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
XX joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
XX cardiant; gene therapy; secretory cell function regulator; promoter;
XX inhibitor; ds.
XX OS Rattus sp.
XX PN WO200102564-A1.
XX PD 11-JAN-2001.
XX PF 29-JUN-2000; 2000WO-JP04278.
XX PR 30-JUN-1999; 99JP-0186718.
XX PA (TAKE ) TAKEDA CHEM IND LTD.
XX PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
XX Tanaka H;
XX WPI; 2001-159271/16.
XX P-PSDB; AAB69131.
XX Safe, low-toxicity secretory cell function-regulatory protein and
XX encoded DNA, applicable as drugs, in diagnosis and development of
XX promoters and inhibitors for preventing or treating e.g. bone and joint
XX diseases -
XX Claim 12; Page 107; 111pp; Japanese.
XX The present invention describes novel MLP proteins and their encoding
XX DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
XX activities, and can be used in gene therapy and as secretory cell
XX function regulators. The MLP proteins and DNAs can be used in drugs, in
XX the diagnosis and development of promoters and inhibitors for preventing
XX or treating bone and joint diseases as well as pathologic angiogenesis.
XX AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
XX in the exemplification of the present invention.
XX Sequence 330 BP; 91 A; 62 C; 91 G; 86 T; 0 other;
XX
Query Match 76.8%; Score 294.8; DB 22; Length 330;
Best Local Similarity 93.3%; Pred. No. 8.7e-85;
Matches 308; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 55 CATGGTGTATTTATGGATAAATCTTCTTAAGAAAGTTGTGCGGATGAGAGTGTGTC 114
|||
Db 1 CATGGCATGTTTATGGATAAATCTTCTTAAGAAAGTTGTGCGGATGAGAGTGTGTC 60
|||

QY 115 TATACATTTCTTCTGCAAGACGACAGGAGATTACAATGCCAGACTGTAGTTTCATC 174
|||
Db 61 TATACATTTCTTCTGCAAGACGACAGGAGATTACAATGCCAGACTGTAGTTTCATC 120
|||

QY 175 GATGTCAAGAAAGGCGAGAGATCTATGTTTACTCCAAGCTGTGTAAACAGAAACGGAGCT 234
|||
```

```
Db 121 AATGTCAAGAAAGGCGAGAGATCTATGTTTATTCCAAGCTGTGTAAACAGAAATGGAGCT 180
|||
QY 235 GGAGAGTTTGGCTGGCAGTGTATGTTGACCAACAGGATGAGATGGGAATTTGAGGT 294
|||
Db 181 GGGGCATTTCTGGGCTGGCAGTGTATGTTGACCAACAGGATGAGATGGGAATTTGAGGT 240
|||
QY 295 TATTTCCCGAGCACTTGGTGAAGGAGCAGCGTGTATACAGGAGGCCACCAAGGAGATC 354
|||
Db 241 TATTTCCCGAGCACTTGGTGAAGGAGCAGCGTGTATACAGGAGGCCACCAAGGAGATT 300
|||
QY 355 CCAACACCGGATATTGACTTCTTCTGTGAA 384
|||
Db 301 CCAACACCGGATATTGACTTCTTCTGTGAA 330
|||

RESULT 6
AAF59065
ID AAF59065 standard; DNA; 384 BP.
XX AC AAF59065;
XX DT 23-APR-2001 (first entry)
XX DE Human MLP nucleotide sequence SEQ ID NO:4.
XX KW MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
XX joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
XX cardiant; gene therapy; secretory cell function regulator; promoter;
XX inhibitor; ds.
XX OS Homo sapiens.
XX PN WO200102564-A1.
XX PD 11-JAN-2001.
XX PF 29-JUN-2000; 2000WO-JP04278.
XX PR 30-JUN-1999; 99JP-0186718.
XX PA (TAKE ) TAKEDA CHEM IND LTD.
XX PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
XX Tanaka H;
XX WPI; 2001-159271/16.
XX P-PSDB; AAB69123.
XX Safe, low-toxicity secretory cell function-regulatory protein and
XX encoded DNA, applicable as drugs, in diagnosis and development of
XX promoters and inhibitors for preventing or treating e.g. bone and joint
XX diseases -
XX Example 1; Page 91; 111pp; Japanese.
XX The present invention describes novel MLP proteins and their encoding
XX DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
XX activities, and can be used in gene therapy and as secretory cell
XX function regulators. The MLP proteins and DNAs can be used in drugs, in
XX the diagnosis and development of promoters and inhibitors for preventing
XX or treating bone and joint diseases as well as pathologic angiogenesis.
XX AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
XX in the exemplification of the present invention.
XX
XX Sequence 384 BP; 99 A; 70 C; 106 G; 109 T; 0 other;
XX
Query Match 74.7%; Score 287; DB 22; Length 384;
Best Local Similarity 84.3%; Pred. No. 3e-82;
Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 ATGGCAAGGATATTGATTCTTTTGTGCGGCGCTGTGTGTTCTATGTGCGGCGATGTT 60
|||
Db 1 ATGGCAAGGATATTGATTCTTTTGTGCGGCGCTGTGTGTTCTATGTGCGGCGATGTT 60
|||
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QY 61 GATTATGATGATAAATCTTCTTCTAAGAGTGTGTGGGATGAGGAGTGTGCTATACT 120  
|||||  
Db 61 ATATTATGACCGTCTAGCTTCCAAGAAAGCTCTGTGCAGATGATGAGTGTGCTATACT 120  
  
QY 121 ATTTCTCTGGCAGACGACAGGAGATTACAATGCCCGACGCTAGGTTTCATCGATGTC 180  
|||||  
Db 121 ATTTCTCTGGCTAGTGTCTCAAGAAGATTATATGCCCCGACGCTGATGATTCATTAAGTT 180  
  
QY 181 AAGAAAGGGCAGCAGATCTATGTTTACTCCCAAGCTGTAAACAGAAACGAGCTGGAGAG 240  
|||||  
Db 181 AAAAAAGGGCAGCAGATCTATGTTTACTCAAGCTGTAAAGAAAGAAATGAGCTGGAGAA 240  
  
QY 241 TTTTGGCTGGCAGTGTATGTTTGTGACCCACAGATGAGATGGAAATTTAGTTATTTTC 300  
|||||  
Db 241 TTTTGGCTGGCAGTGTATGTTTGTGATGGCCAGACGAGATGGGAGTCGTGGGTATTTTC 300  
  
QY 301 CCAGCAACTTGTGTGAAGGACGACGCTGTATACCAGGAGCCACCAAGGAGATCCCAACC 360  
|||||  
Db 301 CCAGGAACTTGTGTCAAGGACACGCTGTATACCAGGAGCTACCAAGGAGTTCCACC 360  
  
QY 361 ACGGATATTGACTTCTTCTGTGA 383  
|||||  
Db 361 ACGGATATTGACTTCTTCTGTGA 383

RESULT 7  
AAH26341  
ID AAS17583 standard; cDNA; 387 BP.  
XX  
AC AAS17583;  
XX  
XX  
XX 26-FEB-2002 (first entry)  
XX  
XX DNA encoding novel secreted protein #12.  
XX  
XX Secreted protein; cytostatic; immunosuppressive; vulnery; vaccine;  
KW antiinflammatory; neuroprotective; nephrotropic; cardiovascular;  
KW human; cancer; autoimmune disease; wound healing disorder; infection;  
KW haematopoietic disorder; inflammatory disorder; infertility;  
KW neurological disease; psychiatric disease; cardiovascular disease;  
KW respiratory disease; renal; gastrointestinal; ss.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH 1..387  
FT /\*tag= a  
FT /product= "Human secreted protein"  
XX  
XX WO200179454-A1.  
XX  
XX 25-OCT-2001.  
XX  
XX 11-APR-2001; 2001WO-US11797.  
XX  
XX 13-APR-2000; 2000US-196603P.  
PR 24-APR-2000; 2000US-199417P.  
XX  
XX (SMIK ) SMITHKLINE BEECHAM CORP.  
XX (SMIK ) SMITHKLINE BEECHAM PLC.  
XX  
XX Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;  
XX  
XX WPI; 2002-061975/08.  
DR P-PSDB; AAU09871.  
XX  
XX New secreted proteins or polypeptides, useful for treating e.g. cancer,  
PT autoimmune diseases, wound healing disorder, infections, haematopoietic  
PT disorders, inflammatory disorders, infertility, cancer -  
XX  
XX Claim 2; Page 44; 92pp; English.

CC The invention relates to an isolated novel secreted polypeptide (I) and  
CC polynucleotide (II). (I) and (II) are useful for treating cancer,  
CC autoimmune diseases, wound healing disorder, infections, haematopoietic  
CC disorders, inflammatory disorders, infertility, neurological and  
CC psychiatric diseases, cardiovascular diseases, these may also be used to  
CC treat diseases, or gastrointestinal diseases. These may also be used to  
CC expression, production, function and/or metabolism of the genes, as  
CC vaccines for inducing immunological response in a mammal, and in  
CC screening methods for detecting the effect of added compounds on the  
CC production of mRNA and polypeptide in cells. The polypeptides can be used  
CC as immunogens to produce antibodies immunospecific for the polypeptides,  
CC and to identify membrane-bound or soluble receptors. The polynucleotides  
CC may be used as diagnostic reagents, in chromosome localisation studies,  
CC and in tissue expression studies. The present sequence represents the  
CC coding sequence of novel human secreted protein #12.  
XX  
SQ Sequence 387 BP; 101 A; 70 C; 106 G; 110 T; 0 other;  
  
Query Match 74.7%; Score 287; DB 24; Length 387;  
Best Local Similarity 84.3%; Pred. No. 3.1e-82;  
Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;  
  
QY 1 ATGGCAAGGATATTGATTTCTTTTCTGGGGCTTGTGGTCTATGTCGGGCGATGGT 60  
|||||  
Db 1 ATGGCAAGGATATTGATTTCTTTCTCCCGGCTTGTGGCTGTATGCTGTGATGGA 60  
  
QY 61 GTATTTATGATTAACATTTCTTTAAGAGTGTGTGGGATGAGGAGTGTGCTATACT 120  
|||||  
Db 61 ATATTTATGAGACGCTCTAGCTTCCAAGAAAGCTCTGTGCAGATGATGATGCTATACT 120  
  
QY 121 ATTTCTCTGGCAGACGACAGGAGATTACAATGCCCGACGCTGTAGGTTTCATCGATGTC 180  
|||||  
Db 121 ATTTCTCTGGCTAGTGTCTCAAGAAGATTATTAAGCCCGACGCTGATTCATTAACGTT 180  
  
QY 181 AAGAAAGGGCAGCAGATCTATGTTTACTCCCAAGCTGTAAACAGAAACGAGCTGGAGAG 240  
|||||  
Db 181 AAAAAAGGGCAGCAGATCTATGTTTACTCAAGCTGTAAAGAAAGAAATGAGCTGGAGAA 240  
  
QY 241 TTTTGGCTGGCAGTGTATGTTTGTGACCCACAGATGAGATGGAAATTTAGTTATTTTC 300  
|||||  
Db 241 TTTTGGCTGGCAGTGTATGTTTGTGATGGCCAGACGAGATGGGAGTCGTGGGTATTTTC 300  
  
QY 301 CCAGCAACTTGTGTGAAGGACGACGCTGTATACCAGGAGCCACCAAGGAGATCCCAACC 360  
|||||  
Db 301 CCAGGAACTTGTGTCAAGGACACGCTGTATACCAGGAGCTACCAAGGAGTTCCACC 360  
  
QY 361 ACGGATATTGACTTCTTCTGTGA 383  
|||||  
Db 361 ACGGATATTGACTTCTTCTGTGA 383  
  
RESULT 8  
AAH26341  
ID AAH26341 standard; cDNA; 426 BP.  
XX  
AC AAH26341;  
XX  
XX 02-OCT-2001 (first entry)  
DT Human growth regulatory-like polypeptide clone 16372272.  
XX  
XX Growth regulatory-like polypeptide; human; cartilage; melanoma;  
KW neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;  
KW ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200155332-A2.  
PN  
XX 02-AUG-2001.  
PD  
XX 25-JAN-2001; 2001WO-US02455.  
PF





CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic  
CC activities, and can be used in gene therapy. The PRO polynucleotides,  
CC proteins, agonists and antagonists are useful for treating or diagnosing  
CC a cardiovascular endothelial or angiogenic disorder in a mammal,  
CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular  
CC degeneration, atherosclerosis, hypertension, arterial restenosis,  
CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,  
CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver  
CC carcinoma) and wound healing. The PRO polynucleotides have applications  
CC in molecular biology, including use as hybridisation probes, and in  
CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and  
CC probes used in the exemplification of the present invention.  
XX  
SQ Sequence 521 BP; 167 A; 86 C; 131 G; 137 T; 0 other;  
Query Match 74.7%; Score 287; DB 24; Length 521;  
Best Local Similarity 84.3%; Pred. No. 3.5e-82;  
Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;  
QY 1 ATGGCAAGGATATTGATCTTTGCTTGGGGGCTTGTGCTTATGTCGGGCGCATGTT 60  
Db ATGGCAAGGATATTGATCTTTGCTTGGGGGCTTGTGCTTATGTCGGGCGCATGTT 97  
QY 61 GTATTATCGATAAATCTTCTCAAGAGTTGTGCGGATGAGGAGTGTGCTATCT 120  
Db ATATTATGACCGCTAGCTTCCAAAGAGCTCTGTGCGATGATGAGTGTGCTATCT 157  
QY 121 ATTTCTCTGGCAGACACAGGAGATTACAATGCCCCAGACTGTAGTTCATCGATGTC 180  
Db ATTTCTCTGGCTAGTGTCTCAAGAGATTATAATGCCCCGAGCTGTAGTTCATTAACGTT 217  
QY 181 AAGAAAGGGCAGCAGATCTATGTTTACTCCAACTGGTAAACAGAAACGAGCTGGAG 240  
Db AAAAAAGGGCAGCAGATCTATGTTGTTACTCAAGAGCTGTGTAAGAAAGAAATGGAGCTGGAGAA 277  
QY 241 TTTTGGGCTGGCAGTGTATTATGTGACCCAGGATGAGATGGGATTTAGTGTATTTC 300  
Db TTTTGGGCTGGCAGTGTATTATGTGATGGCCAGGACGAGATGGGATTTAGTGTATTTC 337  
QY 301 CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACAGAGAGCCACCAAGGAGATCCCAACC 360  
Db CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACAGAGAGCTACCAAGGAGATTTCCACC 397  
QY 361 ACGGATATTGACTTCTTCTGTGA 383  
Db ACGGATATTGACTTCTTCTGTGA 420  
RESULT 11  
ABK33571 standard; cDNA; 521 BP.  
XX AC ABK33571;  
XX  
XX 08-MAY-2002 (first entry)  
XX cDNA encoding human PRO protein, Seq ID No 71.  
DE  
XX Human; secreted protein; PRO; tumour; lung cancer; colon cancer;  
KW breast cancer; prostate tumour; rectal tumour; liver tumour;  
KW pericyte cell proliferation; chondrocyte cell proliferation;  
KW tumour necrosis factor-alpha; gene; ss.  
XX  
OS Homo sapiens.  
XX  
XX WO200208288-A2.  
XX  
XX 31-JAN-2002.  
XX  
XX 29-JUN-2001; 2001WO-US21066.  
XX  
XX 20-JUL-2000; 2000US-219556P.  
XX  
XX 25-JUL-2000; 2000US-220585P.

PR 25-JUL-2000; 2000US-220605P.  
PR 25-JUL-2000; 2000US-220607P.  
PR 25-JUL-2000; 2000US-220624P.  
PR 25-JUL-2000; 2000US-220638P.  
PR 25-JUL-2000; 2000US-220664P.  
PR 25-JUL-2000; 2000US-220666P.  
PR 26-JUL-2000; 2000US-220893P.  
PR 26-JUL-2000; 2000US-220710.  
PR 28-JUL-2000; 2000WO-US23522.  
PR 23-AUG-2000; 2000WO-US23328.  
PR 15-SEP-2000; 2000US-000000P.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 28-NOV-2000; 2000US-253646P.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000US-074259.  
PR 28-FEB-2001; 2000WO-US34956.  
PR 10-MAY-2001; 2001WO-US06520.  
PR 25-MAY-2001; 2001US-0854280.  
XX  
XX (GETH ) GENENTECH INC.  
PA  
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;  
XX  
XX WPI: 2002-172001/22.  
DR P-PSDB; AAU83627.  
XX  
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,  
PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal  
PT tumour or liver tumour -  
XX  
XX Claim 2; Figure 71; 359pp; English.  
XX  
XX The invention relates to one hundred and twenty two nucleic acids  
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides  
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,  
CC agonists and antagonists are useful for treating a PRO related disorder.  
CC The PRO polypeptides are useful for diagnosing tumours, especially lung  
CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or  
CC liver tumour. The PRO polypeptides are useful for stimulating the  
CC proliferation of, or gene expression in, pericyte cells, for stimulating  
CC the proliferation or differentiation of chondrocyte cells, for  
CC stimulating the release of tumour necrosis factor-alpha from human blood,  
CC for stimulating or inhibiting the proliferation of normal human dermal  
CC fibroblast cells. The PRO polypeptide may also be used as molecular  
CC weight markers and for tissue typing. The PRO nucleic acids have  
CC applications in molecular biology, including use as hybridisation probes,  
CC and in chromosome and gene mapping. ABK33536-ABK33657 represent human  
CC PRO protein coding sequences of the invention.  
XX  
XX SQ Sequence 521 BP; 167 A; 86 C; 131 G; 137 T; 0 other;  
Query Match 74.7%; Score 287; DB 24; Length 521;  
Best Local Similarity 84.3%; Pred. No. 3.5e-82;  
Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;  
QY 1 ATGGCAAGGATATTGATCTTTGCTTGGGGGCTTGTGCTTATGTCGGGCGCATGTT 60  
Db ATGGCAAGGATATTGATCTTTGCTTGGGGGCTTGTGCTTATGTCGGGCGCATGTT 97  
QY 61 GTATTATGATAAATCTTCTCAAGAGTTGTGCGGATGAGGAGTGTGCTATCT 120  
Db ATATTATGACCGCTAGCTTCCAAAGAGCTCTGTGCGATGATGAGTGTGCTATCT 157  
QY 121 ATTTCTCTGGCAGACACAGGAGATTACAATGCCCCAGACTGTAGTTCATCGATGTC 180  
Db ATTTCTCTGGCTAGTGTCTCAAGAGATTATAATGCCCCGAGCTGTAGTTCATTAACGTT 217  
QY 181 AAGAAAGGGCAGCAGATCTATGTTTACTCCAACTGGTAAACAGAAACGAGCTGGAG 240  
Db AAAAAAGGGCAGCAGATCTATGTTGTTACTCAAGAGCTGTGTAAGAAAGAAATGGAGCTGGAGAA 277

QY 241 TTTTGGCTGGCAGTCTTTATGCTGACCCAGCAGATGAGATGGAAATTTAGTATTATTC 300  
 DB 278 TTTTGGCTGGCAGTCTTTATGCTGATGGCCAGCAGATGGAGTCGTGGGTATTATTC 337  
 QY 301 CCAGCAACTTGGTGAAGGAGCAGCGTGATACAGGAGGCCACCAAGAGATCCCAACC 360  
 DB 338 CCAGGAACTTGGTCAAGGAAAGCGGTGTACAGAGAGCTACCAAGGAAGTTCCACC 397  
 QY 361 ACGGATATTGACTTCTTCTGTGA 383  
 DB 398 ACGGATATTGACTTCTTCTGTGA 420

RESULT 12  
 AAH98228  
 ID AAH98228 standard; cDNA; 891 BP.  
 AC AAH98228;  
 XX  
 DT 12-OCT-2001 (first entry)  
 DE Human EST-derived coding sequence SEQ ID NO: 85.  
 DE Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;  
 KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;  
 KW diagnostics; forensic test; gene mapping; genetic disorder;  
 KW biodiversity; gene therapy; nutrition; ss.  
 XX Homo sapiens.  
 OS  
 XX WO200154477-A2.  
 PN  
 XX 02-AUG-2001.  
 PD  
 XX 25-JAN-2001; 2001WO-US02687.  
 PF  
 XX 25-JAN-2000; 2000US-0491404.  
 PR 17-JUL-2000; 2000US-0617746.  
 PR 03-AUG-2000; 2000US-0631451.  
 PR 15-SEP-2000; 2000US-0663870.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;  
 PI Cao Y, Drmanac RA, Zhang J, Werhman T;  
 PI  
 XX WPI; 2001-476164/51.  
 DR P-PSDB; AAM23569.  
 DR  
 XX Isolated polypeptide for treatment of diseases, diagnostics, raising  
 PT antibodies and research use -  
 XX  
 PS Claim 1; Page 236; 1275pp; English.  
 XX  
 CC The present invention provides the protein and coding sequences of novel  
 CC proteins from a variety of organisms, including human, dog, cat, horse,  
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea  
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)  
 CC from the organism of interest. They can be used in diagnostics,  
 CC forensics, gene mapping, identification of mutations, to assess  
 CC biodiversity and for nutritional purposes. The present sequence is a cDNA  
 CC of the invention.  
 XX  
 SQ Sequence 891 BP; 272 A; 146 C; 214 G; 259 T; 0 other;  
 XX

Query Match 74.7%; Score 287; DB 22; Length 891;  
 Best Local Similarity 84.3%; Pred. No. 4.4e-82;  
 Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;  
 QY 1 ATGGCAAGATATTGATTTCTTTGCTGGGGCCTTGTGTTCTATGTGCCGGCATGGT 60  
 DB 19 ATGGCAAGATATTGTTTCTTCCCGGGTCTTTGTGCTGTATGTGTGTCATGGA 78

QY 61 GTATTTATGGATAAACTTTTCTTCTAAGAGTTGTTGTCGGATGAGGAGTGTCTCTATACT 120  
 DB 79 ATATTTATGGACCGTCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTATACT 138  
 QY 121 ATTTCCTCTGGCAAGAGCAGCAGGAAGATTACAATGCCCCAGACTGTAGTTTCATCGATGTC 180  
 DB 139 ATTTCCTCTGGCTAGTCTCTAAGAGATTATATATGCCCCGAGCTGTAGATTCNTTAAGTT 198  
 QY 181 AAGAAAGGCGAGCAGATCTATGTTTACTCCAGCTGGTAAACAGAAACCGAGCTGGAGAG 240  
 DB 199 AAAAAAGGCGAGCAGATCTATGTGTACTCAAGCTGTGTAAGAAAGAAATGCGAGCTGGAGAA 258  
 QY 241 TTTTGGCTGGCAGTCTTTATGCTGACCCAGCAGATGAGATGGAAATTTAGTATTATTC 300  
 DB 259 TTTTGGCTGGCAGTCTTTATGCTGATGGCCAGCAGATGGAGTCGTGGGTATTATTC 318  
 QY 301 CCAGCAACTTGGTGAAGGAGCAGCGTGATACAGGAGGCCACCAAGAGATCCCAACC 360  
 DB 319 CCAGGAACTTGGTCAAGGAAAGCGGTGTGTACAGAGAGCTACCAAGGAAGTTCCACC 378  
 QY 361 ACGGATATTGACTTCTTCTGTGA 383  
 DB 379 ACGGATATTGACTTCTTCTGTGA 401

RESULT 13  
 AAH26342  
 ID AAH26342 standard; cDNA; 891 BP.  
 AC AAH26342;  
 XX  
 DT 02-OCT-2001 (first entry)  
 DE Human growth regulatory-like polypeptide partial cDNA clone.  
 DE Human growth regulatory-like polypeptide; human; cartilage; melanoma;  
 KW Growth regulatory-like polypeptide; glioma; cancer; gene therapy; diagnosis;  
 KW neuroectodermal tumour; ss.  
 XX  
 OS Homo sapiens.  
 XX WO200155332-A2.  
 PN  
 XX 02-AUG-2001.  
 PD  
 XX 25-JAN-2001; 2001WO-US02455.  
 PF  
 XX 25-JAN-2000; 2000US-0491404.  
 PR 02-MAY-2000; 2000US-0563786.  
 PR  
 XX (HYSE-) HYSEQ INC.  
 PA  
 XX Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;  
 PI Drmanac RT;  
 PI  
 XX WPI; 2001-483233/52.  
 DR  
 XX Isolated human growth regulatory-like polypeptide useful for treating  
 PT e.g. Alzheimer's disease, cancer, autoimmune disorders,  
 PT hyperproliferative disorders, coagulation disorders, and nervous system  
 PT disorders -  
 XX  
 PS Claim 1; Page 115; 119pp; English.  
 XX  
 CC The present sequence is that of a novel nucleic acid that was  
 CC assembled from human thymus cDNA library-derived Hyseq clone  
 CC identification number 16372272 (see AAH26341). A recursive  
 CC algorithm was used to extend the clone by pulling additional  
 CC sequences from different databases. A full-length sequence (see  
 CC AAH26343) encoding novel human growth regulatory-like polypeptide  
 CC (GRIP, see AAH82671) was subsequently obtained. Human GRIP  
 CC belongs to the same protein family as growth regulatory proteins,  
 CC

```
CC growth factors, human melanoma derived growth regulatory protein
CC precursor (64% similarity and 45% identity over 111 amino acids)
CC or melanoma inhibitory activity, cattle cartilage-derived
CC retinoic acid sensitive protein (CD-RAP, 44% identity and 64%
CC similarity over 126 amino acids) and other retinoic acid-sensitive
CC proteins. GRP polypeptides and polynucleotides of the invention
CC can be used in the prophylaxis, treatment (including gene therapy)
CC and diagnosis of disorders and diseases caused by, or involving,
CC cartilage development and maintenance, inhibition of melanoma cell
CC growth and tumours, including neuroectodermal tumours such as
CC gliomas. The polynucleotides can also be used to design probes
CC and primers, for chromosome and gene mapping, in the recombinant
CC production of protein, in the generation of antisense, ribozyme and
CC peptide-nucleic acid molecules, and to produce transgenic animals.
XX
SQ Sequence 891 BP; 272 A; 146 C; 214 G; 259 T; 0 other;

  Query Match      74.7%; Score 287; DB 22; Length 891;
  Best Local Similarity 84.3%; Pred. No. 4.4e-82;
  Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 ATGGCAAGGATATTGATTCTTTTGGCTTGGGGCCCTTGGTCTATGTCGCGGATCGT 60
DB 19 ATGGCAAGGATATTGATTCTTTTGGCTTGGGGCCCTTGGTCTATGTCGCGATCGA 78

QY 61 GTATTATGGAATAACTTTCTTCTAAGAGTGTGTCGGGATGAGAGTGTCTATACT 120
DB 79 ATATTATGGACCGCTCTAGCTTCCAAAGAGCTCTGTGCAGATGATGATGTCTATACT 138

QY 121 ATTTCTCTGGCAAGACGACAGGAAGATTACATGCCCCAGAGCTGTAGGTTTCATCGATGTC 180
DB 139 ATTTCTCTGGCTAGTGCTCAAGAAATTATATGCCCGGACTGTAGATTCAATACGTT 198

QY 181 AAGAAAGGCGACGACATCTATGTTTACTCCAAAGCTGGTAACAGAAAACGAGCTGGAGAG 240
DB 199 AAAAAAGGCGACGACATCTATGTGACTCAAGAGCTGGTAAGAAAATGGAGCTGGAGAA 258

QY 241 TTTTGGGCTGGCAGGTTTATGTGACCAACAGGATGAGATGGGAATGTAGGTTATTTC 300
DB 259 TTTTGGGCTGGCAGGTTTATGTGATGGCCAGGACGAGATGGGAGTGTGGGTTATTTC 318

QY 301 CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACCAAGGAGGCCACCAAGGAGATCCCAACC 360
DB 319 CCCAGCAACTTGGTCAAGGACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTCCCAACC 378

QY 361 ACGGATATTGACTTCTTCTGTGA 383
DB 379 ACGGATATTGACTTCTTCTGTGGA 401

RESULT 14
AAF59083
ID AAF59083 standard; DNA; 923 BP.
XX
AC AAF59083;
XX
DT 23-APR-2001 (first entry)
XX
DE Human MLP nucleotide sequence SEQ ID NO:29.
XX
KW MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
KW cardiant; gene therapy; secretory cell function regulator; promoter;
KW inhibitor; ds.
XX
OS Homo sapiens.
XX
PN WC200102564-A1.
XX
PD 11-JAN-2001.
XX
PF 29-JUN-2000; 2000WO-JF04278.
XX
```

```
PR 30-JUN-1999; 99JP-0186718.
XX
FA (TAKA ) TAKEDA CHEM IND LTD.
XX
PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
PI Tanaka H;
XX
DR WPI; 2001-159271/16.
XX
PT Safe, low-toxicity secretory cell function-regulatory protein and
PT encoded DNA, applicable as drugs, in diagnosis and development of
PT promoters and inhibitors for preventing or treating e.g. bone and joint
PT diseases -
XX
PS Example 1; Page 99-100; 111pp; Japanese.
XX
CC The present invention describes novel MLP proteins and their encoding
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
CC activities, and can be used in gene therapy and as secretory cell
CC function regulators. The MLP proteins and DNAs can be used in drugs, in
CC the diagnosis and development of promoters and inhibitors for preventing
CC or treating bone and joint diseases as well as pathologic angiogenesis.
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
CC in the exemplification of the present invention.
XX
SQ Sequence 923 BP; 303 A; 147 C; 213 G; 260 T; 0 other;

  Query Match      74.7%; Score 287; DB 22; Length 923;
  Best Local Similarity 84.3%; Pred. No. 4.5e-82;
  Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 ATGGCAAGGATATTGATTCTTTTGGCTTGGGGCCCTTGGTCTATGTCGCGGATCGT 60
DB 34 ATGGCAAGGATATTGATTCTTTTGGCTTGGGGCCCTTGGTCTATGTCGTCATGGA 93

QY 61 GTATTATGGAATAACTTTTCTTAAAGAGTGTGTCGGGATGAGAGTGTCTATACT 120
DB 94 ATATTATGGAACCGCTCTAGCTTCCAAAGAGCTCTGTGCAGATGATGATGTCTATACT 153

QY 121 ATTTCTCTGGCAAGGACAGGAAGATTACATGCCCCAGAGCTGTAGGTTTCATCGATGTC 180
DB 154 ATTTCTCTGGCTAGTGCTCAAGAAATTATATGCCCGGACTGTAGATTCAATACGTT 213

QY 181 AAGAAAGGCGACGACATCTATGTTTACTCCAAAGCTGGTAACAGAAAACGAGCTGGAGAG 240
DB 214 AAAAAAGGCGACGACATCTATGTGACTCAAGCTGGTAAGAAAATGGAGCTGGAGAA 273

QY 241 TTTTGGGCTGGCAGGTTTATGTGTAACCAACAGGATGAGATGGGAATGTAGGTTATTTC 300
DB 274 TTTTGGGCTGGCAGGTTTATGTGATGGCCAGGACGAGATGGGAGTGTGGGTTATTTC 333

QY 301 CCCAGCAACTTGGTGAAGGAGCGGTGTATACCAAGGAGGCCACCAAGGAGATCCCAACC 360
DB 334 CCCAGCAACTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTTACCAAGGAAGTCCCAACC 393

QY 361 ACGGATATTGACTTCTTCTGTGA 383
DB 394 ACGGATATTGACTTCTTCTGTGGA 416

RESULT 15
AAH26343
ID AAH26343 standard; cDNA; 1201 BP.
XX
AC AAH26343;
XX
DT 02-OCT-2001 (first entry)
XX
DE Human growth regulatory-like polypeptide cDNA.
XX
KW Growth regulatory-like polypeptide; human; cartilage; melanoma;
KW neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;
KW ss.
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OM nucleic - nucleic search, using sw model

Run on: December 30, 2003, 04:08:13 ; Search time 315.339 Seconds  
(without alignments)  
4172.254 Million cell updates/sec

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Perfect score: 384  
Sequence: 1 atggcaagatattgattct.....atattgactttctgtgaa 384

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2244575 seqs, 1713117285 residues

Total number of hits satisfying chosen parameters: 4489150

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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  - 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
  - 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
  - 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
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  - 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*
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  - 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*
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  - 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
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  - 18: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	287	74.7	521	13	Sequence 71, Appl
4	287	74.7	521	13	Sequence 71, Appl
5	287	74.7	521	13	Sequence 71, Appl
6	287	74.7	521	13	Sequence 71, Appl
7	287	74.7	521	13	Sequence 71, Appl
8	287	74.7	521	13	Sequence 71, Appl
9	287	74.7	521	13	Sequence 71, Appl
10	287	74.7	521	13	Sequence 71, Appl
11	287	74.7	521	13	Sequence 71, Appl
12	287	74.7	521	13	Sequence 71, Appl
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17	287	74.7	521	13	US-10-219-532-71	Sequence 71, Appl
18	287	74.7	521	13	US-10-219-533-71	Sequence 71, Appl
19	287	74.7	521	13	US-10-223-081-359	Sequence 359, App
20	287	74.7	521	13	US-10-230-437-71	Sequence 71, Appl
21	287	74.7	521	13	US-10-232-228-71	Sequence 71, Appl
22	287	74.7	521	13	US-10-233-082-359	Sequence 359, App
23	287	74.7	521	15	US-10-227-884-71	Sequence 71, Appl
24	287	74.7	521	15	US-10-230-163-71	Sequence 71, Appl
25	287	74.7	521	15	US-10-230-338-71	Sequence 71, Appl
26	287	74.7	521	15	US-10-218-631-71	Sequence 71, Appl
27	287	74.7	521	15	US-10-230-414-71	Sequence 71, Appl
28	287	74.7	521	15	US-10-216-159A-71	Sequence 71, Appl
29	287	74.7	521	15	US-10-218-849-71	Sequence 71, Appl
30	287	74.7	521	15	US-10-227-873-71	Sequence 71, Appl
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32	287	74.7	521	15	US-10-219-076-71	Sequence 71, Appl
33	287	74.7	521	15	US-10-230-434-71	Sequence 71, Appl
34	287	74.7	521	15	US-10-219-003-71	Sequence 71, Appl
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36	287	74.7	521	15	US-10-219-464-71	Sequence 71, Appl
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40	287	74.7	521	15	US-10-230-260-71	Sequence 71, Appl
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ALIGNMENTS

RESULT 1

US-10-216-038-1

; Sequence 1, Application US/10216038

; Publication No. US20030124573A1

; GENERAL INFORMATION:

; APPLICANT: Mize, Nancy K

; APPLICANT: Boyle, Bryan J

; APPLICANT: Ford, John E

; APPLICANT: Aterburn, Matthew C

; APPLICANT: Tang, Y Tom

; APPLICANT: Liu, Chenghua

; APPLICANT: Drmanac, Radoje T

; APPLICANT: Song, Yong

; APPLICANT: Sjastaad, Michael

; TITLE OF INVENTION: Methods and Materials Relating to No. US20030124573A1el Growth 1

; FILE REFERENCE: HVS-7CIP

; CURRENT APPLICATION NUMBER: US/10216,038

; PRIOR FILING DATE: 2002-08-08

; PRIOR APPLICATION NUMBER: US 09/563,786

; PRIOR FILING DATE: 2000-05-02

; PRIOR APPLICATION NUMBER: US 09/491,404

; PRIOR FILING DATE: 2000-01-25

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 426

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (426)..(426)

; OTHER INFORMATION: n = A, T, G, or C

US-10-216-038-1

Query Match 74.7%; Score 287; DB 15; Length 426;  
Best Local Similarity 84.3%; Pred. No. 7.1e-87;  
Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;



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; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
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; PRIOR FILING DATE: 1999-06-22  
; PRIOR APPLICATION NUMBER: 60/140723  
; PRIOR FILING DATE: 1999-06-22  
; PRIOR APPLICATION NUMBER: 60/141037  
; PRIOR FILING DATE: 1999-06-23  
; PRIOR APPLICATION NUMBER: 60/144758

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; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/145698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 60/146222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 60/146963
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/149320
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/149638
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/151733
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/164418
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: 60/166361
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/169445
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835
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Query Match 74.7%; Score 287; DB 13; Length 521;  
Best Local Similarity 84.3%; Pred. No. 7.9e-87;  
Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

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QY 1 ATGGCAAGGATATTGATCTTTGCTTGGGGCCCTTGTGGTCTATGTCCGGGCATGCT 60
DB 38 ATGGCAAGATATTGATCTTTCTCCCGGCTTGTGGCTATGTCTGTGCATGA 97

QY 61 GTATTTATGATAAATCTTTCTTAAGAGATTGTTGTGGGATGAGAGTGTGTCTATCT 120
DB 98 ATATTTATGACCGTCTAGCTTCCAGAGCTCTGTGCAGATGATCAGTGTGTCTATCT 157

QY 121 ATTTCTCTGGCAGACACAGGAGATTCAATGCCCCAGACTGTAGGTTTCATCGATGC 180
DB 158 ATTTCTCTGGCAGTGTATGTGTGATGGCCAGCAGATGGGAGTCTGTGGGTTATTTTC 217

QY 181 AAGAAAGGCGAGCAGATCTATGTTTACTCCAGCTGGTAAACAGAAACCGAGCTGGAGAG 240
DB 218 AAAAAAGGCGAGCAGATCTATGTTACTCAAGCTGGTAAAGAAATGGAGCTGGAGAA 277

QY 241 TTTTGGGCTGGCAGTGTATGTGTGACCAAGAGATGAGATGGGAATTTGTAGTTATTTTC 300
DB 278 TTTTGGGCTGGCAGTGTATGTGTGATGGCCAGCAGATGGGAGTCTGTGGGTTATTTTC 337

QY 301 CCCAGCAACTTGTGAGGAGCAGCTGTATACCAGAGGCCACCAAGGAGATCCCAACC 360
DB 338 CCAGGAACCTTGGTCAAGGAACAGCGTGTGTACAGGAGCTTACCAAGGAGTTCCACC 397

QY 361 ACGGATATTGACTTCTTCTGTGA 383
DB 398 ACGGATATTGACTTCTTCTGCGA 420
```

RESULT 4  
US-10-219-063-71  
; Sequence 71, Application US/10219063  
; Publication No. US20030187202A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3530PIC24  
; CURRENT APPLICATION NUMBER: US/10/219,063  
; CURRENT FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: 10/119,480  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/069873  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 246  
; SEQ ID NO 71  
; LENGTH: 521  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-219-063-71

Query Match 74.7%; Score 287; DB 13; Length 521;  
Best Local Similarity 84.3%; Pred. No. 7.9e-87;  
Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

```
QY 1 ATGGCAAGGATATTGATCTTTGCTTGGGGCCCTTGTGGTCTATGTCCGGGCATGCT 60
DB 38 ATGGCAAGATATTGATCTTTCTCCCGGCTTGTGGCTATGTCTGTGCATGA 97

QY 61 GTATTTATGATAAATCTTTCTTAAGAGATTGTTGTGGGATGAGAGTGTGTCTATCT 120
DB 98 ATATTTATGACCGTCTAGCTTCCAGAGCTCTGTGCAGATGATCAGTGTGTCTATCT 157

QY 121 ATTTCTCTGGCAGACACAGGAGATTCAATGCCCCAGACTGTAGGTTTCATCGATGC 180
DB 158 ATTTCTCTGGCAGTGTATGTGTGATGGCCAGCAGATGGGAGTCTGTAGATTCAATACGTT 217

QY 181 AAGAAAGGCGAGCAGATCTATGTTTACTCCAGCTGGTAAACAGAAACCGAGCTGGAGAG 240
DB 218 AAAAAAGGCGAGCAGATCTATGTTACTCAAGCTGGTAAAGAAATGGAGCTGGAGAA 277

QY 241 TTTTGGGCTGGCAGTGTATGTGTGACCAAGAGATGAGATGGGAATTTGTAGTTATTTTC 300
DB 278 TTTTGGGCTGGCAGTGTATGTGTGATGGCCAGCAGATGGGAGTCTGTGGGTTATTTTC 337

QY 301 CCCAGCAACTTGTGAGGAGCAGCTGTATACCAGAGGCCACCAAGGAGATCCCAACC 360
DB 338 CCAGGAACCTTGGTCAAGGAACAGCGTGTGTACAGGAGCTTACCAAGGAGTTCCACC 397

QY 361 ACGGATATTGACTTCTTCTGTGA 383
DB 398 ACGGATATTGACTTCTTCTGCGA 420
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RESULT 5  
US-10-219-066-71  
; Sequence 71, Application US/10219066  
; Publication No. US20030187203A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary



Db 158 ATTTCTGCTAGTGTCTCAAGAAGATTATATATGCCCCGAGCTGTAGATTCAATTAAGTT 217  
 QY 181 AAGAAAGGGCAGCAGATCTATTTTACTCAAGCTGGTAACAGAAACGAGCTGGAGAG 240  
 Db 218 AAAAAAGGGCAGCAGATCTATGTGTACTCAAGCTGGTAAAGAAAATGGAGCTGGAGAA 277  
 QY 241 TTTTGGGCTGGCAGTGTATTTATGTCACCAAGATGAGATGGGAATTTAGTGTATTTTC 300  
 Db 278 TTTTGGGCTGGCAGTGTATTTATGTCACCAAGATGAGATGGGAATTTAGTGTATTTTC 337  
 QY 301 CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACAGAGAGCCCAAGAGATCCCAACC 360  
 Db 338 CCCAGGAACTTGGTCAAGGAACAGCGTGTGTCTCAGGAAGCTACCAAGGAAGTTCCCAACC 397  
 QY 361 ACGGATATTGACTTCTTCTGTGA 383  
 Db 398 ACGGATATTGACTTCTTCTGTGA 420

RESULT 8  
 US-10-219-069-71  
 ; Sequence 71, Application US/10219069  
 ; Publication No. US20030187206A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Gerritsen, Mary  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stephan, Jean-Philippe F.  
 ; APPLICANT: Watanabe, Colin L.  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P3530P1C40  
 ; CURRENT APPLICATION NUMBER: US/10/219,069  
 ; CURRENT FILING DATE: 2002-08-13  
 ; PRIOR APPLICATION NUMBER: 10/119,480  
 ; PRIOR FILING DATE: 2002-04-09  
 ; PRIOR APPLICATION NUMBER: 60/059113  
 ; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/062287  
 ; PRIOR FILING DATE: 1997-10-17  
 ; PRIOR APPLICATION NUMBER: 60/063549  
 ; PRIOR FILING DATE: 1997-10-28  
 ; PRIOR APPLICATION NUMBER: 60/064103  
 ; PRIOR FILING DATE: 1997-10-31  
 ; PRIOR APPLICATION NUMBER: 60/069873  
 ; PRIOR FILING DATE: 1997-12-17  
 ; PRIOR APPLICATION NUMBER: 60/078910  
 ; PRIOR FILING DATE: 1998-03-20  
 ; PRIOR APPLICATION NUMBER: 60/079294  
 ; PRIOR FILING DATE: 1998-03-25  
 ; PRIOR APPLICATION NUMBER: 60/079656  
 ; PRIOR FILING DATE: 1998-03-26  
 ; PRIOR APPLICATION NUMBER: 60/079728  
 ; PRIOR FILING DATE: 1998-03-27  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 246  
 ; SEQ ID NO 71  
 ; LENGTH: 521  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 US-10-219-069-71

Query Match 74.7%; Score 287; DB 13; Length 521;  
 Best Local Similarity 84.3%; Pred. No. 7.9e-87;  
 Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 ATGGCAAGGATATTGATTTCTTTGCTGGGGGCTTGTGTTCTATGTGCGGGCATGGT 60  
 Db 38 ATGGCAAGATATTGTTACTTTCTCCCGGCTTGTGGCTGTATGTGCTGTGCAATGA 97  
 QY 61 GTATTTATGATAACTTTCTTCAAGAGTTGTGCGGATGAGGAGTGTCTATACT 120  
 Db 98 ATATTTATGACCGTCTAGCTTCCAGAGCTCTGTGCAGATGATGATGTGTCTACT 157  
 QY 121 ATTTCTGTGCAGAGCACAGGAGATTACAATGCCCGGCTTGTGTTCTATGTGCGGGCATGGT 180

QY 301 CCAGCAACTTGGTGAAGGAGCAGCGTGTATACAGAGAGCCACCAAGGAGATCCCAACC 360  
 Db 338 CCCAGGAACTTGGTCAAGGAACAGCGTGTGTACAGAGAGCTACCAAGGAAGTTCCCAACC 397  
 QY 361 ACGGATATTGACTTCTTCTGTGA 383  
 Db 398 ACGGATATTGACTTCTTCTGTGA 420

RESULT 7  
 US-10-219-068-71  
 ; Sequence 71, Application US/10219068  
 ; Publication No. US20030187205A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Gerritsen, Mary  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stephan, Jean-Philippe F.  
 ; APPLICANT: Watanabe, Colin L.  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P3530P1C31  
 ; CURRENT APPLICATION NUMBER: US/10/219,068  
 ; CURRENT FILING DATE: 2002-08-13  
 ; PRIOR APPLICATION NUMBER: 10/119,480  
 ; PRIOR FILING DATE: 2002-04-09  
 ; PRIOR APPLICATION NUMBER: 60/059113  
 ; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/062287  
 ; PRIOR FILING DATE: 1997-10-17  
 ; PRIOR APPLICATION NUMBER: 60/063549  
 ; PRIOR FILING DATE: 1997-10-28  
 ; PRIOR APPLICATION NUMBER: 60/064103  
 ; PRIOR FILING DATE: 1997-10-31  
 ; PRIOR APPLICATION NUMBER: 60/069873  
 ; PRIOR FILING DATE: 1997-12-17  
 ; PRIOR APPLICATION NUMBER: 60/078910  
 ; PRIOR FILING DATE: 1998-03-20  
 ; PRIOR APPLICATION NUMBER: 60/079294  
 ; PRIOR FILING DATE: 1998-03-25  
 ; PRIOR APPLICATION NUMBER: 60/079656  
 ; PRIOR FILING DATE: 1998-03-26  
 ; PRIOR APPLICATION NUMBER: 60/079728  
 ; PRIOR FILING DATE: 1998-03-27  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 246  
 ; SEQ ID NO 71  
 ; LENGTH: 521  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 US-10-219-068-71

Query Match 74.7%; Score 287; DB 13; Length 521;  
 Best Local Similarity 84.3%; Pred. No. 7.9e-87;  
 Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 ATGGCAAGGATATTGATTTCTTTGCTGGGGGCTTGTGTTCTATGTGCGGGCATGGT 60  
 Db 38 ATGGCAAGATATTGTTACTTTCTCCCGGCTTGTGGCTGTATGTGCTGTGCAATGA 97  
 QY 61 GTATTTATGATAACTTTCTTCAAGAGTTGTGCGGATGAGGAGTGTCTATACT 120  
 Db 98 ATATTTATGACCGTCTAGCTTCCAGAGCTCTGTGCAGATGATGATGTGTCTACT 157  
 QY 121 ATTTCTGTGCAGAGCACAGGAGATTACAATGCCCGGCTTGTGTTCTATGTGCGGGCATGGT 180





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; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-475-71

Query Match          74.7%; Score 287; DB 13; Length 521;
Best Local Similarity 84.3%; Pred. No. 7.9e-87;
Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 ATGGCAAGGATATGATCTTTGCTGGGGCCCTTGTGCTATGTCGCGGCATGCT 60
Db 38 ATGGCAAGATATGTTACTTTTCTCCCGGCTCTGTGGCTGTATGCTGTGCATGA 97

QY 61 GTATTATGGAATAACTTCTCTAAGAGTTGTGCGGATGAGGAGTGTCTATACT 120
Db 98 ATATTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTACT 157

QY 121 ATTTCTCTGGCAAGACAGAGATTACAATGCCCCAGACTGTAGGTTCAATGATGC 180
Db 158 ATTTCTCTGGCTAGTGCTCAAGAGATTATAATGCCCGGACTGTAGATTCAATACGTT 217

QY 181 AAGAAAGGCGACAGATCTATGTTTCTTAAAGAGTTGTGCGGATGAGGAGTGTCTATACT 240
Db 218 AAAAAGGCGACAGATCTATGTTTCTTAAAGAGTTATAATGCCCGGACTGTAGATTCAATACGTT 277

QY 241 TTTTGGGCTGGCAGTGTTTATGTTTCTTAAAGAGTTGTGCGGATGAGGAGTGTCTATACT 300
Db 278 TTTTGGGCTGGCAGTGTTTATGTTTCTTAAAGAGTTGTGCGGATGAGGAGTGTCTATACT 337

QY 301 CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACAGGAGGCCACCAAGAGATCCCAACC 360
Db 338 CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACAGGAGGCCACCAAGAGATCCCAACC 397

QY 361 ACGGATATTGACTTCTCTGTGA 383
Db 398 ACGGATATTGACTTCTCTGTGA 420

RESULT 11
US-10-219-480-71
; Sequence 71, Application US/10219480
; Publication No. US20030187209A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C38
; CURRENT APPLICATION NUMBER: US/10/219,480
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17

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; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-480-71

Query Match          74.7%; Score 287; DB 13; Length 521;
Best Local Similarity 84.3%; Pred. No. 7.9e-87;
Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 ATGGCAAGGATATGATCTTTGCTGGGGCCCTTGTGCTATGTCGCGGCATGCT 60
Db 38 ATGGCAAGATATGTTACTTTTCTCCCGGCTCTGTGGCTGTATGCTGTGCATGA 97

QY 61 GTATTATGGAATAACTTCTTAAAGAGTTGTGCGGATGAGGAGTGTCTATACT 120
Db 98 ATATTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTACT 157

QY 121 ATTTCTCTGGCAAGACAGAGATTACAATGCCCCAGACTGTAGGTTCAATGATGC 180
Db 158 ATTTCTCTGGCTAGTGCTCAAGAGATTATAATGCCCGGACTGTAGATTCAATACGTT 217

QY 181 AAGAAAGGCGACAGATCTATGTTTCTTAAAGAGTTGTGCGGATGAGGAGTGTCTATACT 240
Db 218 AAAAAGGCGACAGATCTATGTTTCTTAAAGAGTTATAATGCCCGGACTGTAGATTCAATACGTT 277

QY 241 TTTTGGGCTGGCAGTGTTTATGTTTCTTAAAGAGTTGTGCGGATGAGGAGTGTCTATACT 300
Db 278 TTTTGGGCTGGCAGTGTTTATGTTTCTTAAAGAGTTGTGCGGATGAGGAGTGTCTATACT 337

QY 301 CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACAGGAGGCCACCAAGAGATCCCAACC 360
Db 338 CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACAGGAGGCCACCAAGAGATCCCAACC 397

QY 361 ACGGATATTGACTTCTCTGTGA 383
Db 398 ACGGATATTGACTTCTCTGTGA 420

RESULT 12
US-10-219-483-71
; Sequence 71, Application US/10219483
; Publication No. US20030187210A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C38
; CURRENT APPLICATION NUMBER: US/10/219,480
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17

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Tue Dec 30 10:20:36 2003

FILE REFERENCE: P3530PIC43  
CURRENT APPLICATION NUMBER: US/10/219,483  
CURRENT FILING DATE: 2002-08-13  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 246  
SEQ ID NO 71  
LENGTH: 521  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-219-483-71

Query Match 74.7%; Score 287; DB 13; Length 521;  
Best Local Similarity 84.3%; Pred. No. 7.9e-87;  
Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 ATGGCAAGATATTCATCTTTGCTTGGGGCCCTTGTTCTATGTCGGGCGATGCT 60  
DB 38 ATGGCAAGATATTTACTTTTCTCCGGGTCTTGTGGCTGTATGCTGTGATGGA 97

QY 61 GTATTTATGGATAAACTTTCTTAAAGATTGTGTGGGATGAGAGTGTCTATACT 120  
DB 98 ATATTTATGGACCGTCTAGCTTCCAGAGACTCTGTGCAGATGATGATGCTATACT 157

QY 121 ATTTCTTGGCAAGACAGAGATTAACAATGCCAGACTGTAGTTTCATGATGTC 180  
DB 158 ATTTCTTGGCTAGTGCTCAAGAAGATTATAATGCCCGGACTGTAGATTCAACGTT 217

QY 181 AAGAAAGGSCAGACATCTATCTTAAAGCTGGTAAACAGAAAACGAGCTGAGAG 240  
DB 218 AAAAAAGGSCAGACATCTATCTTAAAGCTGGTAAAGAAAATGGAGCTGAGAA 277

QY 241 TTTTGGCTGGCAGTGTATGATCCACAGGATGAGATGGGAATTGTAGTTATTTC 300  
DB 278 TTTTGGCTGGCAGTGTATGATGGCCAGGACGAGATGGGAGTCTGGGTTATTTC 337

QY 301 CCCAGCACTTGGTGAAGCAGCGTGTATACAGGAGGCCACCAAGAGATCCCAACC 360  
DB 338 CCCAGCACTTGGTCAAGAACAGCGTGTGTACAGGAAGCTTACCAAGAGATCCCAACC 397

QY 361 ACGGATATTGACTTCTCTGTGA 383  
DB 398 ACGGATATTGACTTCTCTGTGA 420

RESULT 13  
US-10-219-525-71  
Sequence 71, Application US/10219525  
Publication No. US2003018721A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Desnoyers, Luc  
APPLICANT: Gerritsen, Mary  
APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
TITLE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3530PIC29  
CURRENT APPLICATION NUMBER: US/10/219,525  
CURRENT FILING DATE: 2002-08-13  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 246  
SEQ ID NO 71  
LENGTH: 521  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-219-525-71

Query Match 74.7%; Score 287; DB 13; Length 521;  
Best Local Similarity 84.3%; Pred. No. 7.9e-87;  
Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 ATGGCAAGATATTCATCTTTGCTTGGGGCCCTTGTTCTATGTCGGGCGATGCT 60  
DB 38 ATGGCAAGATATTTACTTTTCTCCGGGTCTTGTGGCTGTATGCTGTGATGGA 97

QY 61 GTATTTATGGATAAACTTTCTTAAAGATTGTGTGGGATGAGAGTGTCTATACT 120  
DB 98 ATATTTATGGACCGTCTAGCTTCCAGAGACTCTGTGCAGATGATGATGCTATACT 157

QY 121 ATTTCTTGGCAAGACAGAGATTAACAATGCCAGACTGTAGTTTCATGATGTC 180  
DB 158 ATTTCTTGGCTAGTGCTCAAGAAGATTATAATGCCCGGACTGTAGATTCAACGTT 217

QY 181 AAGAAAGGSCAGACATCTATCTTAAAGCTGGTAAACAGAAAACGAGCTGAGAG 240  
DB 218 AAAAAAGGSCAGACATCTATCTTAAAGCTGGTAAAGAAAATGGAGCTGAGAA 277

QY 241 TTTTGGCTGGCAGTGTATGATCCACAGGATGAGATGGGAATTGTAGTTATTTC 300  
DB 278 TTTTGGCTGGCAGTGTATGATGGCCAGGACGAGATGGGAGTCTGGGTTATTTC 337

QY 301 CCCAGCACTTGGTGAAGCAGCGTGTATACAGGAGGCCACCAAGAGATCCCAACC 360  
DB 338 CCCAGCACTTGGTCAAGAACAGCGTGTGTACAGGAAGCTTACCAAGAGATCCCAACC 397

QY 361 ACGGATATTGACTTCTCTGTGA 383  
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Tue Dec 30 10:20:36 2003

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RESULT 14
US-10-219-526-71
; Sequence 71, Application US/10219526
; Publication No. US20030187212A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C41
; CURRENT APPLICATION NUMBER: US/10/219,526
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-526-71

Query Match      74.7%; Score 287; DB 13; Length 521;
Best Local Similarity 84.3%; Pred. No. 7.9e-87;
Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

Qy 1 ATGCGAAGGATATTGATTTCTTTGCTGGGGCCCTTGGTTCATGTCGCGGCATGGT 60
Db 38 ATGCGAAGAAATATTGTTACTTTCTCCCGGCTCTTGGGCTGATGTCGTGCAATGA 97

Qy 61 GTATTTATGGATAAACTTTCTTCTAAGAAAGTTGTGCGGATAGAGGAGTGTCTACT 120
Db 98 ATATTTATGGACCGCTCTAGCTTCCAGAAAGCTCTGTGCAGATGATGATGTCATACT 157

Qy 121 ATTTCTCTGGCAAGACAGCAAGATTAACATCCCGGCTCTGTGCAGATGATGATGTCATGTC 180
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Qy 181 AAGAAAGGCGACAGATCTATGTTTACTCCAAAGCTGTGTAACAGAAAACGAGCTGGAG 240
Db 218 AAAAAGGCGACAGATCTATGTTACTCAAGCTGTGTAAGAAAATGGAGCTGGAG 277

Qy 241 TTTTGGGCTGGCAGTGTATTTAGTGAACACAGAGATGAGATGGGAATTTGTAGGTTATTTTC 300
Db 278 TTTTGGGCTGGCAGTGTATTTAGTGAACACAGAGATGAGATGGGAGTGGGTTATTTTC 337
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Qy 301 CCCAGCAACTTGGTGAAGGACGCGTGTATACAGGAGGCGCACCAAGGAGATCCCAACC 360
Db 338 CCCAGGAACTTTGGTCAAGGAAACGCGTGTATCCAGGAGGTACCAAGGAGTTCGCCACC 397

Qy 361 ACGGATATTGACTTCTTCTGTGA 383
Db 398 ACGGATATTGACTTCTTCTGCGA 420

RESULT 15
US-10-219-530-71
; Sequence 71, Application US/10219530
; Publication No. US20030187213A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C54
; CURRENT APPLICATION NUMBER: US/10/219,530
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-530-71

Query Match      74.7%; Score 287; DB 13; Length 521;
Best Local Similarity 84.3%; Pred. No. 7.9e-87;
Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

Qy 1 ATGCGAAGGATATTGATTTCTTTGCTGGGGCCCTTGGTTCATGTCGCGGCATGGT 60
Db 38 ATGCGAAGAAATATTGTTACTTTCTCCCGGCTCTTGGGCTGATGTCGTGCAATGA 97

Qy 61 GTATTTATGGATAAACTTTCTTCTAAGAAAGTTGTGCGGATAGAGGAGTGTCTACT 120
Db 98 ATATTTATGGACCGCTCTAGCTTCCAGAAAGCTCTGTGCAGATGATGATGTCATACT 157

Qy 121 ATTTCTCTGGCAAGACAGCAAGATTAACATCCCGGCTCTGTGCAGATGATGATGTCATGTC 180
Db 158 ATTTCTCTGGCTAGTGTCTCAAGAAAGATTATTAATGCCCGGACTGTAGATTCAATTAAGCTT 217
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QY 181 AAGAAAGGCGACAGATCTATCTTTACTCCAGCTGGTAACAGAAAAACGAGCTGGAGAG 240
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 218 AAGAAAGGCGACAGATCTATCTTTACTCCAGCTGGTAACAGAAAAATGGAGCTGGAGAA 277
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 241 TTTTGGGCTGGCAGTGTATGTTGATGACACCGAGGATGAGATGGGAATTTAGGTTATTTTC 300
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 278 TTTTGGGCTGGCAGTGTATGTTGATGACACCGAGGATGAGATGGGAATTTAGGTTATTTTC 337
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 301 CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACCAAGGAGGCCACCAAGGAGATCCCAACC 360
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 338 CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACCAAGGAGGCCACCAAGGAGATCCCAACC 397
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 361 ACGGATATTGACTTCTTCTGTGA 383
Db |||||||||||||||||||||||||||
QY 398 ACGGATATTGACTTCTTCTGTGA 420
Db |||||||||||||||||||||||||||
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Search completed: December 30, 2003, 10:03:01  
Job time : 316.339 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 30, 2003, 01:34:27 ; Search time 31.014 Seconds  
(without alignments)  
5464.987 Million cell updates/sec

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Perfect score: 384  
Sequence: 1 atggcaagatattgattct.....atttgactttctgtgaa 384

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:\*

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2: /cgm2\_6/ptodata/2/ina/5B\_COMB.seq:\*

3: /cgm2\_6/ptodata/2/ina/6A\_COMB.seq:\*

4: /cgm2\_6/ptodata/2/ina/6B\_COMB.seq:\*

5: /cgm2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*

6: /cgm2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	66.2	17.2	581	1	US-08-578-649-4
2	60.2	15.7	459	1	US-08-578-649-1
3	55.2	14.4	330	1	US-08-578-649-18
4	52.6	13.7	305	1	US-08-578-649-8
5	35.6	9.3	596	1	US-08-578-649-24
6	35.6	9.3	3565	1	US-08-578-649-3
7	34.4	9.0	2644	4	US-09-399-913-35
8	34.4	9.0	2644	4	US-09-298-731-35
9	34.4	9.0	7218	1	US-08-232-463-14
C 10	32.6	8.5	5822	3	US-08-899-595-4
11	32.6	8.5	5822	3	US-08-899-595-5
12	32.2	8.4	202001	4	US-09-734-674-3
C 13	31.8	8.3	654	4	US-09-280-116-57
C 14	31.8	8.3	654	3	US-09-088-651-3
C 15	31.8	8.3	980	4	US-09-023-942A-30
C 16	31.8	8.3	1109	3	US-09-088-651-1
C 17	31.8	8.3	1109	3	US-09-088-651-6
C 18	31.8	8.3	1110	4	US-09-386-653A-1
C 19	31.8	8.3	1130	4	US-09-386-653A-8
C 20	31.8	8.3	1212	4	US-09-620-312D-431
C 21	31.8	8.3	1751	4	US-09-453-702B-223
22	31.6	8.2	464	4	US-09-615-192A-236
23	31	8.1	2949	3	US-08-433-522A-1
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25	31	8.1	2949	3	US-08-942-046-1
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29	31	8.1	2984	3	US-08-433-522A-3
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31	31	8.1	2984	3	US-08-942-046-3
32	31	8.1	2987	3	US-08-433-522A-55
33	31	8.1	2987	3	US-09-135-166-55
34	31	8.1	2987	3	US-08-942-046-55
C 35	30.8	8.0	1778	1	US-08-416-870C-3
36	30.4	7.9	8789	1	US-08-328-254-5
37	30.4	7.9	10136	1	US-08-353-700-2
38	30.4	7.9	10136	5	PCT-US95-16216-2
39	30.4	7.9	25002	4	US-08-961-527-48
C 40	30	7.8	13158	2	US-08-687-080-105
C 41	30	7.8	36412	4	US-08-311-731A-132
C 42	29.8	7.8	1500	4	US-09-252-991A-4920
43	29.8	7.8	1620	4	US-09-252-991A-4922
C 44	29.8	7.8	2800	3	US-08-714-918-35
C 45	29.8	7.8	2800	3	US-09-265-315-35

ALIGNMENTS

RESULT 1  
US-08-578-649-4  
; Sequence 4, Application US/08578649  
; Patent No. 5770366  
; GENERAL INFORMATION:  
; APPLICANT: Ulrich Bogdan  
; APPLICANT: Reinhard Buttner  
; APPLICANT: Brigitte Kaluza  
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felfe & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: Wordperfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/578,649  
; FILING DATE: 29-July-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE P 43 24 247.2  
; FILING DATE: 20-July-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Andrew L. Tiajolooff  
; REGISTRATION NUMBER: 31,575  
; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 688-9200  
; TELEFAX: (212) 838-3884  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 581 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 110..499  
; FEATURE:  
; NAME/KEY: sig\_peptide  
; LOCATION: 110..178  
; FEATURE:

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; NAME/KEY: mat peptide
; LOCATION: 179..499
US-08-578-649-4

Query Match      17.2%; Score 66.2; DB 1; Length 581;
Best Local Similarity 54.4%; Pred. No. 6.2e-12;
Matches 181; Conservative 0; Mismatches 143; Indels 9; Gaps 2;

QY 51 CGGCGATGGTATTTATGATTAACCTTCTTAAGAAGTTGTGCGGATGAGGAGTG 110
Db 169 CAGGCGTATCGACTATGCCAAGCTGGCTGACTGGAAGCTGTGTGGACGAGGAATG 228
QY 111 TGTCTATATCTTTCTGCGCAAGACAGACAGAAATTAACATGCCCCAGACTGTAGTT 170
Db 229 CAGCCATCTATCTCCATGGCTGTGGCCCTCCAGGACTACGTGGCCCTGATTCGCCGT 288
QY 171 CATGATGTCAGAAAGGCGACAGACTATGTTTACTCCAAGCTGGTAAACAGAAACGG 230
Db 289 CTTGACTATATAGGGCCCAAGTGGTGTATGTCTTCTCCAGTTG-----AAGGGCG 342
QY 231 AGCTGGAGAGTTTGGGCTGGCAGTGTATTATGGTGACCACAGGATGAGATGGGA--AT 287
Db 343 TGGGCGCTTCTTGGGGAGGAGGAGTGTTCAGGGAGGTTACTATGGAGACCTGGCAGCCG 402
QY 288 TGTAGTTATTTCCCAACACTTGGTGAAGGACGAGCGGTATACCAAGAGGCCACCAA 347
Db 403 CTTGGGCTATTTCCCACTAGCATTTGTCGGGAGGACCTGAACCTCGAAACCTGGCAAAAT 462
QY 348 GGAGATCCCAACCGGATATTGACTTCTTCTG 380
Db 463 TGATATGAGACCGATCAATGGGATTTCTACTG 495

RESULT 2
US-08-578-649-1
; Sequence 1, Application US/08578649
; Patent No. 5770366
; GENERAL INFORMATION:
; APPLICANT: Ulrich Bogdan
; APPLICANT: Reinhard Buttner
; APPLICANT: Brigitte Kaluza
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/578,649
; FILING DATE: 29-July-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 24 247.2
; FILING DATE: 20-July-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Andrew L. Tiajolloff
; REGISTRATION NUMBER: 31,575
; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 459 base pairs
; TYPE: nucleic acid
;

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 40..432
; FEATURE:
; NAME/KEY: sig peptide
; LOCATION: 40..111
; FEATURE:
; NAME/KEY: mat peptide
; LOCATION: 112..432
US-08-578-649-1

Query Match      15.7%; Score 60.2; DB 1; Length 459;
Best Local Similarity 56.8%; Pred. No. 5e-10;
Matches 154; Conservative 0; Mismatches 108; Indels 9; Gaps 2;

QY 58 GGTCTATTATGGATAAACTTCTTCTTAAGAAGTTGTGCGGATGAGGAGTGTCTAT 117
Db 109 GTGGTCTATGCCAAGCTGGCTGACCGAAGCTGTGTGGACCGAGGAGTGCAGCCAC 168
QY 118 ACTATTTCTTGGCAAGACAGACAGAAATTAACATGCCCCAGACTGTAGTTTATCGAT 177
Db 169 CCTATCTCATGGCTGTGGCCCTTTCAGGACTACATGGCCCCCAGCTGCCGATTCCTGACC 228
QY 178 GTCAAGAAAGGCGACAGACTATGTTTACTCCAAGCTGTAACAGAAAACGGAGCTGGA 237
Db 229 ATTCAACGGGGCCCAAGTGGTGTATGTCTTCTCCAGCTG-----AAGGGCGTGGGCGG 282
QY 238 GAGTTTGGGCTGGCAGTGTATTATGGTGACCACAGGATGAGATGGGAATT---GTAGGT 294
Db 283 CTCCTCTGGGAGGAGCAGCGTTTCAGGAGATTACTATGGAGATCTGGCTGCTCGCCTGGGC 342
QY 295 TATTTCCCAAGCAACTTGGTGAAGAGCAGC 325
Db 343 TATTTCCCAAGTATGATTCAGGAGGAGC 373

RESULT 3
US-08-578-649-18
; Sequence 18, Application US/08578649
; Patent No. 5770366
; GENERAL INFORMATION:
; APPLICANT: Ulrich Bogdan
; APPLICANT: Reinhard Buttner
; APPLICANT: Brigitte Kaluza
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/578,649
; FILING DATE: 29-July-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 24 247.2
; FILING DATE: 20-July-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Andrew L. Tiajolloff
; REGISTRATION NUMBER: 31,575
; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 459 base pairs
; TYPE: nucleic acid
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; TELEPHONE: (212) 688-3200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 330 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: mat peptide
; LOCATION: 7..327
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; NAME/KEY: misc RNA
; LOCATION: 4..6
; OTHER INFORMATION: /function= "Startcodon Met"
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US-08-578-649-18

Query Match      14.4%; Score 55.2; DB 1; Length 330;
Best Local Similarity 55.4%; Pred. No. 1.8e-08;
Matches 152; Conservative 0; Mismatches 113; Indels 9; Gaps 2;

QY 55 CATGGCTATTATTGGATAAACTTCTTCTAAGAAAGTGTGTGGGATGAGGAGTGTGTC 114
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Db 61 CACCTATCTCCATGGCTGTGGCCCTTCAGGACTACATGGCCCCCGGACTGCCGATTCCTG 120
QY 175 GATGTCGAAGAAGGGCGACGAGATCTATGTTTACTCCAGCTGGTAAACAGAAACGGAGCT 234
Db 121 ACCATTACCCGGGCGCAAGTGGTGTATGTCTTCTCCAAAGCTG-----AAGGGCCGTGGG 174
QY 235 GGAGAGTTTTGGGCTGGCAGTGTTTATGTGTGACCAACAGGATGAGATGGGAATT---GTA 291
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QY 292 GGTATTTCGCCAGCAACTTGGTGAAGGAGCAGC 325
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RESULT 4
US-08-578-649-8
; Sequence 8, Application US/08578649
; Patent No. 5770366
; GENERAL INFORMATION:
; APPLICANT: Ulrich Bogdan
; APPLICANT: Reinhard Butner
; APPLICANT: Brigitte Kaluza
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/578,649
; FILING DATE: 29-July-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 24 247.2
; FILING DATE: 20-July-1993
; ATTORNEY/AGENT INFORMATION:

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; NAME: Andrew L. Tiajolloff
; REGISTRATION NUMBER: 31,575
; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 305 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc RNA
; LOCATION: join(1..29, 277..305)
; OTHER INFORMATION: /function= "Primer"
;
US-08-578-649-8

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Query Match      13.7%; Score 52.6; DB 1; Length 305;
Best Local Similarity 57.3%; Pred. No. 1.2e-07;
Matches 138; Conservative 0; Mismatches 94; Indels 9; Gaps 2;

QY 88 AAGTTGTGTGCGGATGAGGAGTGTCTATACTATTTCTCTGGCAAGACACAGGAAGAT 147
Db 7 AAGTTTCGCGGATCAGGATCGAGCCACCCTATCTCCATGGCTGTGGCCCTTCAGGAC 66
QY 148 TACAATGCCCGACGACTGTAGGTTTCATGATGTCAAGAAAGGCGAGCAGATCTATGTTTAC 207
Db 67 TACATGGCCCCCGACTGCCGATTCTGACCAATTCACCGGGGCCCAAGTGGTGTATGTCTTC 126
QY 208 TCCAAGCTGTATACAGAAACGGAGCTGGAGAGTTTGGGCTGGCAGTGTATTATGGTGAC 267
Db 127 TCCAAGCTG-----AAGGGCCGTGGCGGCTCTTCTGGGAGGCGAGCGTTCAGGGAGAT 180
QY 268 CACCAGATCAGATGGGAATT---GTAGGTTATTTCGCCAGCACTTGGTGAAGGAGCAG 324
Db 181 TACTATGAGATCTGGTTCGCTCGCCTGGCTATTTCGCCAGTAGCATTGTCCGAGAGGAC 240
QY 325 C 325
Db 241 C 241

```

```

RESULT 5
US-08-578-649-24
; Sequence 24, Application US/08578649
; Patent No. 5770366
; GENERAL INFORMATION:
; APPLICANT: Ulrich Bogdan
; APPLICANT: Reinhard Butner
; APPLICANT: Brigitte Kaluza
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/578,649
; FILING DATE: 29-July-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 24 247.2
; FILING DATE: 20-July-1993

```





QY	247	GCTGGCAGTGTTTATCGTGACACACGAGTAGATCGGAATTCTAGGTTATTTCGCCAGC	306
Db	2000	CCAGGCCAACAGGTCACGACAGCCTCAGGAGGAGA - GAGAGCTGTTCCTGCCTCCCAGGC	2058
QY	307	AAC TTGGTGAAGGAGCAGCGTGTATATACGAGGCGCACCAAGGAGATCCCAACCACGGAT	366
Db	2059	CTGCCCCAGAAGAAACAGTGTCCCAAGAGCATGTTTCTCTGGAGGAACATCCCCACA AAA	2118
QY	367	ATTGACTTCTTC	378
Db	2119	GTACATTCCATC	2130

RESULT 9  
 US-08-232-463-14/c  
 ; Sequence 14, Application US/08232463  
 ; Patent No. 5670367  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DORNER, F.  
 ; APPLICANT: SCHEIFLINGER, F.  
 ; APPLICANT: FALKNER, F. G.  
 ; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
 ; NUMBER OF SEQUENCES: 52  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Foley & Lardner  
 ; STREET: 1800 Diagonal Road, Suite 500  
 ; CITY: Alexandria  
 ; STATE: VA  
 ; COUNTRY: USA  
 ; ZIP: 22313-0299  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/232,463  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/935,313  
 ; FILING DATE:  
 ; APPLICATION NUMBER: EP 91 114 300.6  
 ; FILING DATE: 26-AUG-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: BENT, Stephen A.  
 ; REGISTRATION NUMBER: 29,768  
 ; REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (703)836-9300  
 ; TELEFAX: (703)683-4109  
 ; TELEX: 899149  
 ; INFORMATION FOR SEQ ID NO: 14:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 7218 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; CLONE: ptzgpt-Fts  
 US-08-232-463-14

[illegible]

Db	2066	GTACCTCCAGGTAAGAGAGGGGGTGAGGAGATGCAACACACCCCGAGCAAGAGGTGGA	2007
Qy	228	CGAGCTGGAGAGTTTGGCTGGCAGTGTATGTGACACCCAGGATCAGATTGGGAAT	287
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Qy	288	TGTAGGTTATTTCCCGAGCAACTTGGTGAAGGAGCAGCGTGTATACCAGGAGGCCACCAA	347
Db	1946	GGATAATAGTGCCAGAGTACCAGGTAAGGAGGGGCGAGGGGGACAGGAGCAGACTA	1887
Qy	348	GGG 350	
Db	1886	GGG 1884	

RESULT 11

US-08-899-595-5  
; Sequence 5, Application US/08899595  
; Patent No. 611072  
; GENERAL INFORMATION:  
; APPLICANT: Narumiya, Shuh  
; APPLICANT: Takahashi, No. 6111072uaki  
; TITLE OF INVENTION: RHO TARGET PROTEIN HUMAN MDIA AND GENE  
; TITLE OF INVENTION: ENCODING SAME  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/899,595  
; FILING DATE: 24-JUL-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 8-242701  
; FILING DATE: 26-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 9-90170  
; FILING DATE: 25-MAR-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stephen A. Bent  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 049441/0112  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5822 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; ANTI-SENSE: YES  
; ORIGINAL SOURCE:  
; ORGANISM: Human  
; US-08-899-595-5

[illegible]

RESULT 10

US-08-899-595-4/C  
 ? Sequence 4, Application US/08899595  
 ? Patent No. 611072  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Narumiya, Shuh  
 ? APPLICANT: Takahashi, No. 611072uaki  
 ? TITLE OF INVENTION: RHO TARGET PROTEIN HUMAN MDIA AND GENE  
 ? TITLE OF INVENTION: ENCODING SAME  
 ? NUMBER OF SEQUENCES: 14  
 ? CORRESPONDENCE ADDRESS:  
 ? ADDRESSEE: Foley & Lardner  
 ? STREET: 3000 K Street, N.W., Suite 500  
 ? CITY: Washington  
 ? STATE: D.C.  
 ? COUNTRY: USA  
 ? ZIP: 20007-5109  
 ? COMPUTER READABLE FORM:  
 ? MEDIUM TYPE: Floppy disk  
 ? COMPUTER: IBM PC compatible  
 ? OPERATING SYSTEM: PC-DOS/MS-DOS  
 ? SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ? CURRENT APPLICATION DATA:  
 ? APPLICATION NUMBER: US/08/899,595  
 ? FILING DATE: 24-JUL-1997  
 ? CLASSIFICATION: 435  
 ? PRIOR APPLICATION DATA:  
 ? APPLICATION NUMBER: JP 8-242701  
 ? FILING DATE: 26-AUG-1996  
 ? PRIOR APPLICATION DATA:  
 ? APPLICATION NUMBER: JP 9-90170  
 ? FILING DATE: 25-MAR-1997  
 ? ATTORNEY/AGENT INFORMATION:  
 ? NAME: Stephen A. Bent  
 ? REGISTRATION NUMBER: 29,768  
 ? REFERENCE/DOCKET NUMBER: 049441/0112  
 ? TELECOMMUNICATION INFORMATION:  
 ? TELEPHONE: (202)672-5300  
 ? TELEFAX: (202)672-5399  
 ? TELEX: 904136  
 ? INFORMATION FOR SEQ ID NO: 4:  
 ? SEQUENCE CHARACTERISTICS:  
 ? LENGTH: 5822 base pairs  
 ? TYPE: nucleic acid  
 ? STRANDEDNESS: single  
 ? TOPOLOGY: linear  
 ? MOLECULE TYPE: cDNA to mRNA  
 ? ORIGINAL SOURCE:  
 ? ORGANISM: Human  
 ? FEATURE:  
 ? NAME/KEY: CDS  
 ? LOCATION: 28..3972  
 ? US-08-899-595-4

Db 3757 GTACCTCCAGTAAAGAGGGGTGAGGAGATGCAAAACACCCCGAGCAAGAGGTTGGA 3816  
Qy 228 CGGAGCTGGAGAGTTTGGGTGCGCAGTGTATATGTTGACACACAGGATGAGATGGGAAT 287  
Db 3817 GGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTACTATCCCGAGGAGGTTGGT 3876  
Qy 288 TGTAGTTATTTCCCGAGCACTTTGGTGAAGGAGCAGGTTGTATACAGGAGGCGCAAA 347  
Db 3877 GGAATAATAGTGCAGAGTACCAGGTAAAGAGGGGCGAGGGGAACAGGAGCAGCTA 3936  
Qy 348 GGA 350  
Db 3937 GGA 3939  
RESULT 12  
US-09-734-674-3  
; Sequence 3, Application US/09734674  
; Patent No. 6498022  
; GENERAL INFORMATION:  
; APPLICANT: WEI, Ming-Hui et al  
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: CLO01018  
; CURRENT APPLICATION NUMBER: US/09/734,674  
; CURRENT FILING DATE: 2000-12-13  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3 202001  
; LENGTH: 202001  
; TYPE: DNA  
; ORGANISM: Human  
; NAME/KEY: misc feature  
; LOCATION: (1)...(202001)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-734-674-3  
Query Match 8.4%; Score 32.2; DB 4; Length 202001;  
Best Local Similarity 49.7%; Pred. No. 10;  
Matches 82; Conservative 0; Mismatches 83; Indels 0; Gaps 0;  
Qy 119 CTATTTCTGCAAGACAGGAGATACATGCCCCAGACTGTAGTTCATCGATG 178  
Db 183409 CTAGAACTCAGGAGAGGTAAGGAGAGACGTAGTCCGTGGAATCATTAGCAAGTCTGT 183468  
Qy 179 TCAAGAAAGGCGAGCAGATCTATGTTTACTCCAAGCTGTACAGAAACCGAGCTGGAG 238  
Db 183469 GAAAGTCAAGCCATGGGTATGATGACTATTCAGGAGAAAGAAACAGAGATGAG 183528  
Qy 239 AGTTTGGGCTGGCAGTGTATGTTGACCCAGAGATGAGTGG 283  
Db 183529 AGTCCAGGAATCCCAATGTTGAGGGGCAATAAAGAGAGATG 183573  
RESULT 13  
US-09-280-116-57/c  
; Sequence 57, Application US/09280116A  
; Patent No. 6331427  
; GENERAL INFORMATION:  
; APPLICANT: Robison, Keith E.  
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs  
; FILE REFERENCE: 5800-24, 035800/176965  
; CURRENT APPLICATION NUMBER: US/09/280,116A  
; CURRENT FILING DATE: 1999-03-26  
; NUMBER OF SEQ ID NOS: 268  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 57  
; LENGTH: 654  
; TYPE: DNA  
; ORGANISM: Homo sapiens

; FEATURE:  
; OTHER INFORMATION: trypsin-like serine proteases  
US-09-280-116-57  
Query Match 8.3%; Score 31.8; DB 4; Length 654;  
Best Local Similarity 59.3%; Pred. No. 1;  
Matches 54; Conservative 0; Mismatches 37; Indels 0; Gaps 0;  
Qy 252 CAGTGTATGTTGACACACAGGATGAGATGGGAATTTAGTGTATTTCCCGAGCAACTT 311  
Db 625 CGGTGCTTTGCTGTAGACGAGGTTCACCTTGGGTGTGTCATGATGGGCACAGGAGTT 566  
Qy 312 GGTGAAGGACGAGCGTGTATATACACAGGAGGCC 342  
Db 565 TCTGACAGATCCGCGGTTCCGGCAGGAGGTC 535  
RESULT 14  
US-09-088-651-3/c  
; Sequence 3, Application US/09088651  
; Patent No. 6165771  
; GENERAL INFORMATION:  
; APPLICANT: BURGESS, NICOLA A.  
; APPLICANT: CLINKENBEARD, HELEN E.  
; APPLICANT: SOUTHAN, CHRISTOPHER D.  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: RATNER & PRESTIA  
; STREET: P.O. BOX 980  
; CITY: VALLEY FORGE  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19482  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/088,651  
; FILING DATE: JUNE 1, 1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB9712088.5  
; FILING DATE: 10-JUNE-1997  
; APPLICATION NUMBER: EP 97308295.1  
; FILING DATE: 17-OCT-1997  
; APPLICATION NUMBER: GB 9803650.2  
; FILING DATE: 20-FEB-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PRESTIA, PAUL F.  
; REGISTRATION NUMBER: 23,031  
; REFERENCE/DOCKET NUMBER: GH30358  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-407-0700  
; TELEFAX: 610-407-0701  
; TELEX: 846169  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 683 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-09-088-651-3  
Query Match 8.3%; Score 31.8; DB 3; Length 683;  
Best Local Similarity 59.3%; Pred. No. 1.1;  
Matches 54; Conservative 0; Mismatches 37; Indels 0; Gaps 0;  
Qy 252 CAGTGTATGTTGACACACAGGATGAGATGGGAATTTAGTGTATTTCCCGAGCAACTT 311

Tue Dec 30 10:20:36 2003

Db 369 CGGTGCTCTTGTCTAGACGAGTTGCACCTTGGGTGTGTGCGATGATGGGCACAGCGAGTT 310  
QY 312 GGTGAGGAGGAGCGGTGTATACGAGGAGCC 342  
Db 309 TCTGAGGATCCGCGTTCGGGACGAGGTC 279

## RESULT 15

US-09-023-942A-30/C  
; Sequence 30, Application US/09023942A  
; Patent No. 6479274  
; GENERAL INFORMATION:  
; APPLICANT: (US only) ANTALIS Toni Marie and HOOPER John David  
; TITLE OF INVENTION: NOVEL MOLECULES  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER  
; STREET: 400 GARDEN CITY PLAZA  
; CITY: GARDEN CITY  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/023,942A  
; FILING DATE: 13-FEB-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: P05101/97  
; FILING DATE: 13-FEB-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: P04022/97  
; FILING DATE: 18-NOV-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: International PCT Application  
; FILING DATE: 13-FEB-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DIGIGLIO, FRANK S  
; REGISTRATION NUMBER: 31,346  
; REFERENCE/DOCKET NUMBER: 11168  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742 4343  
; TELEFAX: (516) 742 4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 980 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-09-023-942A-30

Query Match 8.3%; Score 31.8; DB 4; Length 980;  
Best Local Similarity 59.3%; Pred. NO. 1.2;  
Matches 54; Conservative 0; Mismatches 37; Indels 0; Gaps 0;  
QY 252 CAGTGTATTATGTTACGACGAGGATGAGATGGGAATTGTAGTTATTTCCTCCAGCACTT 311  
Db 525 CGGTGCTCTTGTCTAGACGAGTTGCACCTTGGGTGTGTGCGATGATGGGCACAGCGAGTT 466  
QY 312 GGTGAAGGAGGAGCGGTGTATACGAGGAGCC 342  
Db 465 TCTGAGGATCCGCGTTTCGGGACGAGGTC 435

Search completed: December 30, 2003, 06:10:40  
Job time : 33.014 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2003, 16:03:18 ; Search time 13.2661 Seconds  
(without alignments)  
927.898 Million cell updates/sec

Title: US-10-019-455A-12  
Perfect score: 676  
Sequence: 1 MARILLILLGLVLCAGH.....RVQEQATKEIPTTIDFFCE 128

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues  
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_76.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	277.5	41.1	131	2 I38019	melanoma-derived growth regulatory protein MIA - human
2	277.5	41.1	131	2 I38019	transforming protein vav - mouse
3	89.5	13.2	839	1 TVHUVV	transforming prote
4	84.5	12.5	878	1 I51940	gene VAV2 protein
5	81.5	12.1	1215	2 T32734	myosin-1A - Acanth
6	79	11.7	722	2 G86746	hypothetical prote
7	78.5	11.6	1589	1 RGBYCS	cell division cont
8	77	11.4	695	2 S66662	protein-glutamine
9	76.5	11.3	176	2 T18921	hypothetical prote
10	76	11.2	259	2 C64427	hypothetical prote
11	75	11.1	406	2 S07164	hypothetical prote
12	74.5	11.0	1097	2 T31504	hypothetical prote
13	74	10.9	332	2 T04200	hypothetical prote
14	73	10.8	344	2 C81920	hypothetical prote
15	73	10.8	994	2 T21356	hypothetical prote
16	72.5	10.7	93	2 F84138	hypothetical prote
17	72	10.7	308	2 T48525	hypothetical prote
18	72	10.7	344	2 E81183	copper ABC transpo
19	72	10.7	585	2 G66995	ATP-dependent RNA
20	72	10.7	636	2 T06793	receptor kinase ho
21	72	10.7	1084	2 T12925	ribonucleotide red
22	71.5	10.6	847	1 A53800	mixed-lineage prec
23	71	10.5	340	2 F64853	yceG protein precu
24	71	10.5	340	2 C90813	probable thymidyla
25	71	10.5	340	2 G98672	dTMP kinase (EC 2.
26	71	10.5	373	2 T39655	VHS domain contain
27	71	10.5	946	1 A47299	ror-related recept
28	70.5	10.4	333	2 A84055	transcription regu
29	70.5	10.4	505	1 S24550	protein-tyrosine k

30	70.5	10.4	506	1 S24553	protein-tyrosine k
31	70.5	10.4	718	2 T02310	hypothetical prote
32	70.5	10.4	780	2 T29580	hypothetical prote
33	70.5	10.4	839	2 G96719	probable chromonet
34	70.5	10.4	859	2 S13030	3',5'-cyclic-GMP p
35	70	10.4	295	2 F90113	cell division cycl
36	70	10.4	486	2 S29302	alliin lyase (EC 4
37	69.5	10.3	396	2 S23589	connexin 45 - mous
38	69.5	10.3	413	2 T02893	S-receptor kinase
39	69.5	10.3	714	2 D65047	ribonucleoside-dip
40	69.5	10.3	714	2 E91071	hypothetical prote
41	69.5	10.3	714	2 E85915	hypothetical prote
42	69	10.2	288	2 T38696	probable peroxisom
43	69	10.2	670	2 S67383	probable signal tr
44	69	10.2	816	2 T17257	hypothetical prote
45	69	10.2	1032	2 D95177	Shf2 family protei

ALIGNMENTS

RESULT 1

I38019  
melanoma-derived growth regulatory protein MIA - human  
C:Species: Homo sapiens (man)  
C:Date: 17-May-1996 #sequence\_revision 17-May-1996 #text\_change 04-Mar-2000  
C:Accession: I38019; S40238  
R:Blesch, A.; Bosserhoff, A.K.; Apfel, R.; Behl, C.; Hessdoerfer, B.; Schmitt, A.; Jac  
Cancer Res. 54, 5695-5701, 1994  
A:Title: Cloning of a novel malignant melanoma-derived growth-regulatory protein, MIA.  
A:Reference number: I38019; MUID:95007612; PMID:7923218  
A:Accession: I38019  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-131 <RES>  
A:Cross-references: EMBL:X75450; NID:9438057; PIDN:CAA53203.1; PID:9438058  
C:Genetics:  
A:Gene: mia  
C:Superfamily: human melanoma-derived growth regulatory protein MIA

Query Match 41.1%; Score 277.5; DB 2; Length 131;  
Best Local Similarity 43.4%; Pred. No. 6.6e-21;  
Matches 59; Conservative 29; Mismatches 35; Indels 13; Gaps 6;

QY	1	MARILLILLGLVLC---AGHGVF---MDKLSSKKLCADBECEVTISLARAQEDYNAPD	54
DB	1	MARSLVCL--GVIIILSAFSGPGVGRGMPKLADEKLCADQECSPISMAVALQDYMAPD	58
QY	55	CRFTDVKKGQOIYYVSKLVTEGAGE--FWAGSVYGDHDEMGII--VGYPFSPNLVKEQRVYQ	112
DB	59	CRFLTIHRGQVYVFSKL---KGRGRLEFGSVQGDYVGDLAARLGYPFSSIVREDQTLK	115
QY	113	EATKEIPTTIDFFCE 128	
DB	116	PGKVDVKTDKWDFYQ 131	

RESULT 2

TVMSVW  
transforming protein vav - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 03-May-1994 #sequence\_revision 16-Feb-1996 #text\_change 18-Jun-1999  
C:Accession: A61187; A39576; S36941; S23669  
R:Coppola, J.; Bryant, S.; Koda, T.; Conway, D.; Barbacid, M.  
Cell Growth Differ. 2, 95-105, 1991  
A:Title: Mechanism of activation of the vav protooncogene.  
A:Reference number: A61187; MUID:91299578; PMID:2069873  
A:Accession: A61187  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-844 <COP>  
R:Katzav, S.; Cleveland, J.L.; Heslop, H.E.; Pulido, D.  
Mol. Cell. Biol. 11, 1912-1920, 1991







QY	63	GGQIVVYSKLVTE	NGAGEF-----	WAGSVYGDHQDEM	GVGYPNSLVKE--	QRVVQ	111
		:	:	:	:	:	:
Db	261	NTAIF-----	NDLGKYKAKVP	FEWQNA-----	HAHSLGIMP	LPPNLVNMSS	EEK 307
		:	:	:	:	:	:
QY	113	EATKEIP	119				
			:				
Db	308	EAILEVP	314				
RESULT 12							
T31504							
hypothetical protein Y116A8C.36 - Caenorhabditis elegans							
C;Species: Caenorhabditis elegans							
C;date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999							
C;Accession: T31504							

**us-10-019-455a-12.rpr**

A;Accession: C81920  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-344 <PAR>  
A;Cross-references: GB:AL162754; GB:AL157959; NID:g7379424; PIDN:CAB84045.1; PID:g737399  
A;Experimental source: serogroup A, strain Z2491  
C;Genetics:  
A;Gene: NMA0762

Query Match 10.8%; Score 73; DB 2; Length 344;  
Best Local Similarity 28.1%; Pred.No. 11;  
Matches 27; Conservative 17; Mismatches 46; Indels 6; Gaps 4;

Qy 17 AGHGVFMDKLSKKLCAD--BECVVTISLARAQEDYNAPDCRFIDYKKGQOIYVYVKLV- 73  
Db 170 AGKCVFAYNANYDKLSANHPENCQIGIHFTAAIEGTSLHDNSFIN-NESQVKYVSTRFLD 228  
Qy 74 -TENGAGFWA-GSVYGDHDEMGIYGVPPSNLVKE 107  
Db 229 WSEGHGNYWSDNSAFDLNGDGFSDSAYRPNGIIDQ 264

RESULT 15  
T21356  
Hypothetical protein F25H2.13 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 29-Oct-1999  
C;Accession: T21356; T21540  
R;Wilkinson, J.  
submitted to the EMBL Data Library, September 1996  
A;Reference number: Z19411  
A;Accession: T21356  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-994 <WIL>  
A;Cross-references: EMBL:Z79754; PIDN:CAB02102.1; GSPDB:GN00019; CESP:F25H2.13  
A;Experimental source: clone F25H2  
R;Wilkinson, J.  
submitted to the EMBL Data Library, December 1996  
A;Reference number: Z19437  
A;Accession: T21540  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-994 <W12>  
A;Cross-references: EMBL:Z83224; PIDN:CAB05720.1; GSPDB:GN00019; CESP:F25H2.13  
A;Experimental source: clone F29C6  
C;Genetics:  
A;Gene: CESP:F25H2.13  
A;Map position: 1  
A;Introns: 129/2; 177/1; 206/2; 349/3; 436/3; 506/2; 626/3; 689/3; 772/3; 845/3; 903/3

Query Match 10.8%; Score 73; DB 2; Length 994;  
Best Local Similarity 27.6%; Pred.No. 34;  
Matches 37; Conservative 20; Mismatches 45; Indels 32; Gaps 9;

Qy 23 MDKL-SKKKL-----CADBECVYVTSLARAQEDYNAPDCRFIDYKKGQOIYVYVK- 71  
Db 339 MDKLFGSSQLKSVPLPSGRASDGE-ILLETAKAGFDANSVE-RLVDVLRDAISYLLSKN 396  
Qy 72 ---LVTENAG-----EFWAGSVYGDH-QDEMGIVG-----YFPSNLVKEQRYQE 113  
Db 397 EEVVALTERGDGMEKVADFL-LSYSTHAQDVAAVGEETVKLVDRDPKTVARNCKLIQ 455  
Qy 114 ATKETPTTDDIFFC 127  
Db 456 KKDNEKLTIKYFC 469

Search completed: December 29, 2003, 16:10:39  
Job time : 14.2661 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2003, 16:03:18 ; Search time 5.01961 Seconds  
(without alignments)  
1199.181 Million cell updates/sec

Title: US-10-019-455A-12  
Perfect score: 676  
Sequence: 1 MARILLILGGLVVLCAHG.....RVYQATKEIPTTIDIFFCE 128

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	676	100.0	128	1	Q9JIE3 mus musculus
2	602	89.1	128	1	Q9HRC9 homo sapien
3	468.5	69.3	132	1	Q9HCP6 gallus gall
4	412	60.9	133	1	Q9H8P5 rana catesb
5	277.5	41.1	131	1	Q16674 homo sapien
6	268	39.6	130	1	Q62946 rattus norv
7	267	39.5	130	1	Q28038 bos taurus
8	251	37.1	130	1	Q61865 mus musculus
9	91.5	13.5	843	1	P54100 rattus norv
10	91.5	13.5	845	1	P27870 mus musculus
11	91.5	13.5	847	1	Q9R0C8 mus musculus
12	89.5	13.2	845	1	P15498 homo sapien
13	89.5	13.2	847	1	Q9UKW4 homo sapien
14	85.5	12.6	868	1	Q60992 mus musculus
15	84.5	12.5	878	1	P52735 homo sapien
16	78.5	11.6	1589	1	P04821 saccharomyc
17	77	11.4	695	1	P52181 pagrus majo
18	77	11.4	2161	1	Q9Y566 homo sapien
19	76	11.2	259	1	Q58426 methanococc
20	75	11.1	406	1	P05729 euglena gra
21	75	11.1	1696	1	Q9NZM3 homo sapien
22	75	11.1	2167	1	Q9WV48 rattus norv
23	74	10.9	1217	1	Q9WVE9 rattus norv
24	73	10.8	451	1	P54401 entamoeba h
25	71	10.5	340	1	P28106 escherichia
26	71	10.5	1714	1	Q9Z0R4 mus musculus
27	71	10.5	1721	1	Q15811 homo sapien
28	71	10.5	1815	1	Q9JIL4 rattus norv
29	70.5	10.4	505	1	P42686 spongilla l
30	70.5	10.4	506	1	P42590 spongilla l
31	70.5	10.4	858	1	Q27664 mus musculus
32	70	10.4	486	1	Q01594 allium sati
33	69.5	10.3	396	1	P28229 mus musculus

34	69.5	10.3	713	1	RIR3_ECOLI	P39452 escherichia
35	69	10.2	670	1	YBY2_SCHPO	Q10199 schizosacch
36	68.5	10.1	358	1	KARG_NORMA	P51544 nordotis ma
37	68.5	10.1	377	1	NCK1_HUMAN	P16333 homo sapien
38	68.5	10.1	399	1	CAQ1_MOUSE	Q09165 mus musculus
39	68	10.1	427	1	AROA_STRP8	Q9P0H1 streptococc
40	68	10.1	430	1	AROA_STRP9	Q99283 streptococc
41	68	10.1	733	1	VINE_MOUSE	Q97128 mus musculus
42	68	10.1	954	1	M3KA_HUMAN	Q02779 homo sapien
43	68	10.1	2183	1	POLG_CXB4E	Q86887 c genome po
44	68	10.1	2183	1	POLG_CXB4J	P08292 c genome po
45	67.5	10.0	383	1	PGL3_ASPNG	Q12554 aspergillus

ALIGNMENTS

RESULT 1

ID	OTOR_MOUSE	STANDARD;	PRT;	128 AA.
AC	Q9JIE3;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Otoraplin precursor (Melanoma inhibitory activity-like protein).			
GN	OTOR OR MIAL.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=20334619; PubMed=10873378;			
RA	Robertson N.G., Heller S., Lin J.S., Resendes B.L., Werenowicz S.,			
RA	Denis C.S., Bell A.M., Hudspeth A.J., Morton C.C.;			
RT	"A novel conserved cochlear gene, OTOR: identification, expression			
RT	analysis, and chromosomal mapping.";			
RL	Genomics 66:242-248(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Fetal;			
RA	MEDLINE=21100875; PubMed=11161796;			
RA	Rendtorff N.D., Frodin M., Attie-Bitach T., Vekemans M., Tommerup N.;			
RT	"Identification and characterization of an inner ear-expressed human			
RT	melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent			
RT	polymorphism that abolishes translation.";			
RL	Genomics 71:40-52(2001).			
CC	-!- SUBCELLULAR LOCATION: Secreted (Potential).			
CC	-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN COCHLEA.			
CC	-!- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.			
CC	-!- SIMILARITY: Contains 1 SH3 domain.			

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CC	EMBL; AF233333; AAF82079.1; -
CC	EMBL; AJ243939; CAC27444.1; -
DR	HSSP; Q16674; 111J
DR	MGI; 188678; Otor.
DR	GO; GO:0001502; P:cartilage condensation; IMP.
DR	InterPro; IPR001452; SH3.
DR	Pfam; PF00018; SH3; 1.
DR	SMART; SM00326; SH3; 1.
DR	PROSITE; PS50002; SH3; 1.
KW	Signal; SH3 domain.
FT	SIGNAL 1 18
FT	CHAIN 19 128
FT	POTENTIAL.
FT	OTORAPLIN.
FT	SH3.
FT	DOMAIN 39 110

Tue Dec 30 10:20:38 2003

FT DISULFID 32 37 BY SIMILARITY.  
 FT DISULFID 55 127 BY SIMILARITY.  
 SQ SEQUENCE 128 AA; 14328 MW; 3DD47D4C77C4A7FD CRC64;  
 Query Match 100.0%; Score 676; DB 1; Length 128;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-59;  
 Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARILLGLLVLCAGHGVFMDKLSKKKLCADEECVYTTISLARAQEDYNAPDCRFIDV 60  
 DB 1 MARILLGLLVLCAGHGVFMDKLSKKKLCADEECVYTTISLARAQEDYNAPDCRFIDV 60  
 QY 61 KKGQIYVYKLVTEGAGFVAGSVYGDHGVFVPSNVLKQRYVQATKEIPT 120  
 DB 61 KKGQIYVYKLVTEGAGFVAGSVYGDHGVFVPSNVLKQRYVQATKEIPT 120  
 QY 121 TDIDFCE 128  
 DB 121 TDIDFCE 128

## RESULT 2

OTOR HUMAN STANDARD; PRT: 128 AA.  
 ID Q9NRC9;  
 AC Q9NRC9;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Otoraplin precursor (Fibrocyte-derived protein) (Melanoma inhibitory  
 DE activity like protein).  
 DE activity like protein).  
 OS Homo sapiens (Human).  
 GN Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=20334619; PubMed=10873378;  
 RX Robertson N.G., Heller S., Lin J.S., Resendes B.L., Weremowicz S.,  
 RA Denis C.S., Bell A.M., Hudspeth A.J., Morton C.C.;  
 RT "A novel conserved cochlear gene, OTOR: identification, expression  
 RT analysis, and chromosomal mapping.";  
 RL Genomics 66:242-248(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20568254; PubMed=10998416;  
 RA Cohen-Salmon M., Frenz D., Liu W., Verpy E., Voegelings S., Petit C.;  
 RT "Fdp, a new fibrocyte-derived protein related to MIA/CO-RAP, has an  
 RT in vitro effect on the early differentiation of the inner ear  
 RT mesenchyme.";  
 RL J. Biol. Chem. 275:40036-40041(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain, and Cochlea;  
 RX MEDLINE=21100875; PubMed=11161796;  
 RA Rendtorff N.D., Frodin M., Attie-Bitach T., Vekemans M., Tommerup N.;  
 RT "Identification and characterization of an inner ear-expressed human  
 RT melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent  
 RT polymorphism that abolishes translation.";  
 RL Genomics 71:40-52(2001).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21639749; PubMed=11780052;  
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,  
 RA Jones M., Stavridis G., Almeida J.P., Babbage A.K., Baguley C.L.,  
 RA Bailey J., Barlow K.F., Bates K.N., Bead L.M., Beare D.M.,  
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,  
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,  
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,  
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,  
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,

RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
 RA Leharvalho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
 RA Marsh V.L., Martin S.L., McConachie L.J., McEay K., McMurray A.A.,  
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,  
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,  
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,  
 RA Swann R.M., Symamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
 RA Tracey A., Tomans A.C., Vaudin M., Wall M., Wallis J.M.,  
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,  
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
 RA Rogers J.;  
 RT "The DNA sequence and comparative analysis of human chromosome 20.";  
 RL Nature 414:865-871(2001).  
 CC -!- SURCELLULAR LOCATION: Secreted (Potential).  
 CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN COCHLEA.  
 CC -!- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.  
 CC -!- SIMILARITY: Contains 1 SH3 domain.  
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 CC  
 CC EMBL; AF233261; AAF82078.1; -;  
 DR EMBL; AF243505; BAG42356.1; -;  
 DR EMBL; AJ242552; CAC27443.1; -;  
 DR EMBL; AJ252324; CAC28085.1; -;  
 DR EMBL; AJ252325; CAC28085.1; JOINED.  
 DR EMBL; AJ252326; CAC28085.1; JOINED.  
 DR EMBL; AJ252327; CAC28085.1; JOINED.  
 DR EMBL; AJ034428; CAC16848.1; -;  
 DR HSSP; Q16674; ILLJ.  
 DR Genew; HGNC=8517; OTOR.  
 DR MIM; 606067; -;  
 DR GO; GO:0007605; P:hearing; TAS.  
 DR InterPro; IPR001452; SH3.  
 DR Pfam; PF00018; SH3; 1.  
 DR SMART; SM00326; SH3; 1.  
 DR PROSITE; PS50002; SH3; FALSE NEG.  
 DR SIGNAL; 1 18 POTENTIAL.  
 KW SIGNAL; 19 128 OTORAPLIN.  
 FT CHAIN 19 128 SH3.  
 FT DOMAIN 39 110 SH3.  
 FT DISULFID 32 37 BY SIMILARITY.  
 FT DISULFID 55 127 BY SIMILARITY.  
 SQ SEQUENCE 128 AA; 14332 MW; 9BB52C7F5D4FB700 CRC64;  
 Query Match 89.1%; Score 602; DB 1; Length 128;  
 Best Local Similarity 86.7%; Pred. No. 5.5e-52;  
 Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 MARILLGLLVLCAGHGVFMDKLSKKKLCADEECVYTTISLARAQEDYNAPDCRFIDV 60  
 DB 1 MARILLGLLVLCAGHGVFMDKLSKKKLCADEECVYTTISLARAQEDYNAPDCRFIDV 60  
 QY 61 KKGQIYVYKLVTEGAGFVAGSVYGDHGVFVPSNVLKQRYVQATKEIPT 120  
 DB 61 KKGQIYVYKLVTEGAGFVAGSVYGDHGVFVPSNVLKQRYVQATKEIPT 120  
 QY 121 TDIDFCE 128  
 DB 121 TDIDFCE 128

RESULT 3

```
OTOR CHICK STANDARD; PRT; 132 AA.
ID Q918P6;
AC Q918P6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Otoraplin precursor.
GN OTOR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
OX [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=20334619; PubMed=10873378;
RX Robertson N.G., Heller S., Lin J.S., Resendes B.L., Weremowicz S.,
RA Denis C.S., Bell A.M., Hudspeth A.J., Morton C.C.;
RT "A novel conserved cochlear gene, OTOR: identification, expression
analysis, and chromosomal mapping.";
RL Genomics 66:242-248(2000).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN COCHLEA.
CC -!- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
CC -!- SIMILARITY: Contains 1 SH3 domain.
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CC -----
DR EMBL; AF233518; AAF82727.1; -.
DR HSP; Q16674; 111J.
DR InterPro; IPR001452; SH3.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS50002; SH3; 1.
DR SIGNAL; SH3 domain.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 132 OTORAPLIN.
FT DOMAIN 42 114 SH3.
FT DISULFID 35 40 BY SIMILARITY.
FT DISULFID 58 131 BY SIMILARITY.
SQ SEQUENCE 132 AA; 15177 MW; 9D1C807FD353CE1C CRC64;

Query Match 69.3%; Score 468.5; DB 1; Length 132;
Best Local Similarity 71.0%; Pred. No. 6.2e-39;
Matches 88; Conservative 14; Mismatches 15; Indels 7; Gaps 2;

Qy 12 LVLCAG-----HGVMFKLSSKKLCADEECVVTISLARAQEDYNAPDCRFIDVKKQQ 65
Db 9 VLFCLFGLNPFATGIFMDKLASKLCADDCVVTISLARAQEDYNAPDCRFINIKKQL 68
Qy 66 IYVYSKLVTEGAGFVAGSYYG-DHDEMGIVGFPNSLVKEQRYVQEAKEIPTDID 124
Db 69 IYVYSKLVKESEGFVAGSYYGVEYEDHMTGTVGFPRSLVSEQHVQEAKEIPTDID 128

Qy 125 PFCE 128
Db 129 PFCE 132

RESULT 4
ID OTOR_RANCA STANDARD; PRT; 133 AA.
AC Q918P5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Otoraplin precursor.
GN OTOR.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OC NCBI_TaxID=8400;
OX [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=20334619; PubMed=10873378;
RX Robertson N.G., Heller S., Lin J.S., Resendes B.L., Weremowicz S.,
RA Denis C.S., Bell A.M., Hudspeth A.J., Morton C.C.;
RT "A novel conserved cochlear gene, OTOR: identification, expression
analysis, and chromosomal mapping.";
RL Genomics 66:242-248(2000).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
CC -!- SIMILARITY: Contains 1 SH3 domain.
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CC -----
DR EMBL; AF233519; AAF82728.1; -.
DR HSP; Q16674; 111J.
DR InterPro; IPR001452; SH3.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS50002; SH3; 1.
DR SIGNAL; SH3 domain.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 133 OTORAPLIN.
FT DOMAIN 48 115 SH3.
FT DISULFID 35 40 BY SIMILARITY.
FT DISULFID 58 132 BY SIMILARITY.
SQ SEQUENCE 133 AA; 15243 MW; 25440C1A3CF911AE CRC64;

Query Match 60.9%; Score 412; DB 1; Length 133;
Best Local Similarity 57.6%; Pred. No. 2.1e-33;
Matches 72; Conservative 28; Mismatches 17; Indels 8; Gaps 3;

Qy 12 LVLCAG-----HGVMFKLSSKKLCADEECVVTISLARAQEDYNAPDCRFIDVKKQQ 65
Db 9 VIVLCGLFIHQKAYGVYMQKLSKCLCADDCEIVASFGRAEDDYNAPDCRFVNLKKGEL 68
Qy 66 IYVYSKLVTEGAGFVAGSYYGCD-HQDEMGIVGFPNSLVKEQRYVQEAKEIPTDI 123
Db 69 VYIYTKLVKENDDAGEFWGSGVSYSDYRDQOGLVGFPSLLVTLTYVDELQELPTTAV 128

Qy 124 DFCE 128
Db 129 DFYCD 133

RESULT 5
MIA_HUMAN
ID MIA_HUMAN STANDARD; PRT; 131 AA.
AC Q16674;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Melanoma derived growth regulatory protein precursor (Melanoma
DE inhibitory activity).
GN MIA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
OX [1]
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RP MEDLINE=95007612; PubMed=7923218;
RX Blesch A., Bosserhoff A.-K., Apfel R., Behl C., Hessdoerfer B.,
```

RA Schmitt A., Jachimczak P., Lottspeich F., Buettner R., Bogdahn U.;  
 RT "Cloning of a novel malignant melanoma-derived growth-regulatory  
 RL protein, MIA.",  
 RN Cancer Res. 54:5695-5701(1994).  
 [2]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Placenta;  
 RC MEDLINE=96132947; PubMed=8550608;  
 RA Bossert A., K., Hein R., Bogdahn U., Buettner R.;  
 RX "Structure and promoter analysis of the gene encoding the human  
 RT melanoma-inhibiting protein MIA.",  
 RL J. Biol. Chem. 271:490-495(1996).  
 [3]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Skin;  
 RC MEDLINE=2238257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmitt J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RL human and mouse cDNA sequences.",  
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [4]  
 RN X-RAY CRYSTALLOGRAPHY (1.39 ANGSTROMS) OF 25-131.  
 RP MEDLINE=21244635; PubMed=11331761;  
 RA Loughheed J.C., Holton J.M., Alber T., Bazan J.F., Handel T.M.;  
 RX "Structure of melanoma inhibitory activity protein, a member of a  
 RT recently identified family of secreted proteins";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:5515-5520(2001).  
 CC -!- FUNCTION: ELICITS GROWTH INHIBITION ON MELANOMA CELLS IN VITRO  
 CC AS WELL AS SOME NEUROECTODERMAL TUMORS, INCLUDING GLIOMAS.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: ALL MALIGNANT MELANOMA CELL LINES TESTED AND  
 CC INFREQUENTLY IN GLIOMA CELL LINES.  
 CC -!- PTM: MAY POSSESS TWO INTRAMOLECULAR DISULFIDE BONDS.  
 CC -!- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.  
 CC -!- SIMILARITY: Contains 1 SH3 domain.  
 CC -----  
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 CC -----  
 DR EMBL; X75450; CAA53203.1; --  
 DR EMBL; X84707; CAA53195.1; --  
 DR EMBL; BC005910; AAH05910.1; --  
 DR PIR; I38019; I38019.  
 DR PDB; 1L1J; 16-MAY-01.  
 DR PDB; 1HJD; 29-JAN-02.  
 DR PDB; 1K0X; 24-JUL-02.  
 DR Genew; HGNC:7076; MIA.  
 DR MIM; 601340; --  
 DR GO; GO:0005615; C:extracellular space; TAS.  
 DR GO; GO:0008283; P:cell proliferation; TAS.  
 DR InterPro; IPR001452; SH3.  
 DR Pfam; PF00018; SH3; 1.

DR SMART: SM00326; SH3; 1.  
 DR PROSITE; PS50002; SH3; 1.  
 KW Growth factor; Signal; SH3 domain; 3D-structure.  
 FT FT SIGNAL 1 24  
 FT FT CHAIN 25 131 MELANOMA DERIVED GROWTH REGULATORY  
 FT FT PROTEIN.  
 FT FT SH3.  
 FT FT DOMAIN 43 113  
 FT FT DISULFID 36 41  
 FT FT DISULFID 59 130  
 FT FT STRAND 33 36  
 FT FT TURN 39 40  
 FT FT STRAND 46 50  
 FT FT STRAND 54 54  
 FT FT TURN 59 60  
 FT FT TURN 61 61  
 FT FT STRAND 64 64  
 FT FT TURN 66 67  
 FT FT STRAND 69 76  
 FT FT STRAND 78 80  
 FT FT HELIX 81 82  
 FT FT TURN 83 89  
 FT FT TURN 93 94  
 FT FT STRAND 96 96  
 FT FT STRAND 101 104  
 FT FT HELIX 105 107  
 FT FT STRAND 108 113  
 FT FT STRAND 119 122  
 FT FT HELIX 126 128  
 FT FT HELIX 131 AA; 14509 MW; 4D3BB30BD6008BDC CRC64;  
 SQ SEQUENCE 131 AA; 14509 MW; 4D3BB30BD6008BDC CRC64;  
 Query Match 41.1%; Score 277.5; DB 1; Length 131;  
 Best Local Similarity 43.4%; Pred. No. 2.8e-20;  
 Matches 59; Conservative 29; Mismatches 35; Indels 13; Gaps 6;  
 QY 1 MARILILLGLGVLC---AGHVF---MDKLSSKKLCADSECVYVITISLARAQEDYNAPD 54  
 Db 1 MARSIVCL--GVIIILSAFSGVGGVGPMPKLADKLCAQDECSHPISNAVALQDYMAPD 58  
 QY 55 CRFTIVKKGQIYVYVSKLVTENGAGE-FWAGSVYGDHDEMGI-VGYFPFNLVKEQRYVQ 112  
 Db 59 CRFTIHRGQVYVFSKL---KGRGLFWGSGVQDYGDLAARLGYPFSSIVREDQTLK 115  
 QY 113 BATKEIPTTDIDFFCE 128  
 Db 116 PGKVDVTKDKWDFYQ 131  
 RESULT 6  
 MIA RAT STANDARD; PRT; 130 AA.  
 ID MIA RAT STANDARD; PRT; 130 AA.  
 AC Q62946; P97591;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Melanoma derived growth regulatory protein precursor (Melanoma  
 DE inhibitory activity) (Cartilage-derived retinoic acid-sensitive  
 DE protein) (CD-RAP).  
 GN MIA OR CD-RAP.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Mammary gland;  
 RA Lu J.X.;  
 RT "Gene expression changes associated with chemically-induced rat  
 RT mammary Carcinogenesis";  
 RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 34-124 FROM N.A.  
 RC TISSUE=Cartilage;  
 RN MEDLINE=96216414; PubMed=8621736;



Tue Dec 30 10:20:38 2003

RA Dietz U.H., Sandell L.J.;  
RT "Cloning of a retinoic acid-sensitive mRNA expressed in cartilage and  
RL during chondrogenesis";  
J. Biol. Chem. 271:3311-3316 (1996).  
CC -1- FUNCTION: MAY FUNCTION DURING CARTILAGE DEVELOPMENT AND  
CC MAINTENANCE.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: CARTILAGE PRIMORDIA AND CARTILAGE.  
CC -1- INDUCTION: Repressed by retinoic acid.  
CC -1- PFM: MAY POSSESS TWO INTRAMOLECULAR DISULFIDE BONDS.  
CC -1- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.  
CC -1- SIMILARITY: Contains 1 SH3 domain.

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EMBL; U51438; AAC52481.1; -;  
DR EMBL; U67884; AAB40659.1; -;  
DR HSSP; Q16674; I11J.  
DR InterPro: IPR001452; SH3.  
DR Pfam; PF00018; SH3; 1.  
DR SMART; SM00326; SH3; 1.  
DR PROSITE; PS00002; SH3; 1.  
KW Growth factor; Signal; SH3 domain.  
FT SIGNAL 1 22  
FT CHAIN 23 130  
FT DOMAIN 42 112  
FT DISULFID 35 40  
FT DISULFID 58 129  
FT CONFLICT 46 47  
SQ SEQUENCE 130 AA; 14536 MW; 5F99149AECF74501 CRC64;

Query Match 39.6%; Score 268; DB 1; Length 130;  
Best Local Similarity 43.0%; Pred. No. 2.3e-19;  
Matches 55; Conservative 27; Mismatches 36; Indels 10; Gaps 4;

QY 8 LGLGLVLCAGHV-----FMDKLSKLCADCECVYTISLARAQEDYNAPDCRIDVKK 62  
Db 6 VLLGIVLSVFGSLGRADRPMPKLAADKLCADCECHPSLMAVALQDYVADPCREFTIYR 65  
QY 63 GQIIVYVSKLVTEGAGE-FWAGSVYGDHDEMGI-VGYFPSNLVKEQRYQEAATKEIPT 120  
Db 66 GQVIVVFSKL---KGRGLFWGSGVQGDYGYGLAAHLGYFPSSIVREDTLTKPGKVDKMT 122  
QY 121 TDIDPFCE 128  
Db 123 DEWDFVCQ 130

RESULT 7  
MIA\_BOVIN  
ID MIA\_BOVIN STANDARD; PRT; 130 AA.  
AC Q28038;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Melanoma derived growth regulatory protein precursor (Melanoma  
DE inhibitory activity) (Cartilage-derived retinoic acid-sensitive  
DE protein) (CD-RAP).  
GN MIA OR CD-RAP.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.

RX MEDLINE=96216414; PubMed=8621736;  
RA Dietz U.H., Sandell L.J.;  
RT "Cloning of a retinoic acid-sensitive mRNA expressed in cartilage and  
RL during chondrogenesis";  
J. Biol. Chem. 271:3311-3316 (1996).  
CC -1- FUNCTION: MAY FUNCTION DURING CARTILAGE DEVELOPMENT AND  
CC MAINTENANCE.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: CARTILAGE PRIMORDIA AND CARTILAGE.  
CC -1- INDUCTION: Repressed by retinoic acid.  
CC -1- PFM: MAY POSSESS TWO INTRAMOLECULAR DISULFIDE BONDS.  
CC -1- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.  
CC -1- SIMILARITY: Contains 1 SH3 domain.

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EMBL; U51437; AAC48523.1; -;  
DR HSSP; Q16674; I11J.  
DR InterPro: IPR001452; SH3.  
DR Pfam; PF00018; SH3; 1.  
DR SMART; SM00326; SH3; 1.  
DR PROSITE; PS00002; SH3; 1.  
KW Growth factor; Signal; SH3 domain.  
FT SIGNAL 1 22  
FT CHAIN 23 130  
FT DOMAIN 42 112  
FT DISULFID 35 40  
FT DISULFID 58 129  
SQ SEQUENCE 130 AA; 14353 MW; 95D153161C78E02A CRC64;

Query Match 39.5%; Score 267; DB 1; Length 130;  
Best Local Similarity 43.7%; Pred. No. 2.9e-19;  
Matches 59; Conservative 26; Mismatches 38; Indels 12; Gaps 5;

QY 1 MARILILGLGLVLC-----GHGVFMDKLSKLCADCECVYTISLARAQEDYNAPDC 55  
Db 1 MAWSLVFL--GWLLSAPFGPSAGRPMPKLAADKLCADCECHPSLMAVALQDYVADPC 58  
QY 56 RFDVKKQQIYVYVSKLVTEGAGE-FWAGSVYGDHDEMGI-VGYFPSNLVKEQRYQEAATKEIPT 113  
Db 59 RFLTHQGVVYVFSKL---KGRGLFWGSGVQGDYGYGLAAHLGYFPSSIVREDTLTKP 115  
QY 114 ATKEIPTTDIDPFCE 128  
Db 116 AKTDVKTIDWDFYCQ 130

RESULT 8  
MIA\_MOUSE  
ID MIA\_MOUSE STANDARD; PRT; 130 AA.  
AC Q61865; O09086; P97495;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Melanoma derived growth regulatory protein precursor (Melanoma  
DE inhibitory activity) (Cartilage-derived retinoic acid-sensitive  
DE protein) (CD-RAP).  
GN MIA OR CD-RAP.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/C;  
RC MEDLINE=95007612; PubMed=7923218;



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DR PROSITE; PSS0003; PH_DOMAIN; 1.
DR PROSITE; PSS0001; SH2; 1.
DR PROSITE; PSS0002; SH3; 2.
KW Proto-oncogene; Phorbol-ester binding; Zinc; SH2 domain; SH3 domain;
KW Guanine-nucleotide releasing factor; Repeat; Phosphorylation.
FT DOMAIN 1 119
FT DOMAIN 194 373
FT DOMAIN 402 504
FT DOMAIN 516 564
FT DOMAIN 615 658
FT DOMAIN 669 763
FT DOMAIN 780 840
SQ SEQUENCE 843 AA; 97953 MW; C4A5ACAD45FCE80E CRC64;
Query Match 13.5%; Score 91.5; DB 1; Length 843;
Best Local Similarity 32.9%; Pred. No. 0.28;
Matches 23; Conservative 14; Mismatches 20; Indels 13; Gaps 3;
Qy 44 ARAQEDYNAPCRIDVKKGOQIVYSLVTENGAGFEWAGSVVGDHDEMGIVGYPPSN 103
Db 785 AKARYDFCARDSELSLEKGDII----KILNKGQGGWWRGEIYGR-----IGWFFPSN 833
Qy 104 LVKEQRTVQE 113
Db 834 YVEED--YSE 841
RESULT 10
VAV_MOUSE STANDARD; PRT; 845 AA.
AC P27670;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DR Vav proto-oncogene.
GN VAV1 OR VAV.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92228488; PubMed=1565462;
RA Adams J.A., Houston H., Allen J., Lints T., Harvey R.;
RT "The hematopoietically expressed vav proto-oncogene shares homology
RT with the db1 GDP-GTP exchange factor, the bcr gene and a yeast gene
RT (CDC24) involved in cytoskeletal organization.";
RL Oncogene 7:611-618(1992).
RN [2]
RP SEQUENCE OF 1-93 FROM N.A.
RX MEDLINE=91172176; PubMed=2005887;
RA Katrav S., Cleveland J.L., Heslop H.E., Pulido D.;
RT "Loss of the amino-terminal helix-loop-helix domain of the vav proto-
RT oncogene activates its transforming potential.";
RL Mol. Cell. Biol. 11:1912-1920(1991).
RN [3]
RP INTERACTION WITH SLA.
RX MEDLINE=20130290; PubMed=10662792;
RA Sosinowski T., Pandey A., Dixit V.M., Weiss A.;
RT "Src-like adaptor protein (SLAP) is a negative regulator of T cell
RT receptor signaling.";
RL J. Exp. Med. 191:463-474(2000).
CC -!- FUNCTION: Couples tyrosine kinase signals with the activation of
CC the Rho/Rac GTPases, thus leading to cell differentiation and/or
CC proliferation.
CC -!- SUBUNIT: Interacts with SLA.
CC -!- TISSUE SPECIFICITY: Widely expressed in hematopoietic cells but
CC not in other cell types.
CC -!- PTM: Phosphorylated on tyrosine residues (By similarity).
CC -!- SIMILARITY: Contains 1 calponin-homology (CH) domain.
CC -!- SIMILARITY: Contains 1 DBL-homology (DH) domain.
CC -!- SIMILARITY: Contains 1 PH domain.
CC -!- SIMILARITY: Contains 1 zinc-dependent phorbol-ester and DAG
```

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CC binding domain.
CC -!- SIMILARITY: Contains 1 SH2 domain.
CC -!- SIMILARITY: Contains 2 SH3 domains.
CC -----
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CC -----
DR EMBL; X64361; CAA45713.1; -.
DR EMBL; M59833; AAA63402.1; -.
DR PIR; A61187; TVMSV.
DR PDB; 1F5X; 15-SEP-00.
DR PDB; 1GCP; 28-JAN-03.
DR PDB; 1GCQ; 28-JAN-03.
DR PDB; 1K1Z; 18-DEC-02.
DR TRANSFAC; T01230; -.
DR MGI; MGI:98923; Vav1. Calponin-like.
DR InterPro; IPR001715; CH type.
DR InterPro; IPR003247; CH type.
DR InterPro; IPR002219; DAG PE-bind.
DR InterPro; IPR001331; GDS_CDC24.
DR InterPro; IPR001849; PH_
DR InterPro; IPR000219; RhoGEF.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR003096; SM22_calponin.
DR Pfam; PF00307; CH; 1.
DR Pfam; PF00130; DAG PE-bind; 1.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00621; RhoGEF; 1.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 2.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR PRINTS; PR00888; SM22CALPONIN.
DR ProDom; PD001527; CH_type; 1.
DR ProDom; PD000093; SH2; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00109; C1; 1.
DR SMART; SM00033; CH; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00325; RhoGEF; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 2.
DR PROSITE; PS00021; CH; 1.
DR PROSITE; PS00479; DAG PE BIND_DOM_1; 1.
DR PROSITE; PS00081; DAG PE BIND_DOM_2; 1.
DR PROSITE; PS00010; DH_2; 1.
DR PROSITE; PS00741; DH_1; 1.
DR PROSITE; PS00003; PH_DOMAIN; 1.
DR PROSITE; PS00001; SH2; 1.
DR PROSITE; PS00002; SH3; 2.
KW Proto-oncogene; Phorbol-ester binding; Zinc; SH2 domain; SH3 domain;
KW Guanine-nucleotide releasing factor; Repeat; Phosphorylation;
KW 3D-structure.
FT DOMAIN 1 119
FT DOMAIN 194 373
FT DOMAIN 402 504
FT DOMAIN 516 564
FT DOMAIN 617 660
FT DOMAIN 671 765
FT DOMAIN 782 842
FT CONFLICT 29
SQ SEQUENCE 845 AA; 98136 MW; 3666DCCD1C5229DA CRC64;
Query Match 13.5%; Score 91.5; DB 1; Length 845;
Best Local Similarity 32.9%; Pred. No. 0.28;
Matches 23; Conservative 14; Mismatches 20; Indels 13; Gaps 3;
```



RT oncogene activates its transforming potential.";  
 RL Mol. Cell. Biol. 11:1912-1920(1991).  
 RN [4].  
 RP SEQUENCE OF 299-837 FROM N.A.  
 RA Romero F., Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.  
 RL [5].  
 RP SEQUENCE OF 299-334 FROM N.A.  
 RX MEDLINE=96038895; PubMed=7478592;  
 RA Ramos-Morales F., Romero F., Schweighoffer F., Bismuth G., Camonis J.,  
 RA Tortolero M., Fischer S.;  
 RL "The proline-rich region of Vav binds to Grb2 and Grb3-3.";  
 RT Oncogene 11:1665-1669(1995).  
 RN [6].  
 RP SIMILARITY TO CDC24 FAMILY.  
 RX AEDLINE=92228488; PubMed=1565462;  
 RA Adams J.M., Houston H., Allen J., Lints T., Harvey R.;  
 RT "The hematopoietically expressed vav proto-oncogene shares homology  
 with the db1 GDP-GTP exchange factor, the bcr gene and a yeast gene  
 (CDC24) involved in cytoskeletal organization.";  
 RT Oncogene 7:611-618(1992).  
 RL CC -i- FUNCTION: Couples tyrosine kinase signals with the activation of  
 the Rho/Rac GTPases, thus leading to cell differentiation and/or  
 proliferation.  
 CC -i- SUBUNIT: Interacts with SLA (By similarity). Interacts with Grb2  
 and Grb3.  
 CC -i- TISSUE SPECIFICITY: WIDELY EXPRESSED IN HEMATOPOIETIC CELLS BUT  
 NOT IN OTHER CELL TYPES.  
 CC -i- PM: Phosphorylated on tyrosine residues.  
 CC -i- MISCELLANEOUS: 'Vav' stands for the sixth letter of the Hebrew  
 alphabet.  
 CC -i- SIMILARITY: Contains 1 calponin-homology (CH) domain.  
 CC -i- SIMILARITY: Contains 1 DBL-homology (DH) domain.  
 CC -i- SIMILARITY: Contains 1 PH domain.  
 CC -i- SIMILARITY: Contains 1 zinc-dependent phosphol-ester and DAG  
 binding domain.  
 CC -i- SIMILARITY: Contains 1 SH2 domain.  
 CC -i- SIMILARITY: Contains 2 SH3 domains.  
 CC -i- CAUTION: Ref.2 sequence differs from that shown due to frameshifts  
 in position 322 and 355.  
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 CC  
 DR EMBL; AF030227; AAC25011.1; -;  
 DR EMBL; AF030201; AAC25011.1; JOINED.  
 DR EMBL; AF030202; AAC25011.1; JOINED.  
 DR EMBL; AF030203; AAC25011.1; JOINED.  
 DR EMBL; AF030204; AAC25011.1; JOINED.  
 DR EMBL; AF030205; AAC25011.1; JOINED.  
 DR EMBL; AF030206; AAC25011.1; JOINED.  
 DR EMBL; AF030207; AAC25011.1; JOINED.  
 DR EMBL; AF030208; AAC25011.1; JOINED.  
 DR EMBL; AF030209; AAC25011.1; JOINED.  
 DR EMBL; AF030210; AAC25011.1; JOINED.  
 DR EMBL; AF030211; AAC25011.1; JOINED.  
 DR EMBL; AF030212; AAC25011.1; JOINED.  
 DR EMBL; AF030213; AAC25011.1; JOINED.  
 DR EMBL; AF030214; AAC25011.1; JOINED.  
 DR EMBL; AF030215; AAC25011.1; JOINED.  
 DR EMBL; AF030216; AAC25011.1; JOINED.  
 DR EMBL; AF030217; AAC25011.1; JOINED.  
 DR EMBL; AF030218; AAC25011.1; JOINED.  
 DR EMBL; AF030219; AAC25011.1; JOINED.  
 DR EMBL; AF030220; AAC25011.1; JOINED.  
 DR EMBL; AF030221; AAC25011.1; JOINED.  
 DR EMBL; AF030222; AAC25011.1; JOINED.  
 DR EMBL; AF030223; AAC25011.1; JOINED.  
 DR EMBL; AF030224; AAC25011.1; JOINED.  
 DR EMBL; AF030225; AAC25011.1; JOINED.  
 DR EMBL; AF030226; AAC25011.1; JOINED.  
 DR EMBL; X16316; CAA34383.1; ALT\_FRAME.  
 DR EMBL; MS9834; AAA63267.1; -;  
 DR EMBL; X83931; CAA58783.1; -;  
 DR PIR; B39576; TVHUVV.  
 DR HSSP; P29354; IGRI.  
 DR TRANSFAC; T00880; -;  
 DR Genew; HGNC:12857; VAV1.  
 DR MIM; 164875; -;  
 DR GO; GO:0003700; F:transcription factor activity; TAS.  
 DR GO; GO:0007048; P:oncogenesis; TAS.  
 DR InterPro; IPR001715; Calponin-like.  
 DR InterPro; IPR003247; CH type.  
 DR InterPro; IPR002219; DAG\_PE-bind.  
 DR InterPro; IPR001331; GDS\_CDC24.  
 DR InterPro; IPR001849; PH.  
 DR InterPro; IPR002119; RhoGEF.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001452; SH3.  
 DR InterPro; IPR003096; SM22\_calponin.  
 DR Pfam; PF00307; CH; 1.  
 DR Pfam; PF00130; DAG\_PE-bind; 1.  
 DR Pfam; PF00169; PH; 1.  
 DR Pfam; PF00621; RhoGEF; 1.  
 DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00018; SH3; 2.  
 DR PRINTS; PR00401; SH2DOMAIN.  
 DR PRINTS; PR00452; SH3DOMAIN.  
 DR PRINTS; PR00888; SM22CALPONIN.  
 DR ProDom; PD001527; CH type; 1.  
 DR ProDom; PD00092; SH2; 1.  
 DR ProDom; PD00066; SH3; 1.  
 DR SMART; SM00109; C1; 1.  
 DR SMART; SM00033; CH; 1.  
 DR SMART; SM00325; RhoGEF; 1.  
 DR SMART; SM00233; PH; 1.  
 DR SMART; SM00252; SH2; 1.  
 DR SMART; SM00326; SH3; 2.  
 DR PROSITE; PS00021; CH; 1.  
 DR PROSITE; PS00479; DAG\_PE\_BIND\_DOM\_1; 1.  
 DR PROSITE; PS00081; DAG\_PE\_BIND\_DOM\_2; 1.  
 DR PROSITE; PS0010; DH 2; 1.  
 DR PROSITE; PS00741; DH 1; 1.  
 DR PROSITE; PS00003; PH\_DOMAIN; 1.  
 DR PROSITE; PS00001; SH2; 1.  
 DR PROSITE; PS00002; SH3; 2.  
 KW Proto-oncogene; Phorbol-ester binding; Zinc; SH2 domain; SH3 domain;  
 KW Guanine-nucleotide releasing factor; Repeat; Phosphorylation.  
 FT DOMAIN 1 119  
 FT DOMAIN 194 373  
 FT DOMAIN 402 504  
 FT DOMAIN 516 564  
 FT DOMAIN 617 660  
 FT DOMAIN 671 765  
 FT DOMAIN 782 842  
 FT DOMAIN 845 885  
 FT CONFLICT 264 264  
 FT CONFLICT 718 718  
 SQ SEQUENCE 845 AA; 98313 MW; AC3BC9736FD2F138 CRC64;  
 Query Match 13.2%; Score 89.5; DB 1; Length 845;  
 Best Local Similarity 32.9%; Pred. No. 0.44;  
 Matches 23; Conservative 14; Mismatches 13; Gaps 3;  
 QY 44 ARAQSDYNAPCRFDIVKKGQOYVYKLVTEGAGEFWAGSVYGDHDEMGIVGFFSN 103  
 Db 787 AKARYDFCARDSELSLKEGDI-----KILNKKGGQGGWRGRIYGR-----VGWFFAN 835  
 QY 104 LVKEQRTVQE 113  
 Db 836 YVEED--YSE 843

[illegible]





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DR InterPro; IPR002219; DAG PE-bind.
DR InterPro; IPR001331; GDS_CDC24.
DR InterPro; IPR001849; PH.
DR InterPro; IPR000219; RhogEF.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00307; CH; 1.
DR Pfam; PF00130; DAG PE-bind; 1.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00621; RhogEF; 1.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 2.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR ProDom; PD001527; CH type; 1.
DR ProDom; PD000093; SH2; 1.
DR ProDom; PD000066; SH3; 2.
DR SMART; SM00109; Cl; 1.
DR SMART; SM00033; CH; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00325; RhogEF; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 2.
DR PROSITE; PS00021; CH; 1.
DR PROSITE; PS00479; DAG PE BIND_DOM_1; 1.
DR PROSITE; PS00081; DAG PE BIND_DOM_2; 1.
DR PROSITE; PS00010; DH; 2; 1.
DR PROSITE; PS00741; DH; 1; 1.
DR PROSITE; PS00003; PH DOMAIN; 1.
DR PROSITE; PS00001; SH2; 1.
DR PROSITE; PS00002; SH3; 2.
KW Phorbol-ester binding; Zinc; SH2 domain; SH3 domain;
KW Guanine-nucleotide releasing CH.
FT DOMAIN 1 119
FT DOMAIN 198 376
FT DOMAIN 405 512
FT DOMAIN 524 572
FT DOMAIN 586 652
FT DOMAIN 673 767
FT DOMAIN 816 877
FT MOD RES 142 142
FT MOD RES 159 159
FT MOD RES 172 172
SQ SEQUENCE 878 AA; 101256 MW; C8FF7681032146B4 CRC64;
Query Match 12.5%; Score 84.5; DB 1; Length 878;
Best Local Similarity 27.6%; Pred. No. 1.4;
Matches 21; Conservative 20; Mismatches 22; Indels 13; Gaps 3;
QY 38 VYT---ISLARAQEDYNAPDCRFIDVKKGQIYVYKLVTEAGAGFEWAGSVYGDHQDEM 94
Db 812 VFTPRVIGTAVARYNFAARDMRELRLREGDVVRYISRGDQG---WKKG-----ETN 861
QY 95 GIVGYFSPNLVKEQRV 110
Db 862 GRIGWFPSTYVEEGI 877

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Search completed: December 29, 2003, 16:04:13  
 Job time : 6.01961 secs



Db 28 HG---RPFSLKVCDECSMLVYRGKALEFTGDCRFVNFKGGDDVYVYKLA--GGS 82  
 QY 79 GEFWAGSVYGDHDEMGIYGVFNSLVKEQVYQATKEIPTTDDIDFFC 127  
 Db 83 LELWAGSV--EHS-----FGYFPKDLIKVLKHYTEELHHPADETDFVC 124

RESULT 4

Q8C899 PRELIMINARY; PRT; 68 AA.  
 AC Q8C899;  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Otoraplin.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Head;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs."  
 RL Nature 420:563-573(2002).  
 DR EMBL; AK047965; BAC33202.1;  
 SQ SEQUENCE 68 AA; 7431 MW; 3CBE75527D3CBF7F CRC64;

Query Match 29.0%; Score 196; DB 11; Length 68;  
 Best Local Similarity 64.6%; Pred. No. 3.1e-13;  
 Matches 42; Conservative

QY 1 MARILLLLGGLVLCAGHGVFMDKLSKKLCADECV-----YTISLARAQSDYNA 52  
 Db 1 MARILLLLGGLVLCAGHGVFMDKLSKKLCADECVCKKLLTVNFSLSFYHMGNLISG 60  
 QY 53 --PDC 55  
 Db 61 KQPDG 65

RESULT 5

Q921X3 PRELIMINARY; PRT; 137 AA.  
 AC Q921X3;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Similar to cartilage derived retinoic acid sensitive protein.  
 GN CDRA.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAUSBERG R.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC009815; AA009815.1;  
 DR MGI; MGI:109615; Cdrap.  
 DR InterPro; IPR001452; SH3.  
 DR Pfam; PF00018; SH3; 1.  
 DR SMART; SM00326; SH3; 1.  
 SQ SEQUENCE 137 AA; 15441 MW; 971415552E6FD536 CRC64;

Query Match 27.7%; Score 187.5; DB 11; Length 137;  
 Best Local Similarity 50.6%; Pred. No. 5.7e-22;  
 Matches 43; Conservative 11; Mismatches 22; Indels 9; Gaps 3;

QY 85 SVYGDHDEMGI--VGYFNSLVKEQVYQATKEIPT 120  
 Db 58 SVQGDYDGLAARLGVFSSIVREDQTLKPGKVDYKT 94

RESULT 2

Q8BJE9 PRELIMINARY; PRT; 268 AA.  
 AC Q8BJE9;  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Weakly similar to NP1P-like protein (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Eye;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs."  
 RL Nature 420:563-573(2002).  
 DR EMBL; AK084344; BAC39164.1;  
 FT NON\_TER 268  
 SQ SEQUENCE 268 AA; 29722 MW; 67339C562F684402 CRC64;

Query Match 32.2%; Score 218; DB 11; Length 268;  
 Best Local Similarity 42.2%; Pred. No. 7.6e-15;  
 Matches 46; Conservative 13; Mismatches 38; Indels 12; Gaps 4;

QY 19 HGVFMDKLSKKLCADECVYTISLARAQSDYNAQDRCFIDVKKGQIYVYSLKLVTENGA 78  
 Db 28 HG---RPFSLKVCDECSMLVYRGKALEFTGDCRFVNFKGGDDVYVYKLA--GGS 82  
 QY 79 GEFWAGSVYGDHDEMGIYGVFNSLVKEQVYQATKEIPTTDDIDFFC 127  
 Db 83 LELWAGSV--EHS-----FGYFPKDLIKVLKHYTEELHHPADETDFVC 124

RESULT 3

Q8BI84 PRELIMINARY; PRT; 1239 AA.  
 AC Q8BI84;  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Weakly similar to NP1P-like protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Retina;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs."  
 RL Nature 420:563-573(2002).  
 DR EMBL; AK044749; BAC32064.1;  
 SQ SEQUENCE 1239 AA; 136350 MW; 6E16F9D42ECCFF05 CRC64;

Query Match 32.2%; Score 218; DB 11; Length 1239;  
 Best Local Similarity 42.2%; Pred. No. 4.8e-14;  
 Matches 46; Conservative 13; Mismatches 38; Indels 12; Gaps 4;

QY 19 HGVFMDKLSKKLCADECVYTISLARAQSDYNAQDRCFIDVKKGQIYVYSLKLVTENGA 78

QY 8 LLLGLVLCAGHV-----FMDKLSKKLCADBEVCVYTTISLARAQEDYNAPDCRFIDVKK 62  
Db 6 VLLGIVLVSVFSGPSRADRAMPKADKLCADBECSHPISMAVALQDYVAPDCRFITYYR 65  
QY 63 GQOIYVYKLVTEGAGE-FWAGSV 86  
Db 66 GQVYVFSKL----KGRGLFWGGSV 87  
RESULT 6  
Q90XFI PRELIMINARY; PRT; 88 AA.  
ID Q90XFI  
AC Q90XFI  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Melanoma inhibitory activity protein (Fragment).  
OS Tetraodon nigroviridis (Green puffer).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Telostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
OC Tetraodontidae; Tetraodontidae; Tetraodon.  
OX NCBI\_TaxID=99883;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Bosserhoff A.K., Buettner R.;  
RT "Characterization of the MIA gene family.";  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF390176; AAL26991.1; -;  
DR InterPro; IPR001452; SH3.  
DR Pfam; PF00018; SH3; 1  
DR SMART; SM00326; SH3; 1  
DR NON TER 1  
FT SEQUENCE 88 AA; 10080 MW; C355C1FE04DA22EA CRC64;  
Query Match 26.6%; Score 179.5; DB 13; Length 88;  
Best Local Similarity 42.4%; Pred. No. 2.3e-11;  
Matches 39; Conservative 17; Mismatches 25; Indels 11; Gaps 4;  
QY 41 ISLARAQEDYNAPDCRFIDVKKGQOIYVYKLVTEGAG-EFWAGSV-----YGDHQDEMG 95  
Db 3 IMIARALQDYVPADCKFPPIRQGLIYVYAML---KGRGQFWAGSVQDSYVGQOEAR--- 57  
QY 96 IVGYPFSLVKEQRYQVQATKEIPTDDIDFFC 127  
Db 58 -IGHFPFSIVEETHPLMAAQTEVTSNMDFYC 88  
RESULT 7  
Q96PCS PRELIMINARY; PRT; 119 AA.  
ID Q96PCS  
AC Q96PCS  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Melanoma inhibitory activity protein 2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Bosserhoff A.K., Buettner R.;  
RT "Characterization of the MIA gene family.";  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF390175; AAL26990.1; -;  
DR InterPro; IPR001452; SH3.  
DR SMART; SM00326; SH3; 1  
SQ SEQUENCE 119 AA; 13535 MW; AEF29762D880AC5 CRC64;  
Query Match 24.4%; Score 165; DB 4; Length 119;  
Best Local Similarity 33.6%; Pred. No. 1.1e-09;

Matches 43; Conservative 16; Mismatches 45; Indels 24; Gaps 4;  
QY 6 ILLGLVLCAGHVFMKLSKKL-----CADBEVCVYTTISLARAQEDYNAPDCRFID 59  
Db 9 ILLLAISLTKC-----LESTKLADLKCGDLECEALINRVSAMRDYRGDPDCRYLN 59  
QY 60 VKRQGOIYVYKLVTEGAGEFWAGSVYGDHQDEMGIVGPPSNLVKEQRYQVQATKEIP 119  
Db 60 FTGGEISVYVVKLAGER--EDLWAGSKGK-----FGYFPRDAVQIEEVFISEIQMS 110  
QY 120 TTDIDFFC 127  
Db 111 TKESDFLC 118  
RESULT 8  
Q91ZV0 PRELIMINARY; PRT; 119 AA.  
ID Q91ZV0  
AC Q91ZV0  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Melanoma inhibitory activity protein 2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA TISSUE=Embryo;  
RT "Characterization of the MIA gene family.";  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF390177; AAL26992.1; -;  
DR InterPro; IPR001452; SH3.  
DR SMART; SM00326; SH3; 1  
SQ SEQUENCE 119 AA; 13397 MW; 589F390C0B49D1C7 CRC64;  
Query Match 23.1%; Score 156; DB 11; Length 119;  
Best Local Similarity 33.6%; Pred. No. 1e-08;  
Matches 42; Conservative 20; Mismatches 49; Indels 14; Gaps 5;  
QY 3 RILILLGLVLCAGHVFMKLSKKLCADBEVCVYTTISLARAQEDYNAPDCRFIDVKK 62  
Db 8 RILLVVS--LAKCL-EGTKL--LAHLKKCGDLECEALISRVIALRDYTGDPDCRYLNFT 62  
QY 63 GQOIYVYKLVTEGAGEFWAGSVYGDHQDEMGIVGPPSNLVKEQRYQVQATKEIPTD 122  
Db 63 GGEISVYVVKLGDDR--EDLWAGSKGD-----FGYFPRDAVQIEEVFISEIQMS 113  
QY 123 IDFFC 127  
Db 114 SDFLC 118  
RESULT 9  
O08526 PRELIMINARY; PRT; 166 AA.  
ID O08526  
AC O08526  
DT 01-JUL-1997 (TrEMBLrel. 04, Created)  
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Vav-T.  
GN VAV.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN=ddy; TISSUE=Testis;  
RX MEDLINE=97190224; PubMed=9038379;  
RA Okumura K., Kaneko Y., Nonogushi K., Nishiyama H., Yokoi H.,



Tue Dec 30 10:20:39 2003

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Db      797 YVEED--YSE 804

RESULT 12
QBTV7      PRELIMINARY;      PRT;      845 AA.
ID QBTV7
AC Q8BTW7;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE VAV proto-oncogene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK088586; BAC40436.1; -. 5D0DE0D93111DFB8B CRC64;
SQ SEQUENCE 845 AA; 98093 MW; 5D0DE0D93111DFB8B CRC64;

Query Match      13.5%; Score 91.5; DB 11; Length 845;
Best Local Similarity 32.9%; Pred. No. 0.7;
Matches 23; Conservative 14; Mismatches 20; Indels 13; Gaps 3;

QY      44 ARAQEDYNAPDPCRFIDVKKGQIYVYKLVTEGAGFEWAGSVYGDHDEMGIYGVYPSN 103
Db      787 AKARYDFPCARDSELSLKEGDII----KILNKKGGQGWGRGIYGR-----IGWFPSPN 835
QY      104 LVKEQRYQVE 113
Db      836 YVEED--YSE 843

RESULT 13
QBUX6      PRELIMINARY;      PRT;      846 AA.
ID QBUX6
AC Q8UUX6;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE GDP/GTP exchange factor VAV3.
GN VAV3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=11805146;
RA Inabe K., Ishiai M., Scharenberg A.M., Freshney N., Downward J.,
RA Kurosaki T.;
RT "Vav3 Modulates B Cell Receptor Responses by Regulating
RT Phosphoinositide 3-Kinase Activation.";
RL J. Exp. Med. 195:189-200 (2002).
CC -!- SIMILARITY: CONTAINS 2 SH3 DOMAINS.
CC -!- SIMILARITY: CONTAINS 1 PH DOMAIN.
DR EMBL; AV046915; AAL06249.1; -.
DR InterPro; IPR001715; Calponin-like.
DR InterPro; IPR003247; CH_type.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR001331; GDS CDC24.
DR InterPro; IPR001849; PH.
DR InterPro; IPR000219; RhoGEF.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.

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DR      InterPro; IPR003096; SM22_calponin.
DR      Pfam; PF00307; CH; 1.
DR      Pfam; PF00130; DAG_PE-bind; 1.
DR      Pfam; PF00169; PH; 1.
DR      Pfam; PF00621; RhoGEF; 1.
DR      Pfam; PF00017; SH2; 1.
DR      Pfam; PF00018; SH3; 1.
DR      PRINTS; PR00401; SH2DOMAIN.
DR      PRINTS; PR00452; SH3DOMAIN.
DR      PRINTS; PR00888; SM22CALPONIN.
DR      ProDom; PD001527; CH_type; 1.
DR      ProDom; PD000093; SH2; 1.
DR      ProDom; PD000066; SH3; 1.
DR      SMART; SM00109; C1; 1.
DR      SMART; SM00033; CH; 1.
DR      SMART; SM00233; PH; 1.
DR      SMART; SM00325; RhoGEF; 1.
DR      SMART; SM00252; SH2; 1.
DR      SMART; SM00326; SH3; 2.
DR      PROSITE; PS00021; CH; 1.
DR      PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR      PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.
DR      PROSITE; PS00741; DH_1; 1.
DR      PROSITE; PS00010; DH_2; 1.
DR      PROSITE; PS00003; PH_DOMAIN; 1.
DR      PROSITE; PS00001; SH2; 1.
DR      PROSITE; PS00002; SH3; 2.
KW      SH3 domain.
SQ      SEQUENCE 846 AA; 97815 MW; C47EE949D873821B CRC64;

Query Match      13.5%; Score 91.5; DB 13; Length 846;
Best Local Similarity 34.3%; Pred. No. 0.7;
Matches 23; Conservative 12; Mismatches 21; Indels 11; Gaps 2;

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ID Q9VWA8
AC Q9VWA8;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE CG11098 protein.
GN CG11635 OR CG13768 OR CG13769.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

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RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Gosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Holstad D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarly C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RA "The genome sequence of *Drosophila melanogaster*.";  
RA Science 287:2185-2195(2000).  
RL  
RN  
RP SEQUENCE FROM N.A.  
RA Celniker S.E., Adams M.D., Krontz B., Wan K.H., Holt R.A.,  
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,  
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,  
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,  
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,  
RA Ferrera S., Frise E., Galle R.F., Garg N.S., George R.A.,  
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,  
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,  
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,  
RA Pacleb J., Parasag V., Park S., Patel S., Pfeiffer B., Scheeler F.,  
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,  
RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,  
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;  
RA "Sequencing of *Drosophila melanogaster* genome.";  
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN  
RP SEQUENCE FROM N.A.  
RA Mixa S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,  
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,  
RA Tupy J.L., Bergman C., Beran B., Carlson J.W., Celniker S.E.,  
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,  
RA Krontz B., Marshall B., Millburn G., Richter J., Russo S.,  
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,  
RA Ashburner M., Gelbart W.M., Rubin G.M., Murgall C.J., Lewis S.E.;  
RA "Annotation of *Drosophila melanogaster* genome.";  
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RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN  
RP SEQUENCE FROM N.A.  
RA FlyBase;  
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AE003614; AAF52413.2;  
DR FlyBase; FBgn0051635; CG31635.  
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Query Match 13.38; Score 90; DB 5; Length 1257;  
Best Local Similarity 25.68; Preq. No. 1.6;  
Matches 30; Conservative 19; Mismatches 56; Indels 12; Gaps 3;  
6 ILLIGLVLVLCAGHGVFMDLSSKKLCADECVYTISLARAQEDYNAPDCRFIDVKKGQ 65  
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DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE CG11098 protein.  
GN CG11098  
OS *Drosophila melanogaster* (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
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RC STRAIN=Berkeley;  
RX MEDLINE=20196006; PubMed=10731132;  
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RA Merkulov G., Milshina N.V., Mobarly C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
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RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
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RN SEQUENCE FROM N.A.  
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RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,  
RA Tupy J.L., Bergman C., Beran B., Carlson J.W., Celniker S.E.,  
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,  
RA Krontz B., Marshall B., Millburn G., Richter J., Russo S.,  
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,  
RA Ashburner M., Gelbart W.M., Rubin G.M., Murgall C.J., Lewis S.E.;  
RA "Annotation of *Drosophila melanogaster* genome.";  
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
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RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;  
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RP SEQUENCE FROM N.A.  
RA FlyBase;  
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AE003614; AAF52413.2;  
DR FlyBase; FBgn0051635; CG31635.  
SQ SEQUENCE 1257 AA; 139136 MW; 5843F0540EEA9511 CRC64;  
Query Match 13.38; Score 90; DB 5; Length 1257;  
Best Local Similarity 25.68; Preq. No. 1.6;  
Matches 30; Conservative 19; Mismatches 56; Indels 12; Gaps 3;  
6 ILLIGLVLVLCAGHGVFMDLSSKKLCADECVYTISLARAQEDYNAPDCRFIDVKKGQ 65  
17 LALVIGLLICLPLTTLTAATLSDKRLCAKPCQEIISMGIAKITAYTGGGLISFKINS 76





GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2003, 16:03:18 ; Search time 25.098 Seconds  
(without alignments)  
809.506 Million cell updates/sec

Title: US-10-019-455A-12  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	676	100.0	128	22	Mouse MLP protein
2	655	96.9	128	22	Rat MLP protein se
3	602	89.1	128	22	Human growth regul
4	602	89.1	128	22	Human MLP protein
5	602	89.1	128	23	Human angiogenesis
6	602	89.1	128	23	Human PRO9873 prot
7	602	89.1	128	23	Human PRO protein,
8	602	89.1	128	23	Novel human secret
9	591	87.4	110	22	Mouse MLP protein

10	574	84.9	110	22	AAB69131	Rat MLP protein se
11	547	80.9	110	22	AAB69126	Human MLP protein
12	519	76.8	105	22	AAB82672	Human growth regul
13	449	66.4	87	22	AAB69129	Rat MLP protein se
14	277.5	41.1	131	16	AAR69811	Melanoma inhibitor
15	277.5	41.1	131	22	AAG65614	Human MIA protein
16	275.5	40.8	137	22	AAG65615	Recombinant human
17	247	36.5	130	16	AAB69812	Melanoma inhibitor
18	218	32.2	125	23	ABB82119	Mouse TANGO 130 MI
19	218	32.2	303	22	AAU29304	Human PRO polypept
20	218	32.2	303	22	AAB87608	Human PRO19670. H
21	218	32.2	303	23	ABG93933	Human secreted/tra
22	218	32.2	303	23	ABG95600	Human angiogenesis
23	218	32.2	303	23	ABB84994	Human PRO19670 pro
24	218	32.2	303	24	ABU71392	Human secreted pol
25	218	32.2	303	24	ABU71588	Human secreted/tra
26	218	32.2	303	24	ABU72034	Novel human secret
27	218	32.2	303	24	ABU72191	Human PRO polypept
28	218	32.2	303	24	ABU65849	Human secreted/tra
29	218	32.2	303	24	ABU66182	Novel human secret
30	218	32.2	303	24	ABU67686	Human secreted/tra
31	218	32.2	303	24	ABU65544	Human PRO polypept
32	218	32.2	303	24	ABU58680	Human secreted/tra
33	218	32.2	303	24	ABU56216	Human PRO polypept
34	218	32.2	303	24	ABU57211	Human secreted/tra
35	218	32.2	303	24	ABU10790	Human secreted/tra
36	218	32.2	714	23	ABY70209	Murine TANGO 130 p
37	218	32.2	714	23	ABB82117	Mouse TANGO 130 po
38	209.5	31.0	138	22	AM25834	Human protein sequ
39	208.5	30.8	125	23	ABB82120	Human TANGO 130 MI
40	208.5	30.8	410	21	AA70210	Human TANGO 130 pr
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43	200	29.6	499	22	AAU29319	Human PRO polypept
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ALIGNMENTS

RESULT 1

AAB69125  
ID AAB69125 standard; Protein; 128 AA.

XX AAB69125;

AC AAB69125;

DT 23-APR-2001 (first entry)

DE Mouse MLP protein sequence SEQ ID NO:12.

KW MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
cardiant; gene therapy; secretory cell function regulator; promoter;  
inhibitor.

OS Mus musculus.

XX WO200102564-A1.

XX 11-JAN-2001.

XX 29-JUN-2000; 2000WO-JP04278.

XX 30-JUN-1999; 99JP-0186718.

XX (TAKE ) TAKEDA CHEM IND LTD.

PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
Tanaka H;

DR WPI; 2001-159271/16.

DR N-PSDB; AAF59068.



disorders -

Claim 10; Page 116-117; 119pp; English.

The present sequence is that of a novel human growth regulatory-like polypeptide (GRLP). The amino acid sequence is predicted from a novel assembled cDNA (see AAH26343) based on Hyseq clone number 16372272. The protein has a mol.wt. of 14 kDa unglycosylated. GRLP belongs to the same protein family as growth regulatory proteins, growth factors, human melanoma derived growth regulatory protein precursor (64% similarity and 45% identity over 111 amino acids) or melanoma inhibitory activity, cattle cartilage-derived retinoic acid sensitive protein (CD-RAP, 44% identity and 64% similarity over 126 amino acids) and other retinoic acid-sensitive proteins. GRLP polypeptides and polynucleotides of the invention can be used in the prophylaxis, treatment (including gene therapy) and diagnosis of disorders and diseases caused by, or involving, cartilage development and maintenance, inhibition of melanoma cell growth and tumours, including neuroectodermal tumours such as gliomas. The polypeptides, which include the GRLP mature protein, may also have nutritional uses, cytokine and cell proliferation or differentiation activity, stem cell growth factor activity, haematopoiesis regulating activity, tissue growth activity, immunosuppressive or immunostimulant activity, activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, use in cancer diagnosis and therapy, drug screening, receptor/ligand activity, antiinflammatory activity, and treatment of leukaemia, nervous system disorders, arthritis and inflammation.

Sequence 128 AA;

Query Match 89.1%; Score 602; DB 22; Length 128;  
Best Local Similarity 86.7%; Pred. No. 2.1e-65;  
Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

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Db 1 MARILLLLGLVLCAGHGVFMDKLSKKLCADECVYTISLARAQEDYNAPDPRFIDV 60

QY 61 KKGQIYVYVKLVTEGAGFAGSVYGDHDEMGIVGYFPSNLVKQRVYQEAATKEIPT 120  
Db 61 KKGQIYVYVKLVTEGAGFAGSVYGDHDEMGIVGYFPSNLVKQRVYQEAATKEIPT 120

QY 121 TDIDFFCE 128  
Db 121 TDIDFFCE 128

RESULT 4  
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XX AC AAB69123;  
XX DT 23-APR-2001 (first entry)  
XX DE Human MLP protein sequence SEQ ID NO:6.  
XX KW MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
XX KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
XX KW cardiant; gene therapy; secretory cell function regulator; promoter;  
XX KW inhibitor.  
XX OS Homo sapiens.  
XX PN WO200102564-A1.  
XX PD 11-JAN-2001.  
XX PF 29-JUN-2000; 2000WO-JP04278.  
XX PR 30-JUN-1999; 95JP-0186718.

(TAKE ) TAKEDA CHEM IND LTD.

PA Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
PI Tanaka H;  
DR WPI; 2001-159271/16.  
DR N-PSDB; AAF59065.  
XX Safe, low-toxicity secretory cell function-regulatory protein and  
PT encoded DNA, applicable as drugs, in diagnosis and development of  
PT promoters and inhibitors for preventing or treating e.g. bone and joint  
PT diseases -  
XX Claim 2; Page 91-92; 111pp; Japanese.  
XX The present invention describes novel MLP proteins and their encoding  
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
CC activities, and can be used in gene therapy and as secretory cell  
CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
CC the diagnosis and development of promoters and inhibitors for preventing  
CC or treating bone and joint diseases as well as pathologic angiogenesis.  
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
CC in the exemplification of the present invention.  
XX SQ Sequence 128 AA;  
Query Match 89.1%; Score 602; DB 22; Length 128;  
Best Local Similarity 86.7%; Pred. No. 2.1e-65;  
Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 MARILLLLGLVLCAGHGVFMDKLSKKLCADECVYTISLARAQEDYNAPDPRFIDV 60  
Db 1 MARILLLLGLVLCAGHGVFMDKLSKKLCADECVYTISLARAQEDYNAPDPRFIDV 60

QY 61 KKGQIYVYVKLVTEGAGFAGSVYGDHDEMGIVGYFPSNLVKQRVYQEAATKEIPT 120  
Db 61 KKGQIYVYVKLVTEGAGFAGSVYGDHDEMGIVGYFPSNLVKQRVYQEAATKEIPT 120

QY 121 TDIDFFCE 128  
Db 121 TDIDFFCE 128

RESULT 5  
ABB95602  
ID ABB95602 standard; Protein; 128 AA.  
XX AC ABB95602;  
XX DT 19-JUL-2002 (first entry)  
XX DE Human angiogenesis related protein PRO9873 SEQ ID NO: 360.  
XX KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
XX KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
XX KW cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;  
XX KW antiarteriosclerotic.  
XX OS Homo sapiens.  
XX PN WO200208284-A2.  
XX PD 31-JAN-2002.  
XX PF 09-JUL-2001; 2001WO-US21735.  
XX PR 20-JUL-2000; 2000US-219556P.  
XX PR 25-JUL-2000; 2000US-220624P.  
XX PR 25-JUL-2000; 2000US-220664P.  
XX PR 28-JUL-2000; 2000WO-US20710.  
XX PR 02-AUG-2000; 2000US-222695P.  
XX PR 17-AUG-2000; 2000US-0643657.



PR	25-MAY-2001; 2001US-0866028.	FN	WO200208298-A2.
PR	25-MAY-2001; 2001US-0866034.	XX	
PR	25-MAY-2001; 2001US-0866034.	PD	
PR	25-MAY-2001; 2001US-0866034.	XX	31-JAN-2002.
PR	25-MAY-2001; 2001US-0866034.	PF	
PR	25-MAY-2001; 2001US-0866034.	XX	29-JUN-2001; 2001WO-US21066.
PR	25-MAY-2001; 2001US-0866034.	XX	
PR	25-MAY-2001; 2001US-0866034.	PR	20-JUL-2000; 2000US-219556P.
PR	25-MAY-2001; 2001US-0866034.	PR	25-JUL-2000; 2000US-220585P.
PR	25-MAY-2001; 2001US-0866034.	PR	25-JUL-2000; 2000US-220605P.
PR	25-MAY-2001; 2001US-0866034.	PR	25-JUL-2000; 2000US-220607P.
PR	25-MAY-2001; 2001US-0866034.	PR	25-JUL-2000; 2000US-220624P.
PR	25-MAY-2001; 2001US-0866034.	PR	25-JUL-2000; 2000US-220638P.
PR	25-MAY-2001; 2001US-0866034.	PR	25-JUL-2000; 2000US-220664P.
PR	25-MAY-2001; 2001US-0866034.	PR	25-JUL-2000; 2000US-220666P.
PR	25-MAY-2001; 2001US-0866034.	PR	26-JUL-2000; 2000US-220893P.
PR	25-MAY-2001; 2001US-0866034.	PR	28-JUL-2000; 2000WO-US20710.
PR	25-MAY-2001; 2001US-0866034.	PR	23-AUG-2000; 2000WO-US23522.
PR	25-MAY-2001; 2001US-0866034.	PR	24-AUG-2000; 2000WO-US23328.
PR	25-MAY-2001; 2001US-0866034.	PR	15-SEP-2000; 2000US-000000P.
PR	25-MAY-2001; 2001US-0866034.	PR	10-NOV-2000; 2000WO-US30873.
PR	25-MAY-2001; 2001US-0866034.	PR	28-NOV-2000; 2000US-253646P.
PR	25-MAY-2001; 2001US-0866034.	PR	01-DEC-2000; 2000WO-US32678.
PR	25-MAY-2001; 2001US-0866034.	PR	20-DEC-2000; 2000US-0747259.
PR	25-MAY-2001; 2001US-0866034.	PR	20-DEC-2000; 2000WO-US34956.
PR	25-MAY-2001; 2001US-0866034.	PR	28-FEB-2001; 2001WO-US06520.
PR	25-MAY-2001; 2001US-0866034.	PR	10-MAY-2001; 2001US-0854280.
PR	25-MAY-2001; 2001US-0866034.	PR	25-MAY-2001; 2001WO-US17092.
XX		XX	(GETH ) GENENTECH INC.
XX		PA	Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
XX		PI	Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX		PI	N-PSDB; ABK33571.
XX		XX	WPI; 2002-172001/22.
XX		XX	One hundred and twenty two nucleic acids encoding PRO polypeptides,
XX		XX	useful for treating a PRO related disorder and for diagnosing tumours
XX		XX	such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
XX		XX	tumour or liver tumour -
XX		XX	Claim 11; Figure 72; 359pp; English.
XX		XX	The invention relates to one hundred and twenty two nucleic acids
XX		XX	encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
XX		XX	encode human secreted proteins. The PRO nucleic acids, polypeptides,
XX		XX	agonists and antagonists are useful for treating a PRO related disorder.
XX		XX	The PRO polypeptides are useful for diagnosing tumours, especially lung
XX		XX	cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
XX		XX	liver tumour. The PRO polypeptides are useful for stimulating the
XX		XX	proliferation of, or gene expression in, pericyte cells, for stimulating
XX		XX	the proliferation or differentiation of chondrocyte cells, for
XX		XX	stimulating the release of tumour necrosis factor-alpha from human blood,
XX		XX	for stimulating or inhibiting the proliferation of normal human dermal
XX		XX	fibroblast cells. The PRO polypeptide may also be used as molecular
XX		XX	weight markers and for tissue typing. The PRO nucleic acids have
XX		XX	applications in molecular biology, including use as hybridisation probes,
XX		XX	and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
XX		XX	protein sequences of the invention.
XX		XX	Sequence 128 AA;
XX		XX	Query Match 89.1%; Score 602; DB 23; Length 128;
XX		XX	Best Local Similarity 86.7%; Pred. No. 2.le-65;
XX		XX	Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;
QY	1 MARILLILGLVLCAGHGVFMDKLSSKKLCADCECVYTISLASAQEDYNAPDCRFDV 60	QY	1 MARILLILGLVLCAGHGVFMDKLSSKKLCADCECVYTISLASAQEDYNAPDCRFDV 60
DB	1 MARILLILFLPGLVAVCAVHGIFMDRLASKKLCADCECVYTISLASAQEDYNAPDCRFINV 60	DB	1 MARILLILFLPGLVAVCAVHGIFMDRLASKKLCADCECVYTISLASAQEDYNAPDCRFINV 60
QY	61 KKGQIYVYVSKLVTENGAGFAGSVYGDHDEMGIVGYFPSPNIVKQRYVQATKEIPT 120	QY	61 KKGQIYVYVSKLVTENGAGFAGSVYGDHDEMGIVGYFPSPNIVKQRYVQATKEIPT 120
DB	61 KKGQIYVYVSKLVKENGAGFAGSVYGDGQDGVVGYFPRLIVKQRYVQATKEVPT 120	DB	61 KKGQIYVYVSKLVKENGAGFAGSVYGDGQDGVVGYFPRLIVKQRYVQATKEVPT 120
QY	121 TDIDFFCE 128	QY	121 TDIDFFCE 128
DB	121 TDIDFFCE 128	DB	121 TDIDFFCE 128
RESULT 7		XX	
AAU83627		XX	
ID	AAU83627 standard; Protein; 128 AA.	XX	
AC	AAU83627;	XX	
XX		XX	
DT	08-MAY-2002 (first entry)	XX	
XX		XX	
DE	Human PRO protein, Seq ID No 72.	XX	
XX		XX	
KW	Human; secreted protein; PRO; tumour; lung cancer; colon cancer;	XX	
KW	breast cancer; prostate tumour; rectal tumour; liver tumour;	XX	
KW	pericyte cell proliferation; chondrocyte cell proliferation;	XX	
KW	tumour necrosis factor-alpha.	XX	
XX		XX	
OS	Homo sapiens.	XX	
XX		XX	

1 MRRILLIGGLVVLGAGHGVFMDKSSKXLCADBECVYTISLARQEDVNAPDRFIDV 60



```

RESULT 10
AAB69131
ID AAB69131 standard; Protein; 110 AA.
XX
AC AAB69131;
XX
DT 23-APR-2001 (first entry)
XX
DE Rat MLP protein sequence SEQ ID NO:49.
XX
KW MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
KW cardiant; gene therapy; secretory cell function regulator; promoter;
KW inhibitor.
XX
OS Rattus sp.
XX
PN WO200102564-A1.
XX
PD 11-JAN-2001.
XX
PF 29-JUN-2000; 2000WO-JP04278.
XX
PR 30-JUN-1999; 99JP-0186718.
XX
PA (TAKE ) TAKEDA CHEM IND LTD.
XX
PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
PI Tanaka H;
XX
DR N-PSDB; AAF59099.
XX
CC Safe, low-toxicity secretory cell function-regulatory protein and
CC encoded DNA, applicable as drugs, in diagnosis and development of
CC promoters and inhibitors for preventing or treating e.g. bone and joint
CC diseases -
XX
PS Claim 5; Page 107; 111pp; Japanese.
XX
CC The present invention describes novel MLP proteins and their encoding
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
CC activities, and can be used in gene therapy and as secretory cell
CC function regulators. The MLP proteins and DNAs can be used in drugs, in
CC the diagnosis and development of promoters and inhibitors for preventing
CC or treating bone and joint diseases as well as pathologic angiogenesis.
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
CC in the exemplification of the present invention.
XX
SQ Sequence 110 AA;
Query Match 84.9%; Score 574; DB 22; Length 110;
Best Local Similarity 96.4%; Pred. No. 4.5e-62;
Matches 106; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Qy 19 HGVFMDKLSKKLCADDECVYTTISLARAQEDYNAPDCRFIDVKKGQOIYVYSKLVTEGA 78
Db 1 HGMFMDKLSKKLCADDECVYTTISLARAQEDYNAPDCRFIDVKKGQOIYVYSKLVTEGA 60
Qy 79 GEFWAGSVYGDHDEMGIYGVFPNSLVKEQRYQVQATKEIPTTIDPFCE 128
Db 61 GAFWAGSVYGDHDEMGIYGVFPNSLVKEQRYQVQATKEIPTTIDPFCE 110
RESULT 11
AAB69126
ID AAB69126 standard; Protein; 110 AA.
XX
AC AAB69126;
XX
DT 23-APR-2001 (first entry)
XX
DE Human MLP protein sequence SEQ ID NO:24.
XX
KW MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
KW cardiant; gene therapy; secretory cell function regulator; promoter;
KW inhibitor.
XX
OS Homo sapiens.
XX
PN WO200102564-A1.
XX
PD 11-JAN-2001.
XX
PF 29-JUN-2000; 2000WO-JP04278.
XX
PR 30-JUN-1999; 99JP-0186718.
XX
PA (TAKE ) TAKEDA CHEM IND LTD.
XX
PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
PI Tanaka H;
XX
DR N-PSDB; AAF59079.
XX
CC Safe, low-toxicity secretory cell function-regulatory protein and
CC encoded DNA, applicable as drugs, in diagnosis and development of
CC promoters and inhibitors for preventing or treating e.g. bone and joint
CC diseases -
XX
PS Claim 1; Page 97-98; 111pp; Japanese.
XX
CC The present invention describes novel MLP proteins and their encoding
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
CC activities, and can be used in gene therapy and as secretory cell
CC function regulators. The MLP proteins and DNAs can be used in drugs, in
CC the diagnosis and development of promoters and inhibitors for preventing
CC or treating bone and joint diseases as well as pathologic angiogenesis.
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
CC in the exemplification of the present invention.
XX
SQ Sequence 110 AA;
Query Match 80.9%; Score 547; DB 22; Length 110;
Best Local Similarity 90.0%; Pred. No. 9e-59;
Matches 99; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
Qy 19 HGVFMDKLSKKLCADDECVYTTISLARAQEDYNAPDCRFIDVKKGQOIYVYSKLVTEGA 78
Db 1 HGIFMDRLASKKLCADDECVYTTISLARAQEDYNAPDCRFIDVKKGQOIYVYSKLVTEGA 60
Qy 79 GEFWAGSVYGDHDEMGIYGVFPNSLVKEQRYQVQATKEIPTTIDPFCE 128
Db 61 GEFWAGSVYGDHDEMGIYGVFPNSLVKEQRYQVQATKEIPTTIDPFCE 110
RESULT 12
AAB82672
ID AAB82672 standard; Protein; 105 AA.
XX
AC AAB82672;
XX
DT 02-OCT-2001 (first entry)
XX
DE Human growth regulatory-like polypeptide (mature protein).
XX
KW Growth regulatory-like polypeptide; human; cartilage; melanoma;
KW neuroectodermal tumour; glioma; cancer; therapy; diagnosis.
XX
OS Homo sapiens.
XX
PN WO200155332-A2.
```

```

XX
DE Human MLP protein sequence SEQ ID NO:24.
XX
KW MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
KW cardiant; gene therapy; secretory cell function regulator; promoter;
KW inhibitor.
XX
OS Homo sapiens.
XX
PN WO200102564-A1.
XX
PD 11-JAN-2001.
XX
PF 29-JUN-2000; 2000WO-JP04278.
XX
PR 30-JUN-1999; 99JP-0186718.
XX
PA (TAKE ) TAKEDA CHEM IND LTD.
XX
PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
PI Tanaka H;
XX
DR N-PSDB; AAF59079.
XX
CC Safe, low-toxicity secretory cell function-regulatory protein and
CC encoded DNA, applicable as drugs, in diagnosis and development of
CC promoters and inhibitors for preventing or treating e.g. bone and joint
CC diseases -
XX
PS Claim 1; Page 97-98; 111pp; Japanese.
XX
CC The present invention describes novel MLP proteins and their encoding
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
CC activities, and can be used in gene therapy and as secretory cell
CC function regulators. The MLP proteins and DNAs can be used in drugs, in
CC the diagnosis and development of promoters and inhibitors for preventing
CC or treating bone and joint diseases as well as pathologic angiogenesis.
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
CC in the exemplification of the present invention.
XX
SQ Sequence 110 AA;
Query Match 80.9%; Score 547; DB 22; Length 110;
Best Local Similarity 90.0%; Pred. No. 9e-59;
Matches 99; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
Qy 19 HGVFMDKLSKKLCADDECVYTTISLARAQEDYNAPDCRFIDVKKGQOIYVYSKLVTEGA 78
Db 1 HGIFMDRLASKKLCADDECVYTTISLARAQEDYNAPDCRFIDVKKGQOIYVYSKLVTEGA 60
Qy 79 GEFWAGSVYGDHDEMGIYGVFPNSLVKEQRYQVQATKEIPTTIDPFCE 128
Db 61 GEFWAGSVYGDHDEMGIYGVFPNSLVKEQRYQVQATKEIPTTIDPFCE 110
RESULT 12
AAB82672
ID AAB82672 standard; Protein; 105 AA.
XX
AC AAB82672;
XX
DT 02-OCT-2001 (first entry)
XX
DE Human growth regulatory-like polypeptide (mature protein).
XX
KW Growth regulatory-like polypeptide; human; cartilage; melanoma;
KW neuroectodermal tumour; glioma; cancer; therapy; diagnosis.
XX
OS Homo sapiens.
XX
PN WO200155332-A2.
```

XX PD 02-AUG-2001.  
 XX PF 25-JAN-2001; 2001WO-US02455.  
 XX PR 25-JAN-2000; 2000US-0491404.  
 XX PR 02-MAY-2000; 2000US-0563786.  
 XX PA (HYSE-) HYSEQ INC.  
 XX PI Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;  
 XX PI Drmanac RT;  
 XX PR WPI; 2001-483233/52.  
 XX DR N-PSDB; AAH26343.  
 XX XX Isolated human growth regulatory-like polypeptide useful for treating  
 XX PT e.g. Alzheimer's disease, cancer, autoimmune disorders,  
 XX PT hyperproliferative disorders, coagulation disorders, and nervous system  
 XX PT disorders -  
 XX XX Claim 10; Page 117; 119pp; English.  
 XX PS The present sequence is that of a novel human growth regulatory-like  
 XX CC polypeptide (GRLP) mature protein. The sequence is predicted from  
 XX CC a novel assembled cDNA (see AAH26343) based on Hyseq clone number  
 XX CC 16372272. The protein has a mol.wt. of 14 kDa and is glycosylated. GRLP  
 XX CC belongs to the same protein family as growth regulatory proteins,  
 XX CC growth factors, human melanoma derived growth regulatory protein  
 XX CC precursor (64% similarity and 45% identity over 111 amino acids)  
 XX CC or melanoma inhibitory protein (CD-RAP, 44% identity and 64%  
 XX CC retinoic acid sensitive protein) and other retinoic acid-sensitive  
 XX CC proteins. GRLP polypeptides and polynucleotides of the invention  
 XX CC can be used in the prophylaxis, treatment (including gene therapy)  
 XX CC and diagnosis of disorders and diseases caused by, or involving,  
 XX CC cartilage development and maintenance, inhibition of melanoma cell  
 XX CC growth and tumours, including neuroectodermal tumours such as  
 XX CC gliomas. The polypeptides, which include the GRLP mature protein,  
 XX CC may also have nutritional uses, cytokine and cell proliferation  
 XX CC or differentiation activity, stem cell growth factor activity,  
 XX CC haematopoiesis regulating activity, tissue growth activity,  
 XX CC immunosuppressive or immunostimulant activity, activin/inhibin  
 XX CC activity, chemotactic/chemokinetic activity, haemostatic and  
 XX CC thrombolytic activity, use in cancer diagnosis and therapy,  
 XX CC drug screening, receptor/ligand activity, antiinflammatory  
 XX CC activity, and treatment of leukaemia, nervous system disorders,  
 XX CC arthritis and inflammation.  
 XX SQ Sequence 105 AA;  
 Query Match 76.8%; Score 519; DB 22; Length 105;  
 Best Local Similarity 90.5%; Pred. No. 2.3e-55;  
 Matches 95; Conservative 6; Mismatches 4; Indels 0; Gaps 0;  
 QY 24 DKLSKKLCADDECVYTISLARAQEDYNAPDCRFIDVKKQQIYVYVKLVTEGAGFEWA 83  
 Db 1 DRLASKKLCADDECVYTISLARAQEDYNAPDCRFIDVKKQQIYVYVKLVTEGAGFEWA 60  
 QY 84 GSVYGDHODEMGIVGYPFNSLVKEQRYQVQATKEIPTTIDDFCE 128  
 Db 61 GSVYGDQDQDEMGVGFPRNLVKEQRYQVQATKEVPTTIDDFCE 105  
 RESULT 13  
 AAB69129  
 ID AAB69129 standard; Protein; 87 AA.  
 XX AC AAB69129;  
 XX XX 23-APR-2001 (first entry)  
 XX DE Rat MLP protein sequence SEQ ID NO:39.  
 XX MIP; MIA; melanoma inhibitory activity; cancer; bone disease;  
 KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
 KW cardiant; gene therapy; secretory cell function regulator; promoter;  
 KW inhibitor.  
 XX OS Rattus sp.  
 XX XX WO200102564-A1.  
 XX PN 11-JAN-2001.  
 XX PD 29-JUN-2000; 2000WO-JP04278.  
 XX PF 30-JUN-1999; 99JP-0186718.  
 XX PR (TAKE ) TAKEDA CHEM IND LTD.  
 XX PA Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
 XX PI Tanaka H;  
 XX PI WPI; 2001-159271/16.  
 XX DR Safe, low-toxicity secretory cell function-regulatory protein and  
 XX PT encoded DNA, applicable as drugs, in diagnosis and development of  
 XX PT promoters and inhibitors for preventing or treating e.g. bone and joint  
 XX PT diseases -  
 XX PS Example 9; Page 103; 111pp; Japanese.  
 XX CC The present invention describes novel MLP proteins and their encoding  
 XX CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
 XX CC activities, and can be used in gene therapy and as secretory cell  
 XX CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
 XX CC the diagnosis and development of promoters and inhibitors for preventing  
 XX CC or treating bone and joint diseases as well as pathologic angiogenesis.  
 XX CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
 XX CC in the exemplification of the present invention.  
 XX SQ Sequence 87 AA;  
 Query Match 66.4%; Score 449; DB 22; Length 87;  
 Best Local Similarity 96.6%; Pred. No. 6.5e-47;  
 Matches 84; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 24 DKLSKKLCADDECVYTISLARAQEDYNAPDCRFIDVKKQQIYVYVKLVTEGAGFEWA 83  
 Db 1 DKLSKKLCADDECVYTISLARAQEDYNAPDCRFIDVKKQQIYVYVKLVTEGAGFEWA 60  
 QY 84 GSVYGDHODEMGIVGYPFNSLVKEQRY 110  
 Db 61 GSVYGDHODEMGIVGYPFNSLVKEQRY 87  
 RESULT 14  
 AAB69811  
 ID AAB69811 standard; Protein; 131 AA.  
 XX AC AAB69811;  
 XX XX 25-MAR-2003 (updated)  
 XX DT 26-OCT-1995 (first entry)  
 XX DE Melanoma inhibiting protein (human).  
 XX Melanoma; inhibition; cancer; melanoma; glioblastoma; neuroblastoma;  
 KW small cell lung cancer; neuroectodermal tumours; immunosuppressant;  
 KW phytohaemagglutinin; lymphocyte; interleukin 2; IL-2; detection;  
 KW probe; fusion protein.  
 XX OS Homo sapiens.  
 XX XX WO9503328-A2.

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XX PD 02-FEB-1995.
XX PF 19-JUL-1994; 94WO-EP02369.
XX PR 20-JUL-1993; 93DE-4324247.
XX PA (BOEF ) BOEHRINGER MANNHEIM GMBH.
XX PI Bogdahn U, Buettner R, Kaluza B;
XX WPI; 1995-075191/10.
DR N-PSDB; AAQ84050, AAQ84051.
XX
XX New melanoma inhibiting protein and related nucleic acid -
PT vectors, transformed cells, antibodies etc., useful for treating
PT tumours and as immunosuppressant e.g. by gene therapy
XX
XX Claim 1; Page 54; 85pp; German.
XX
XX This protein has melanoma-inhibiting activity and can be used to
CC treat cancer (melanoma, glioblastoma, neuroblastoma, small cell
CC lung cancer, neuroectodermal tumours) or as an immunosuppressant
CC (it inhibits IL-2 or phytohaemagglutinin induced proliferation of
CC peripheral blood lymphocytes). Antibodies raised against the
CC protein can be used to detect cell producing the protein and also
CC for protein purification. Probes derived from DNA encoding the
CC protein (AAQ84050, AAQ84051) can be used to detect sequences encoding
CC the protein or related proteins. The protein may be expressed as
CC a fusion protein (conjugated with dihydrofolate reductase (DHFR)).
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX SQ Sequence 131 AA;
Query Match 41.1%; Score 277.5; DB 16; Length 131;
Best Local Similarity 43.4%; Pred. No. 1.1e-25;
Matches 59; Conservative 29; Mismatches 35; Indels 13; Gaps 6;
Qy 1 MARILILLGLLVLC---AGHGVF---MDKLSKKLCADCECVYTISLARAQEDYNAPD 54
Db 1 MARSLVCL--GVIIILSAFSGPGVGRGMPKLDRLKLCADQECSPISMAVALQDYNAPD 58
Qy 55 CRFIDVKKGOIYVYVSKLVTENGAGE-FWAGSVYGDHQDEMG1-VGYFPPSNLVKEQRYQ 112
Db 59 CRFTIHRGQVYVFSKL---KGRGLFWGSGVQGDYGDIAARLGYFPSPSIVREDQTLK 115
Qy 113 EATKEIPTTIDDFCE 128
Db 116 PGKVDVTKDKWDFYCQ 131
RESULT 15
AAG65614
ID AAG65614 standard; Protein; 131 AA.
AC AAG65614;
XX
XX DT 07-JAN-2002 (first entry)
XX DE Human MIA protein sequence.
XX
XX MIA: melanoma inhibiting activity protein; antiinflammatory; human;
KW antiarthritic; antirheumatic; antithyroid; osteopathic; nephrotropic;
KW immunosuppressive; ophthalmological; dermatological; antidiabetic;
KW neuroprotective; immune tolerance; T-cell tolerance.
XX
XX OS Homo sapiens.
XX
XX PN WO200170253-A1.
XX
XX PD 27-SEP-2001.
XX
XX PF 15-MAR-2001; 2001WO-EP02991.

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XX PR 23-MAR-2000; 2000EP-0201063.
XX PA (ALKU ) AKZO NOBEL NV.
XX PI Nelissen RLH, Verheijden GFM;
XX WPI; 2001-611446/70.
DR N-PSDB; AAH47783.
XX
XX Use of melanoma inhibiting activity protein or its derivatives as
PT immune modulatory agents for the treatment of inflammatory diseases,
PT specifically rheumatoid arthritis -
XX
XX Example 4; Page 34; 41pp; English.
XX
XX The invention relates to the use of melanoma inhibiting activity (MIA)
CC protein and/or its fragments that have anti-inflammatory effects and
CC induce systemic immune tolerance or specific T-cell tolerance to MIA
CC antigen, for manufacturing a preparation against inflammatory diseases
CC and for induction of systemic immune tolerance or specific T-cell
CC tolerance in patients suffering from or susceptible to inflammatory
CC diseases. A fragment of MIA is useful as a therapeutic substance and is
CC useful for manufacture of pharmaceutical preparations against
CC inflammatory diseases such as an immune-cell mediated cartilage
CC destruction disease, specifically rheumatoid arthritis, autoimmune
CC diseases like Graves' disease, juvenile arthritis, primary
CC glomerulonephritis, polyarthritis, osteoarthritis, Sjogren's syndrome,
CC myasthenia gravis, Addison's disease, primary biliary sclerosis,
CC myelitis, systemic lupus erythematosus, inflammatory bowel disease,
CC multiple sclerosis or diabetes. The MIA polypeptides have specific
CC effect on the autoreactive T-cells thus leaving the other components of
CC the immune system intact as compared to the non-specific suppressive
CC effect of immunosuppressive drugs. The present sequence represents a
CC human MIA protein.
XX
XX SQ Sequence 131 AA;
Query Match 41.1%; Score 277.5; DB 22; Length 131;
Best Local Similarity 43.4%; Pred. No. 1.1e-25;
Matches 59; Conservative 29; Mismatches 35; Indels 13; Gaps 6;
Qy 1 MARILILLGLLVLC---AGHGVF---MDKLSKKLCADCECVYTISLARAQEDYNAPD 54
Db 1 MARSLVCL--GVIIILSAFSGPGVGRGMPKLDRLKLCADQECSPISMAVALQDYNAPD 58
Qy 55 CRFIDVKKGOIYVYVSKLVTENGAGE-FWAGSVYGDHQDEMG1-VGYFPPSNLVKEQRYQ 112
Db 59 CRFTIHRGQVYVFSKL---KGRGLFWGSGVQGDYGDIAARLGYFPSPSIVREDQTLK 115
Qy 113 EATKEIPTTIDDFCE 128
Db 116 PGKVDVTKDKWDFYCQ 131
Search completed: December 29, 2003, 16:09:02
Job time : 25.098 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2003, 16:09:08 ; Search time 17.5686 Seconds  
(without alignments)  
1449.984 Million cell updates/sec

Title: US-10-019-455a-12  
Perfect score: 676  
Sequence: 1 MARILLGLGLVLCAGHG.....RVQEKATKIPITDIDFFCE 128

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 724715 seqs, 199017464 residues 724715  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	602	89.1	128	12	US-10-216-163-72 Sequence 72, Appl
2	602	89.1	128	12	US-10-218-765-72 Sequence 72, Appl
3	602	89.1	128	12	US-10-219-063-72 Sequence 72, Appl
4	602	89.1	128	12	US-10-219-066-72 Sequence 72, Appl
5	602	89.1	128	12	US-10-219-067-72 Sequence 72, Appl
6	602	89.1	128	12	US-10-219-068-72 Sequence 72, Appl
7	602	89.1	128	12	US-10-219-069-72 Sequence 72, Appl
8	602	89.1	128	12	US-10-219-073-72 Sequence 72, Appl
9	602	89.1	128	12	US-10-219-475-72 Sequence 72, Appl
10	602	89.1	128	12	US-10-219-480-72 Sequence 72, Appl
11	602	89.1	128	12	US-10-219-483-72 Sequence 72, Appl
12	602	89.1	128	12	US-10-219-525-72 Sequence 72, Appl
13	602	89.1	128	12	US-10-219-526-72 Sequence 72, Appl
14	602	89.1	128	12	US-10-219-530-72 Sequence 72, Appl
15	602	89.1	128	12	US-10-219-531-72 Sequence 72, Appl

16	602	89.1	128	12	US-10-219-532-72 Sequence 72, Appl
17	602	89.1	128	12	US-10-219-533-72 Sequence 72, Appl
18	602	89.1	128	12	US-10-223-081-360 Sequence 360, App
19	602	89.1	128	12	US-10-230-437-72 Sequence 72, Appl
20	602	89.1	128	12	US-10-232-228-72 Sequence 72, Appl
21	602	89.1	128	12	US-10-223-082-360 Sequence 360, App
22	602	89.1	128	15	US-10-227-884-72 Sequence 72, Appl
23	602	89.1	128	15	US-10-230-163-72 Sequence 72, Appl
24	602	89.1	128	15	US-10-230-338-72 Sequence 72, Appl
25	602	89.1	128	15	US-10-218-631-72 Sequence 72, Appl
26	602	89.1	128	15	US-10-230-414-72 Sequence 72, Appl
27	602	89.1	128	15	US-10-216-159A-72 Sequence 72, Appl
28	602	89.1	128	15	US-10-218-849-72 Sequence 72, Appl
29	602	89.1	128	15	US-10-227-873-72 Sequence 72, Appl
30	602	89.1	128	15	US-10-227-883-72 Sequence 72, Appl
31	602	89.1	128	15	US-10-219-076-72 Sequence 72, Appl
32	602	89.1	128	15	US-10-230-434-72 Sequence 72, Appl
33	602	89.1	128	15	US-10-219-003-72 Sequence 72, Appl
34	602	89.1	128	15	US-10-219-075-72 Sequence 72, Appl
35	602	89.1	128	15	US-10-219-464-72 Sequence 72, Appl
36	602	89.1	128	15	US-10-219-466-72 Sequence 72, Appl
37	602	89.1	128	15	US-10-219-479-72 Sequence 72, Appl
38	602	89.1	128	15	US-10-219-481-72 Sequence 72, Appl
39	602	89.1	128	15	US-10-230-260-72 Sequence 72, Appl
40	602	89.1	128	15	US-10-232-231-72 Sequence 72, Appl
41	602	89.1	128	15	US-10-232-233-72 Sequence 72, Appl
42	602	89.1	128	15	US-10-216-165-72 Sequence 72, Appl
43	602	89.1	128	15	US-10-218-956-72 Sequence 72, Appl
44	602	89.1	128	15	US-10-219-468-72 Sequence 72, Appl
45	602	89.1	128	15	US-10-219-478-72 Sequence 72, Appl

ALIGNMENTS

RESULT 1

US-10-216-163-72  
; Sequence 72, Application US/10216163  
; Publication No. US20030149239A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3530F1C3  
; CURRENT APPLICATION NUMBER: US/10/216,163  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR FILING DATE: 10/119,480  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR FILING DATE: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR FILING DATE: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR FILING DATE: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR FILING DATE: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR FILING DATE: 60/069873  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR FILING DATE: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR FILING DATE: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR FILING DATE: 60/079656

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us-10-019-455a-12.rapb

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; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-163-72

Query Match      89.1%; Score 602; DB 12; Length 128;
Best Local Similarity 86.7%; Pred. No. 2.7e-64;
Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MARILLLLGLVLCAGHGVFMDKLSKKLCADEECVYTISLARAQEDYNAPDCRFIDV 60
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Db 1 MARILLPLGLVAVCAVHGIFMDRLASKKLCADEECVYTISLASAQEDYNAPCRFINV 60
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Qy 61 KKGQIYVYSKLVTENGAGFEWAGSVYGDHDEMGIVGYFSPNLYKGRVYQEAATKEIPT 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 KKGQIYVYSKLKVENGAGFEWAGSVYGDGDENGVGVPFRNLVKEQRYQEAATKEVPT 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 121 TDIDFFCE 128
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Db 121 TDIDFFCE 128
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RESULT 2
US-10-218-765-72
; Sequence 72, Application US/10218765
; Publication No. US20030187201A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P:C19
; CURRENT APPLICATION NUMBER: US/10/218,765
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
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; PRIOR APPLICATION NUMBER: 60/085579
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; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090691
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; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/091982
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; PRIOR APPLICATION NUMBER: 60/097986
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; PRIOR APPLICATION NUMBER: 60/099598
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; PRIOR FILING DATE: 1998-09-15
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; PRIOR FILING DATE: 1998-09-15
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; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: 60/101916
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; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101922
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/106178
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/106248
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 60/106464
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/106905
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: 60/108787
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; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835

Query Match      89.1%; Score 602; DB 12; Length 128;
Best Local Similarity 86.7%; Pred. No. 2.7e-64;
Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MARIILLGLVVLCAHGVMFKLSKLCADBEVCYTISLASAQEDYNAPDCRFIDV 60
Db 1 MARIILLFLPGLVAVCAVHGIFMDRLASKKLCADBEVCYTISLASAQEDYNAPDCRFINV 60

Qy 61 KKGQIYVYKLVKENGAGFWAGSVYGDHODENGIVGYFPSNLVKEQVYQEAATKEPT 120
Db 61 KKGQIYVYKLVKENGAGFWAGSVYGDHODENGIVGYFPSNLVKEQVYQEAATKEPT 120

Qy 121 TDIDFFCE 128
Db 121 TDIDFFCE 128

RESULT 3
US-10-219-063-72
; Sequence 72, Application US/10219063
; Publication No. US20030187202A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C24
; CURRENT APPLICATION NUMBER: US/10/219,063
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
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Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MARILLILLGLVLCAGHGVFMDKLSKKLCADEECVYTISLARAQEDYNAPDCRFIDV 60  
Db 1 MARILLFLPLGAVCAVGHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINV 60

Qy 61 KKGQIYVYVKLVTEGAGFEWAGSVYGDHDEMGIVGYFPPSNLVKEQRYVQEATKEIPT 120  
Db 61 KKGQIYVYVKLVTEGAGFEWAGSVYGDHDEMGIVGYFPPSNLVKEQRYVQEATKEIPT 120

Qy 121 TDIDFFCE 128  
Db 121 TDIDFFCE 128

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US-10-219-067-72  
; Sequence 72, Application US/10219067  
; Publication No. US20030187204A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3530PIC27  
; CURRENT APPLICATION NUMBER: US/10/219,067  
; CURRENT FILING DATE: 2002-08-14  
; PRIOR APPLICATION NUMBER: 10/119,480  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/059113  
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; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/069873  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 246  
; SEQ ID NO 72  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-219-067-72

Query Match 89.1%; Score 602; DB 12; Length 128;  
Best Local Similarity 86.7%; Pred. No. 2.7e-64;  
Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MARILLILLGLVLCAGHGVFMDKLSKKLCADEECVYTISLARAQEDYNAPDCRFIDV 60  
Db 1 MARILLFLPLGAVCAVGHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINV 60

Qy 61 KKGQIYVYVKLVTEGAGFEWAGSVYGDHDEMGIVGYFPPSNLVKEQRYVQEATKEIPT 120  
Db 61 KKGQIYVYVKLVTEGAGFEWAGSVYGDHDEMGIVGYFPPSNLVKEQRYVQEATKEIPT 120

Qy 121 TDIDFFCE 128  
Db 121 TDIDFFCE 128

RESULT 4  
US-10-219-066-72  
; Sequence 72, Application US/10219066  
; Publication No. US20030187203A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3530PIC27  
; CURRENT APPLICATION NUMBER: US/10/219,066  
; CURRENT FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: 10/119,480  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/069873  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 246  
; SEQ ID NO 72  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-219-066-72

Query Match 89.1%; Score 602; DB 12; Length 128;  
Best Local Similarity 86.7%; Pred. No. 2.7e-64;

LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-219-063-72

Query Match 89.1%; Score 602; DB 12; Length 128;  
Best Local Similarity 86.7%; Pred. No. 2.7e-64;  
Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MARILLILLGLVLCAGHGVFMDKLSKKLCADEECVYTISLARAQEDYNAPDCRFIDV 60  
Db 1 MARILLFLPLGAVCAVGHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINV 60

Qy 61 KKGQIYVYVKLVTEGAGFEWAGSVYGDHDEMGIVGYFPPSNLVKEQRYVQEATKEIPT 120  
Db 61 KKGQIYVYVKLVTEGAGFEWAGSVYGDHDEMGIVGYFPPSNLVKEQRYVQEATKEIPT 120

Qy 121 TDIDFFCE 128  
Db 121 TDIDFFCE 128

RESULT 4  
US-10-219-066-72  
; Sequence 72, Application US/10219066  
; Publication No. US20030187203A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3530PIC27  
; CURRENT APPLICATION NUMBER: US/10/219,066  
; CURRENT FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: 10/119,480  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/069873  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 246  
; SEQ ID NO 72  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-219-066-72

Query Match 89.1%; Score 602; DB 12; Length 128;  
Best Local Similarity 86.7%; Pred. No. 2.7e-64;





```

; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC52
; CURRENT APPLICATION NUMBER: US/10/219,073
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-073-72

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Query Match      89.1%; Score 602; DB 12; Length 128;
Best Local Similarity 86.7%; Pred. No. 2.7e-64;
Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MARILLGLVLCAGHGVFMDKLSKKLCADDECVYTISLARAQEDYNAPDCRFIDV 60
Db 1 MARILLFLPLVAVCAVHGIFMDRLASKKLCADDECVYTISLARAQEDYNAPDCRFIN 60

Qy 61 KKGQIYVYVKLVKENGAGFEWAGSVYGDHDEMGIVGFPSNLVKEQRYVQEAATKEIPT 120
Db 61 KKGQIYVYVKLVKENGAGFEWAGSVYGDHDEMGIVGFPSNLVKEQRYVQEAATKEIPT 120

Qy 121 TDIDFCE 128
Db 121 TDIDFCE 128

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RESULT 9
US-10-219-475-72
; Sequence 72, Application US/10219475
; Publication No. US20030187208A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria

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; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC49
; CURRENT APPLICATION NUMBER: US/10/219,475
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-475-72

```

```

Query Match      89.1%; Score 602; DB 12; Length 128;
Best Local Similarity 86.7%; Pred. No. 2.7e-64;
Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MARILLGLVLCAGHGVFMDKLSKKLCADDECVYTISLARAQEDYNAPDCRFIDV 60
Db 1 MARILLFLPLVAVCAVHGIFMDRLASKKLCADDECVYTISLARAQEDYNAPDCRFIN 60

Qy 61 KKGQIYVYVKLVKENGAGFEWAGSVYGDHDEMGIVGFPSNLVKEQRYVQEAATKEIPT 120
Db 61 KKGQIYVYVKLVKENGAGFEWAGSVYGDHDEMGIVGFPSNLVKEQRYVQEAATKEIPT 120

Qy 121 TDIDFCE 128
Db 121 TDIDFCE 128

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```

RESULT 10
US-10-219-480-72
; Sequence 72, Application US/10219480
; Publication No. US20030187209A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC38
; CURRENT APPLICATION NUMBER: US/10/219,480

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; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-480-72

Query Match      89.1%; Score 602; DB 12; Length 128;
Best Local Similarity 86.7%; Pred. No. 2.7e-64;
Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MARILLGLGVLCAGHGVFMDKLSKKLCADEECVYTISLARAQEDYNAPDCRFIDV 60
Db 1 MARILLGLGVLCAGHGVFMDKLSKKLCADEECVYTISLARAQEDYNAPDCRFIDV 60

Qy 61 KKGQIYVYKLVTVENGAGFVWAGSVYGDGQDGVGVYFPRNLVKQRYVQEAATKEIPT 120
Db 61 KKGQIYVYKLVTVENGAGFVWAGSVYGDGQDGVGVYFPRNLVKQRYVQEAATKEIPT 120

Qy 121 TDIDFFCE 128
Db 121 TDIDFFCE 128

RESULT 11
US-10-219-483-72
; Sequence 72, Application US/10219483
; Publication No. US20030187210A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C43
; CURRENT APPLICATION NUMBER: US/10/219,483
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-480-72

Query Match      89.1%; Score 602; DB 12; Length 128;
Best Local Similarity 86.7%; Pred. No. 2.7e-64;
Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MARILLGLGVLCAGHGVFMDKLSKKLCADEECVYTISLARAQEDYNAPDCRFIDV 60
Db 1 MARILLGLGVLCAGHGVFMDKLSKKLCADEECVYTISLARAQEDYNAPDCRFIDV 60

Qy 61 KKGQIYVYKLVTVENGAGFVWAGSVYGDGQDGVGVYFPRNLVKQRYVQEAATKEIPT 120
Db 61 KKGQIYVYKLVTVENGAGFVWAGSVYGDGQDGVGVYFPRNLVKQRYVQEAATKEIPT 120

Qy 121 TDIDFFCE 128
Db 121 TDIDFFCE 128

RESULT 12
US-10-219-525-72
; Sequence 72, Application US/10219525
; Publication No. US20030187211A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C29
; CURRENT APPLICATION NUMBER: US/10/219,525
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-483-72
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Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 246  
; SEQ ID NO 72  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-219-526-72  
Query Match 89.1%; Score 602; DB 12; Length 128;  
Best Local Similarity 86.7%; Pred. No. 2.7e-64;  
Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;  
QY 1 MARILILLGLVVLVLCAGHGVFMDKLSKKLCADEECVYTISLARAQEDYNAPDCRFIDV 60  
Db 1 MARILILLFLPGLVAVCAVHGIFMDRLASKKLCADEECVYTISLARAQEDYNAPDCRFIN 60  
QY 61 KKGQIIVYVKLVKENGAGFVAGSVYGDQDGVGVYFPRNLVKEQRYVQEAATKEIPT 120  
Db 61 KKGQIIVYVKLVKENGAGFVAGSVYGDQDGVGVYFPRNLVKEQRYVQEAATKEVPT 120  
QY 121 TDIDFFCE 128  
Db 121 TDIDFFCE 128  
RESULT 14  
US-10-219-530-72  
; Sequence 72, Application US/10219530  
; Publication No. US20030187213A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P35301C54  
; CURRENT APPLICATION NUMBER: US/10/219,530  
; CURRENT FILING DATE: 2002-08-14  
; PRIOR APPLICATION NUMBER: 10/119,480  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/069873  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 246  
; SEQ ID NO 72  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-219-530-72

Prior Filing Date: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 246  
; SEQ ID NO 72  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-219-525-72  
Query Match 89.1%; Score 602; DB 12; Length 128;  
Best Local Similarity 86.7%; Pred. No. 2.7e-64;  
Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;  
QY 1 MARILILLGLVVLVLCAGHGVFMDKLSKKLCADEECVYTISLARAQEDYNAPDCRFIDV 60  
Db 1 MARILILLFLPGLVAVCAVHGIFMDRLASKKLCADEECVYTISLARAQEDYNAPDCRFIN 60  
QY 61 KKGQIIVYVKLVKENGAGFVAGSVYGDQDGVGVYFPRNLVKEQRYVQEAATKEIPT 120  
Db 61 KKGQIIVYVKLVKENGAGFVAGSVYGDQDGVGVYFPRNLVKEQRYVQEAATKEVPT 120  
QY 121 TDIDFFCE 128  
Db 121 TDIDFFCE 128  
RESULT 13  
US-10-219-526-72  
; Sequence 72, Application US/10219526  
; Publication No. US20030187212A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P35301C41  
; CURRENT APPLICATION NUMBER: US/10/219,526  
; CURRENT FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: 10/119,480  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/069873  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27

Query Match	89.1%;	Score	602;	DB	12;	Length	128;	
Best Local Similarity	86.7%;	Pred. No.	2.7e-64;					
Matches	111;	Conservative	9;	Mismatches	8;	Indels	0; Gaps	0;
Qy	1	MARILLLLGGVLVCLAGHGVFMDKLSKKLCADDECVYITISLARAQEDYNAPCRFTDV	60					
Dd	1	MARILLFLPGLVAVCAVHGIFMDRLASKKLCADECVYITISLASAQEDYNAPCRFINV	60					
Qy	61	KKGQOIIVYSKLVNTENGAGEFWAGSVYGDHQDEMGI VGYFPSPNLVKQRVVYEATKEIPT	120					
Dd	61	KKGQOIIVYSKLVKENGAGEFWAGSVYGDGDENGVGYPFRNLVKQRVVYEATKEVPPT	120					
Qy	121	TDIDFFCE	128					
Dd	121	TDIDFFCE	128					

```

RESULT 15
US-10-219-531-72
  ? Sequence 72, Application US/10219531
  ? Publication No. US20030187214A1
  ? GENERAL INFORMATION:
  ? APPLICANT: Baker, Kevin P.
  ? APPLICANT: Desnoyers, Luc
  ? APPLICANT: Gerritsen, Mary
  ? APPLICANT: Goddard, Audrey
  ? APPLICANT: Godowski, Paul J.
  ? APPLICANT: Grimaldi, J. Christopher
  ? APPLICANT: Gurney, Austin L.
  ? APPLICANT: Smith, Victoria
  ? APPLICANT: Stephan, Jean-Philippe F.
  ? APPLICANT: Watanabe, Colin L.
  ? APPLICANT: Wood, William I.
  ? TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
  ? FILE REFERENCE: P3530P1C66
  ? CURRENT APPLICATION NUMBER: US/10/219,531
  ? CURRENT FILING DATE: 2002-08-14
  ? PRIOR APPLICATION NUMBER: 10/119,480
  ? PRIOR FILING DATE: 2002-04-09
  ? PRIOR APPLICATION NUMBER: 60/059113
  ? PRIOR FILING DATE: 1997-09-17
  ? PRIOR APPLICATION NUMBER: 60/062287
  ? PRIOR FILING DATE: 1997-10-17
  ? PRIOR APPLICATION NUMBER: 60/063549
  ? PRIOR FILING DATE: 1997-10-28
  ? PRIOR APPLICATION NUMBER: 60/064103
  ? PRIOR FILING DATE: 1997-10-31
  ? PRIOR APPLICATION NUMBER: 60/069873
  ? PRIOR FILING DATE: 1997-12-17
  ? PRIOR APPLICATION NUMBER: 60/078910
  ? PRIOR FILING DATE: 1998-03-20
  ? PRIOR APPLICATION NUMBER: 60/079294
  ? PRIOR FILING DATE: 1998-03-25
  ? PRIOR APPLICATION NUMBER: 60/079656
  ? PRIOR FILING DATE: 1998-03-26
  ? PRIOR APPLICATION NUMBER: 60/079728
  ? PRIOR FILING DATE: 1998-03-27
  ? Remaining Prior Application data removed - See File Wrapper or PALM.
  ? NUMBER OF SEQ ID NOS: 246
  ? SEQ ID NO 72
  ? LENGTH: 128
  ? TYPE: PRT
  ? ORGANISM: Homo Sapien
US-10-219-531-72

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Db      1  MARILLFLPGLVAVCAHGFPMORLASKKLCADDECYVTTISLASAQEDYNAPDCFFINV 60
Qy      61  KKGQOIYVYSKLVKTENGAGFEWAGSVYGDHODEMGI VGYFPFNLVKQEVYQEATKEIPT 120
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61  KKGQOIYVYSKLVKENGAGFEWAGSVYGDGDEMGVGYFPFNLVKQEVYQEATKEVPT 120
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      121  TDIDFFCE 128
          |||||
Db      121  TDIDFFCE 128
          |||||

Search completed: December 29, 2003, 16:26:15
Job time : 18.5686 secs

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Tue Dec 30 10:20:37 2003

us-10-019-455a-12.ra1

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Db      1  MARSLVCL--GVILLGAFSGPVRGGMPLKADRLKLCADQECSHPI SMAVALQDYNWAPD 58
Qy      55  CRFTDVKKGQIYVYVSKLVTEGAGE--FWAGSVYGDHDEMGI--VGYPFNSNLVKEQRYVQ 112
Db      59  CRFTIHRGQVYVYVSKL---XGRGRUFWGSGVQGYDGLAARLGYPFNSIVREDQTLK 115
Qy      113  EATKEIPTDIDDFCE 128
Db      116  PGKVDVTKDKWDFYCQ 131

RESULT 2
US-08-578-649-5
; Sequence 5, Application US/08578649
; Patent No. 5770366
; GENERAL INFORMATION:
; APPLICANT: Ulrich Bogdan
; APPLICANT: Reinhard Buttner
; APPLICANT: Brigitte Kaluza
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/578,649
; FILING DATE: 29-July-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: DE P 43 24 247.2
; FILING DATE: 20-July-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Andrew L. Tiejoloff
; REGISTRATION NUMBER: 31,575
; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-578-649-5

Query Match      36.5%; Score 247; DB 1; Length 130;
Best Local Similarity 43.0%; Pred. No. 1.8e-23;
Matches 55; Conservative 23; Mismatches 40; Indels 10; Gaps 4;

Qy      8  LLGLVLVLCAGHGV-----FMDKLSSKKLCADEECVYTTISLARAEQEDYNAPDCRFIDVKK 62
Db      6  VLLGIVLVSPGSPRADRPKPLADWKLCADDECSHPISMAVALQDYNAPDCRFILYR 65
Qy      63  GQQTYYVSKLVTEGAGE--FWAGSVYGDHDEMGI--VGYPFNSNLVKEQRYVQEAKEIPT 120
Db      66  GQVYVYVSKL---XGRGRUFWGSGVQGYDGLAARLGYPFNSIVREDLNSKPGKIDMKT 122

Qy      121  TDIDFFCE 128
Db      123  DQWDFYCQ 130

RESULT 3
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US-07-646-537B-2
; Sequence 2, Application US/07646537B
; Patent No. 5348664
; GENERAL INFORMATION:
; APPLICANT: Barbacid, Mariano
; TITLE OF INVENTION: Vav Proto-Oncogene Protein
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company
; STREET: P.O. Box 4000
; CITY: Princeton
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 08543-4000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/646,537B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaul, Timothy J.
; REGISTRATION NUMBER: 33,111
; REFERENCE/DOCKET NUMBER: DC10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 921-5901
; TELEFAX: (609) 921-4526
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 844 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-646-537B-2

Query Match      13.5%; Score 91.5; DB 1; Length 844;
Best Local Similarity 32.9%; Pred. No. 0.013;
Matches 23; Conservative 14; Mismatches 20; Indels 13; Gaps 3;

Qy      44  ARAQEDYNAPDCRFIDVKKGQIYVYVSKLVTEGAGEFWAGSVYGDHDEMGIYVFPNS 103
Db      786  AKARYDFCARDSELSKESDII---KILNKKGQGGWRRGEIYGR-----IGWFPNS 834
Qy      104  LVKEQRYVQE 113
Db      835  YVEED--YSE 842

RESULT 4
US-09-346-510B-21
; Sequence 21, Application US/09346510B
; Patent No. 6281014
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Wang, Yinxiang
; TITLE OF INVENTION: SH3-Containing Protein, DNA and Uses Thereof
; FILE REFERENCE: D6221CIP
; CURRENT APPLICATION NUMBER: US/09/346,510B
; CURRENT FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: 08/871,732
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 21
; LENGTH: 54
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; NAME/KEY: Domain
; OTHER INFORMATION: amino acid sequence of Vav SH3 domain
US-09-346-510B-21
```





```

; FILING DATE: 14-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5607849man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-599-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)412-3000
; TELEFAX: (703)413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 694 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-583-799-4

Query Match 11.4%; Score 77; DB 1; Length 694;
Best Local Similarity 27.5%; Pred. No. 0.69;
Matches 22; Conservative 20; Mismatches 28; Indels 10; Gaps 3;

Qy 49 DYNAPDCRFIDVKKGQOIYVYKLVTEGAG---EFWAGSVYGDHQMDEMGIVGFFPSNLV 105
Db 392 EVNADTIYVQKQGR-----RKITEDHASVGKNISTKSVYGNHREDVTILHYKYPEGSQ 446
Qy 106 KEQRYVQBATKEI--PTTDDI 123
Db 447 KEREYKKGAGRRVTEPSNEI 466

RESULT 8
US-08-164-839-6
; Sequence 6, Application US/08164839
; Patent No. 5514573
; GENERAL INFORMATION:
; APPLICANT: YASUEDA, HISASHI
; APPLICANT: NAKANISHI, KAZUO
; APPLICANT: MOTOKI, MASAO
; APPLICANT: NAGASE, KAZUO
; APPLICANT: MATSUI, HIROSHI
; TITLE OF INVENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED
; FROM FISH
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/164,839
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/004,729
; FILING DATE: 14-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5514573man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-599-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)412-3000
; TELEFAX: (703)413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 694 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-583-799-4

Query Match 11.4%; Score 77; DB 1; Length 694;
Best Local Similarity 27.5%; Pred. No. 0.69;
Matches 22; Conservative 20; Mismatches 28; Indels 10; Gaps 3;

Qy 49 DYNAPDCRFIDVKKGQOIYVYKLVTEGAG---EFWAGSVYGDHQMDEMGIVGFFPSNLV 105
Db 392 EVNADTIYVQKQGR-----RKITEDHASVGKNISTKSVYGNHREDVTILHYKYPEGSQ 446
Qy 106 KEQRYVQBATKEI--PTTDDI 123
Db 447 KEREYKKGAGRRVTEPSNEI 466

RESULT 9
US-08-583-799-6
; Sequence 6, Application US/08583799
; Patent No. 5607849
; GENERAL INFORMATION:
; APPLICANT: YASUEDA, HISASHI
; APPLICANT: NAKANISHI, KAZUO
; APPLICANT: MOTOKI, MASAO
; APPLICANT: NAGASE, KAZUO
; APPLICANT: MATSUI, HIROSHI
; TITLE OF INVENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED
; FROM FISH
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,799
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/004,729
; FILING DATE: 14-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5607849man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-599-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)412-3000
; TELEFAX: (703)413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 695 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-583-799-6

Query Match 11.4%; Score 77; DB 1; Length 695;
Best Local Similarity 27.5%; Pred. No. 0.69;
Matches 22; Conservative 20; Mismatches 28; Indels 10; Gaps 3;

Qy 49 DYNAPDCRFIDVKKGQOIYVYKLVTEGAG---EFWAGSVYGDHQMDEMGIVGFFPSNLV 105
Db 393 EVNADTIYVQKQGR-----RKITEDHASVGKNISTKSVYGNHREDVTILHYKYPEGSQ 447
Qy 106 KEQRYVQBATKEI--PTTDDI 123
Db 448 KEREYKKGAGRRVTEPSNEI 467
```

Db 393 EVNADTIYVQKQGR-----RKTFEDHASVGKNISTKSVYGNHREDVTLHKYKPSGQ 447

Qy 106 KEORVYQKATKEI--PTTDI 123

Db 448 KEREVYKAGRRVTFESNEI 467

RESULT 10

US-08-630-915A-194

Sequence 194, Application US/08630915A

Patent No. 6309820

GENERAL INFORMATION:

APPLICANT: SPARKS, Andrew B.

APPLICANT: HOFFMAN, No. 6309820h

APPLICANT: KAY, Brian K.

APPLICANT: FOWLKES, Dana M.

APPLICANT: MCCONNELL, Stephen J.

TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL

TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND

TITLE OF INVENTION: USING SAME

NUMBER OF SEQUENCES: 227

CORRESPONDENCE ADDRESS:

ADDRESSEE: pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/630,915A

FILING DATE: 03-APR-1996

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Mistrock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 1101-174

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-8864/9741

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 194:

SEQUENCE CHARACTERISTICS:

LENGTH: 509 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-630-915A-194

Query Match 11.1%; Score 75; DB 4; Length 509;

Best Local Similarity 22.1%; Pred. No. 0.8;

Matches 36; Conservative 22; Mismatches 33; Indels 72; Gaps 10;

Qy 18 GHGVFMDKLSSKKLCA-----DEECVYT-----ISLARAQEDY----- 50

Db 210 GQGQVVENLKAQALCSWTAKXNDHNLNFSKDHDIITVLEQQENWFWGEVHGGRGWFPKSYVK 269

Qy 51 -----NAPDCRFIDVKK-----GQQ-----IYVYSK-----LYTE 75

Db 270 IIPGSEVKREBEALYAAVNNKPTSAAYSVGEEYIALYPYSEVPEGLDTFTTEGEILVTQ 329

Qy 76 NGAGEFFAGSVYGDHQDEMGIVGVPFNSLV--KEORVYQKATK 116

Db 330 KD-GEWWTGSI--GDRS-----GIFPSNVYKPKQDESFGSASK 364

RESULT 11

US-09-328-352-4886

Sequence 4886, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 4886

LENGTH: 1326

TYPE: PRT

ORGANISM: Acinetobacter baumannii

US-09-328-352-4886

Query Match 11.0%; Score 74.5; DB 4; Length 1326;

Best Local Similarity 26.3%; Pred. No. 3.7;

Matches 36; Conservative 17; Mismatches 47; Indels 37; Gaps 9;

Qy 11 GLVVLGAGHGVFMDKLSSKKLCADEECVYTI-----SLARAQEDYNAPDCRFIDV 60

Db 739 GLTALCGEA--LDTILAELKLGKVGCLMNVYGTETTVWSSAAR-----ITDAKCIDL 790

Qy 61 KK--GQOIYV--YSKLVTENGAGEFWAGSVVGD-----HQDEMGIVGY--FPPNSLV 105

Db 791 GEPLANTQLVLDDEQQRLVPPGVMGELWIG--GDGLAVDYWHRPELTDAQFRTLPS-LP 846

Qy 106 KEORVYQKATKEIPTTD 122

Db 847 NAGRLYRTGDKVCLRTD 863

RESULT 12

US-09-346-510B-24

Sequence 24, Application US/09346510B

Patent No. 6281014

GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

TITLE OF INVENTION: SH3-Containing Protein, DNA and Uses Thereof

FILE REFERENCE: D6221CIP

CURRENT APPLICATION NUMBER: US/09/346,510B

CURRENT FILING DATE: 1999-07-01

PRIOR APPLICATION NUMBER: 08/871,732

PRIOR FILING DATE: 1997-06-09

NUMBER OF SEQ ID NOS: 32

SEQ ID NO 24

LENGTH: 48

TYPE: PRT

ORGANISM: unknown

FEATURE:

NAME/KEY: Domain

LOCATION: 2...49

OTHER INFORMATION: amino acid sequence of Vav SH3 domain at position 2

OTHER INFORMATION: through position 49 of SEQ ID No. 6281014 21

US-09-346-510B-24

Query Match 10.9%; Score 73.5; DB 3; Length 48;

Best Local Similarity 31.6%; Pred. No. 0.041;

Matches 18; Conservative 11; Mismatches 17; Indels 11; Gaps 2;

Qy 49 DYNAPDCRFIDVKKGQOIYVYVYSLVTENGAGEFWAGSVVGDHQDEMGIVGVPFNSLV 105

Db 3 DFCARDRSELKSGDII-----KIILKKGQGGWRRGEIYGR-----VGWFPANYV 48

RESULT 13

US-08-630-915A-40

Sequence 40, Application US/08630915A

Patent No. 6309820

GENERAL INFORMATION:

```

APPLICANT: SPARKS, Andrew B.
APPLICANT: HOFFMAN, No. 6309820h
APPLICANT: KAY, Brian K. M.
APPLICANT: FOMLIES, Dana M.
APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
TITLE OF INVENTION: USING SAME
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-APR-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 869-8864/9741
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-630-915A-40
Query Match 10.6%; Score 71.5; DB 4; Length 248;
Best Local Similarity 36.8%; Pred. No. 0.78;
Matches 21; Conservative 8; Mismatches 13; Indels 15; Gaps 4;
QY 62 KCQIIVTVSKLVENGACFEWAGSVYGDHDEMGIYGFPSNLV--KEQRVYQEATK 116
DB 60 EGEELVTQK-----DGEWTGSI-GDRSS-----GIFFSNVYKPKDQESFGSASK 103
RESULT 14
US-08-164-839-31
Sequence 31, Application US/08164839
Patent No. 5514573
GENERAL INFORMATION:
APPLICANT: YASUEDA, HISASHI
APPLICANT: NAKANISHI, KAZUO
APPLICANT: MOTOKI, MASAO
APPLICANT: NAGASE, KAZUO
APPLICANT: MATSUJI, HIROSHI
TITLE OF INVENTION: GENE ENCODING TRANSGLUAMINASE DERIVED
FROM FISH
TITLE OF INVENTION: FROM FISH
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/164,839
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/004,729
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5514573man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-599-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 412-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 687 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-164-839-31
Query Match 10.6%; Score 71.5; DB 1; Length 687;
Best Local Similarity 26.0%; Pred. No. 3.4;
Matches 27; Conservative 19; Mismatches 45; Indels 13; Gaps 4;
QY 25 KLSKKLCADCECVYTISLARAEQEDYNAPDCRFIDVKKGQQIYVY-----SKL-VTE 75
DB 356 ELSDGEYCPCPVTAIKEGNLSVKYDAP---FIFAEVNADIYYMMAGFGGERKKIDVDQ 412
QY 76 NCAGE-FWAGSVYGDHDEMGIYGFPSNLVKEQRVYQEATKEI 118
DB 413 SGVGKNISTKSILYGYREDVTLLHYKYPEGSKKEREVYQAGHRI 456
RESULT 15
US-08-164-839-33
Sequence 33, Application US/08164839
Patent No. 5514573
GENERAL INFORMATION:
APPLICANT: YASUEDA, HISASHI
APPLICANT: NAKANISHI, KAZUO
APPLICANT: MOTOKI, MASAO
APPLICANT: NAGASE, KAZUO
APPLICANT: MATSUJI, HIROSHI
TITLE OF INVENTION: GENE ENCODING TRANSGLUAMINASE DERIVED
FROM FISH
TITLE OF INVENTION: FROM FISH
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/164,839
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/004,729
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5514573man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-599-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 412-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 687 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-164-839-31

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Tue Dec 30 10:20:37 2003

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;
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5514573man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-599-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)412-3000
; TELEFAX: (703)413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 687 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-164-839-33

Query Match      10.6%; Score 71.5; DB 1; Length 687;
Best Local Similarity 26.0%; Pred. No. 3.4;
Matches 27; Conservative 19; Mismatches 45; Indels 13; Gaps 4;

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Db      356 ELSGGEYCCGCPVTAIKEGNLSVKYDAP---FIFAEVNADIIYWMAGPGGERKKIDVDQ 412

Qy      76 NGAGE-FWAGSVYGDHODEMGIVGVFSPNLVKEQRYQVQATKEI 118
Db      413 SGVGKNISTKSLYGDYREDVTLHYKIPGSKKEREVYQKAGHRI 456

Search completed: December 29, 2003, 16:11:50
Job time : 10.3221 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 29, 2003, 16:11:59 ; Search time 2106.98 Seconds  
(without alignments)  
2485.278 Million cell updates/sec

Title: US-10-019-455A-12  
Perfect score: 676  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
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Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Database : GenEmbl:  
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34: em.htg.pln:\*  
35: em.htg.rod:\*  
36: em.htg.mam:\*  
37: em.htg.vrt:\*  
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41: em.htgo.other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	676	100.0	384	6	BD093106 Novel pol
3	676	100.0	929	10	AF243504 Mus muscu
4	676	100.0	947	6	BD010821 Novel pol
5	676	100.0	947	6	BD093122 Novel pol
6	676	100.0	958	10	MMU243939 Mus muscu
7	676	100.0	1054	10	AF233333 Mus muscu
8	655	96.9	384	6	BD010835 Novel pol
9	655	96.9	384	6	BD093136 Novel pol
10	602	89.1	384	6	BD010802 Novel pol
11	602	89.1	384	6	BD093103 Novel pol
12	602	89.1	521	6	AX358818 Sequence
13	602	89.1	521	6	AX362311 Sequence
14	602	89.1	521	6	AX454774 Sequence
15	602	89.1	521	6	AX491252 Sequence
16	602	89.1	846	9	AF233261 Homo sapi
17	602	89.1	865	9	AF243505 Homo sapi
18	602	89.1	923	6	BD010820 Novel pol
19	602	89.1	923	6	BD093121 Novel pol
20	602	89.1	1422	9	HSA242552 Homo sapi
21	591	87.4	330	6	BD010817 Novel pol
22	591	87.4	330	6	BD093118 Novel pol
23	574	84.9	330	6	BD010836 Novel pol
24	574	84.9	330	6	BD093137 Novel pol
25	547	80.9	330	6	BD010816 Novel pol
26	547	80.9	330	6	BD093117 Novel pol
27	515	76.2	307	6	BD010830 Novel pol
28	515	76.2	307	6	BD093131 Novel pol
29	468.5	69.3	484	5	AF233518 Gallus ga
30	445	65.8	261	6	BD010829 Novel pol
31	445	65.8	261	6	BD093130 Novel pol
32	412	60.9	466	5	AF233519 Rana cate
33	379.5	56.1	215581	2	AC106161 Rattus no
34	378.5	56.0	144765	2	BX510362 Mus muscu
35	294	43.5	121151	9	HS705D16 Human DNA
36	277.5	41.1	396	9	BT007044 Homo sapi
37	277.5	41.1	396	12	BT007775 Synthetic
38	277.5	41.1	459	6	AX2942 Sequence 1
39	277.5	41.1	459	6	AX016785 Sequence
40	277.5	41.1	459	6	AX252508 Sequence
41	277.5	41.1	459	6	AX287209 Sequence
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ALIGNMENTS

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Db	301	CCCAGCAACTTGGTGAAGGACGCGGTATACAGAGGACCAAGGAGATCCCAACC	360
QY	121	ThrAspIleAspPheCysGlu	128
Db	361	ACGATATTGACTTCTTCTGTGAA	384
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DEFINITION	Mus musculus fibrocyte-derived protein (Fdp) mRNA, complete cds.		
ACCESSION	AF243504		
VERSION	AF243504.1	GI:11991841	
KEYWORDS			
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	1	(bases 1 to 929)	
AUTHORS	Cohen-Salmon, M., Frensz, D., Liu, W., Verpy, E., Voegelings, S. and Petit, C.		
TITLE	Fdp, a new fibrocyte-derived protein related to MIA/CD-RAP, has an in vitro effect on the early differentiation of the inner ear mesenchyme		
JOURNAL	J. Biol. Chem. 275 (51), 40036-40041	(2000)	
MEDLINE	20568254		
PUBMED	10998416		
REFERENCE	2	(bases 1 to 929)	
AUTHORS	Cohen-Salmon, M., Frensz, D., Verpy, E., Voegelings, S. and Petit, C.		
TITLE	Direct Submission		
JOURNAL	Submitted (09-MAR-2000) Biotechnologies, Institut Pasteur, 25 rue du Dr. Roux, Paris 75015, France		
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Score:	676.00	Matches:	128
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0
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QY	1	MetAlaArgIleLeuIleLeuLeuGlyLeuValValLeuCysAlaGlyHisGly	20
Db	9	ATGGCAAGGATATTGATCTTTTGTCTGGGGGCTTGTGTTCTATGTCGCGGATGCT	68
QY	21	ValPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValTyrThr	40
Db	69	GTATTATTGATTAACCTTCTTCTAAGAGCTTGTGCGGATGAGGAGTGTGCTACTACT	128
QY	41	IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysAspPheIleAspVal	60
Db	129	ATTTCCTGCGAAGACACAGGAAGATTACAATGCCCCAGACTGTAGGTTTCATCGATGTC	188
QY	61	LysIleGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu	80
Db	189	ARGAAGGGCAGCAGATCTATGTTTACTCCAGCTGTTAACAAGAAACGGAGCTGGAGAG	248
QY	81	PheTriAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe	100
Db	249	TTTTGGCTGGCAGTGTATTGATGGTACCACAGGATGAGATGGGAATTTGAGTTATTTC	308
QY	101	ProSerAsnLeuVallyysGluGlnArgValTyrGlnGluAlaThrlyysGluIleProThr	120
Db	309	CCCAGCAACTTGGTGAAGGACGCGGTATACAGAGGACCAAGGAGATCCCAACC	368
QY	121	ThrAspIleAspPheCysGlu	128
Db	369	ACGATATTGACTTCTTCTGTGAA	392
RESULT 4			
LOCUS	BD010821	947 bp DNA linear	PAT 31-JAN-2002
DEFINITION	Novel polypeptide and DNA thereof.		
ACCESSION	BD010821		
VERSION	BD010821.1	GI:18639194	
KEYWORDS	JP 2001069994-A/22.		
SOURCE	Mus sp.		
ORGANISM	Mus sp.		
REFERENCE	1	(bases 1 to 947)	
AUTHORS	Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y., Yoshimura, K. and Tanaka, H.		
TITLE	Novel polypeptide and DNA thereof		
JOURNAL	Patent: JP 2001069994-A 22 21-MAR-2001;		
COMMENT	TAKEDA CHEMICAL INDUSTRIES LTD		
	OS Mus sp. (mouse)		
	PN JP 2001069994-A/22		
	PD 21-MAR-2001		
	PF 29-JUN-2000 JP 2000195911		
	PR		
	PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI SHINICHI MOGI,		
	PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA		
	PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC A61P19/08,		
	PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC G01N33/53//		
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US-10-019-455A-12 (1-128) x BD010821 (1-947)

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QY	21	ValPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValTyrThr	40
DB	71	GTATTATGGATAAATCTTCTTAAGAAAGTTGTGTGGGATGAGAGTGTCTATACT	130
QY	41	IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal	60
DB	131	ATTCTCTGGCAAGACACAGAAAGATTACAATGCCCCAGACTGTAGGTTCATCGATGTC	190
QY	61	LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu	80
DB	191	AAGAAGGGCAGCAGATCTATGTTTACTCAAGCTGGTAACAGAAAACGGAGCTGAGAG	250
QY	81	PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe	100
DB	251	TTTTGGCTGGCAGTCTTTATGTTGACCAACAGATGAGATGGGAATTGTAGTTATTTC	310
QY	101	ProSerAsnLeuValLysGlnArgValTyrGlnGluAlaThrLysGluIleProThr	120
DB	311	CCAGCAACTTGGTGAAGGACGCGGTATACAGAGGCCACCAAGAGATCCCAACC	370
QY	121	ThrAspIleAspPheCysGlu	128
DB	371	ACGGATATTGACTTCTCTGTGAA	394

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DEFINITION BD093122.1 GI:22638710  
ACCESSION BD093122.1 GI:22638710  
VERSION WO 0102564-A/22.  
KEYWORDS Mus sp.  
SOURCE Mus sp.

ORGANISM Mus sp.  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y., Yoshimura, K. and Tanaka, H.  
TITLE Novel polypeptide and its DNA  
JOURNAL Patent: WO 0102564-A 22 11-JAN-2001;  
TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA  
COMMENT OS Mus sp. (mouse)  
PN WO 0102564-A/22  
PD 11-JAN-2001  
PF 29-JUN-2000 WO 2000JP004278  
PR 30-JUN-1999 JP 99P 186718  
PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI MOGI,  
YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA  
PC C12N15/12, C12N5/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC A61K38/17  
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Pred. No.: 1,43e-71 Length: 947  
Score: 676.00 Matches: 128  
Percent Similarity: 100.00% Conservative: 0  
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Query Match: 100.00% Indels: 0  
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US-10-019-455A-12 (1-128) x BD093122 (1-947)

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QY	21	ValPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValTyrThr	40
DB	71	GTATTATGGATAAATCTTCTTAAGAAAGTTGTGTGGGATGAGAGTGTCTATACT	130
QY	41	IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal	60
DB	131	ATTCTCTGGCAAGACACAGAAAGATTACAATGCCCCAGACTGTAGGTTCATCGATGTC	190
QY	61	LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu	80
DB	191	AAGAAGGGCAGCAGATCTATGTTTACTCAAGCTGGTAACAGAAAACGGAGCTGAGAG	250
QY	81	PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe	100
DB	251	TTTTGGCTGGCAGTCTTTATGTTGACCAACAGATGAGATGGGAATTGTAGTTATTTC	310
QY	101	ProSerAsnLeuValLysGlnArgValTyrGlnGluAlaThrLysGluIleProThr	120
DB	311	CCAGCAACTTGGTGAAGGACGCGGTATACAGAGGCCACCAAGAGATCCCAACC	370
QY	121	ThrAspIleAspPheCysGlu	128
DB	371	ACGGATATTGACTTCTCTGTGAA	394

RESULT 6

MMU243939

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. 958

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Related sequence: AJ242552.

Location/Qualifiers

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AJ243939.1 GI:12619174  
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Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 Rendtorff, N.D., Frodin, M., Attie-Bitach, T., Vekemans, M. and Tommerup, N.  
Identification and characterization of an inner ear-expressed human melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent polymorphism that abolishes translation  
Genomics 71 (1), 40-52 (2001)  
21100875  
11161796  
Rendtorff, N.D.  
Direct Submission  
Submitted (20-JUL-1999) Rendtorff N.D., Department of Medical Genetics, Institute of Medical Biochemistry and Genetics, Blegdamsvej 3, 2200 Copenhagen N, DENMARK  
Related sequence: AJ242552.  
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DEFINITION
ACCESSION BD093136
VERSION   BD093136.1 GI:22638724
KEYWORDS WO 0102564-A/36.
SOURCE   Rattus sp.
ORGANISM Rattus sp.
REFERENCE
AUTHORS Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
        Yoshimura, K. and Tanaka, H.
TITLE    Novel polypeptide and its DNA
JOURNAL  Patent: WO 0102564-A 36 11-JAN-2001;
        TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO
        OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,
        HIDEYUKI TANAKA
COMMENT  OS Rattus sp. (rat)
        PN WO 0102564-A/36
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        PF 29-JUN-2000 WO 2000JP004278
        PR 30-JUN-1999 JP 99P 186718
        PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
        PI MOGI,
        PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
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        A61K38/17,
        PC A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7088// (C12P21/
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BASE COUNT      98 a 72 c 109 g 105 t

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Alignment Scores:
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Score:          655.00      Matches:    123
Percent Similarity: 98.4%      Conservative: 3
Best local Similarity: 96.0%      Mismatches: 2
Query Match:    96.8%      Indels:      0
DB:             6      Gaps:      0

US-10-019-455A-12 (1-128) x BD093136 (1-384)

QY      1 MetAlaArgIleLeuIleLeuLeuLeuGlyGlyLeuValValLeuCysAlaGlyHisGly 20
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QY      21 ValPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValTyrThr 40
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QY      41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal 60
Dbb     121 ATTTCTCTGGCAAGAGCAGAGAAGACTACAATGCCCGGACCTGTAGTTTCATCATGTC 180
QY      61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu 80
Dbb     181 AAGAAGGGCAGCAGATCTATGTTTATTCCAAAGCTGTTAACAAATGGAGCTGGGGCA 240
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Db      241 TTCTGGCTGGCAGTGTATGTTGACCAACAGGATGAGATGGAAATTTGGGTATTTC 300
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Db      301 CCCAGCAACTGGTTAGAGACACAGAGTGTACCAAGAGGCCACCAAGAGATTCCAAAC 360
Qy      121 ThrAspIleAspPheCysGlu 128
Db      361 ACGGATATTGACTTCTTCTGTGAA 384

RESULT 10
LOCUS   BD010802 384 bp DNA linear PAT 31-JAN-2002
DEFINITION Novel polypeptide and DNA thereof.
ACCESSION BD010802
VERSION   BD010802.1 GI:18639175
KEYWORDS JP 2001069994-A/3.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 384)
Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
Yoshimura, K. and Tanaka, H.
Novel polypeptide and DNA thereof
Patent: JP 2001069994-A 3 21-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD
OS Homo sapiens (human)
PN JP 2001069994-A/3
PD 21-MAR-2001
PF 29-JUN-2000 JP 2000195911
PR YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI
SHINICHI MOGI,
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC
A61P19/08,
PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC
G01N33/53//
CC C12P21/08, C12N15/00, A61K37/02, C12N5/00
CQ Key Location/Qualifiers
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FT /organism="Homo sapiens (human)".
FT Location/Qualifiers
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BASE COUNT 99 a 70 c 106 g 109 t
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Score: 602.00 Matches: 111
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Qy      1 MetAlaArgIleLeuIleLeuLeuGlyLeuValValLeuCysAlaGlyHisGly 20
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Qy      21 ValPheMetAspLysLeuSerLysLysLeuCysAlaAspGluCysValTyrThr 40
Db      61 ATATTATGGACCGTCTAGCTTCCAAAGAGCTCTGTGAGATGATGATGCTCTACT 120
Qy      41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal 60
Db      121 ATTTCTCTGGCTAGTGTCTCAGAGAGATTATATGCCCCGGGACTGTAGATTCAATTAACGTT 180

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Qy      61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAenGlyAlaGlyGlu 80
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Qy      81 PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
Db      241 TTTTGGCTGGCAGTGTATTGTTGATGGCCAGGACGAGATGGGAGTCGTGGGTATTTC 300
Qy      101 ProSerAsnLeuValLysGluArgValTyrGlnGluAlaThrLysGluIleProThr 120
Db      301 CCCAGCAACTGGTTAGAGACACAGAGTGTACCAAGAGGCCACCAAGAGATTCCCAAC 360
Qy      121 ThrAspIleAspPheCysGlu 128
Db      361 ACGGATATTGACTTCTTCTGTGAG 384

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LOCUS   BD093103 384 bp DNA linear PAT 27-AUG-2002
DEFINITION Novel polypeptide and its DNA..
ACCESSION BD093103
VERSION   BD093103.1 GI:22638691
KEYWORDS WO 0102564-A/3.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 384)
Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
Yoshimura, K. and Tanaka, H.
Novel polypeptide and its DNA
Patent: WO 0102564-A 3 11-JAN-2001;
TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO
OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,
HIDEYUKI TANAKA
OS Homo sapiens (human)
PN WO 0102564-A/3
PD 11-JAN-2001
PF 29-JUN-2000 WO 2000JP004278
PR 30-JUN-1999 JP 99P 186718
PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
PI MOGI,
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/12, C12N5/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC
A61K38/17,
PC A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7088// (C12P21/
CC 02, C12R1:19)
CQ Key Location/Qualifiers.
FT source 1..384
FT /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 99 a 70 c 106 g 109 t
ORIGIN
Alignment Scores:
Pred. No.: 3.97e-63 Length: 384
Score: 602.00 Matches: 111
Percent Similarity: 93.75% Conservative: 9
Best Local Similarity: 86.72% Mismatches: 8
Query Match: 89.05% Indels: 0
DB: Gaps: 0
US-10-019-455A-12 (1-128) x BD093103 (1-384)
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Search completed: December 29, 2003, 19:57:16  
Job time : 2108.98 secs

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 29, 2003, 16:23:14 ; Search time 1324.28 Seconds  
(without alignments)  
2349.180 Million cell updates/sec

Title: US-10-019-455A-12  
Perfect score: 676  
Sequence: 1 MARIILLGLGLVLCAGHG.....RVQEKATKPTTIDDFCE 128

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Ygapop 10.0 , Ygapext 0.5  
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Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: gb\_estfun:\*  
16: em\_eston:\*  
17: em\_gss\_hum:\*  
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20: em\_gss\_vrt:\*  
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27: em\_gss\_vrl:\*  
28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	676	100.0	488	13	BQ564607	BQ564607 gi119h02.y
3	676	100.0	514	13	BQ568498	BQ568498 gi109c02..
4	676	100.0	534	13	BQ564134	BQ564134 gi114d01.y
5	676	100.0	560	13	BQ569741	BQ569741 gi135f01..
6	676	100.0	608	13	BQ564944	BQ564944 gi27909.y
7	676	100.0	630	13	BQ568471	BQ568471 gi108g04..
8	676	100.0	696	10	BB611549	BB611549 BB611549
9	671	99.3	474	13	BQ565637	BQ565637 gi142g03.y
10	669	99.0	684	13	BQ563768	BQ563768 gi106c09.y
11	646	95.6	409	13	BQ566932	BQ566932 gi173g09.y
12	611	90.4	490	13	BQ565411	BQ565411 gi137h12.y
13	585	86.5	365	13	BY232622	BY232622 BY232622
14	539	79.7	604	13	BQ567343	BQ567343 gi188d08.y
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16	447	66.1	280	13	BQ568785	BQ568785 gi114f04..
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38	268	39.6	594	14	CA509768	CA509768 UI-R-FS0-
39	267	39.5	517	10	BE665724	BE665724 154861 MA
40	266.5	39.4	533	14	W74647	W74647 zd77e05..s1
41	266.5	39.4	633	14	CD360404	CD360404 AGENCOURT
42	265.5	39.3	391	9	AI275598	AI275598 qm48a04.x
43	263	38.9	170	13	BQ569268	BQ569268 gi125a12..
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45	263	38.9	442	9	AA282143	AA282143 zt02b05.s

ALIGNMENTS

RESULT 1  
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LOCUS gi143b10.y1 Mouse Organ of Corti cdna pBluescript Mus musculus CDNA  
DEFINITION clone gi143b10 5', mRNA sequence.  
ACCESSION BQ570035  
VERSION BQ570035.1 GI:21473352  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 398)



us-10-019-455a-12.rst

Location/Qualifiers  
1. .488

1. 488

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/strain="BALB/c"
/db_xref="taxon:10090"
/clone="g19h02"
/sex="male and female"
/dev_stage="Post natal day 5 to 13"
/notes="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was clipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fastrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA). according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR GigaPack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on XL Blue MRF+ cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's EXSist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAAGACGTCATGACC) and 25th strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, WA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have know function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."
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83 c 135 q 127 t

BASE COUNT	143
ORIGIN	
Alignment Scores:	
Pred. No.:	
Score:	
Percent Similarity:	

Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	13	Gaps:	0
US-10-019-455A-12 (1-128) x BQ564607 (1-488)			
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Db	67	GTATTTATGATAACTTCTTCTTAAGAGTTGTGTGGGATGAGGAGTGTGTCTATACT	126
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Db	127	ATTTCTCTGGCAAGAGCACAGGAAGATTACAATGCCCCAGACTGTAGGTTCAATCGATGC	186
Qy	61	LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu	80
Db	187	AAGAAAGGGCAGCAGATCTATGTTTACTTCAAGCTGGTAAACAGAAACCGAGGTGGAGAG	246
Qy	81	PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe	100
Db	247	TTTTGGGCTGGCAGTGTTTAAGTGTACCAACAGATGAGATGGGAATTGTAGGTATTTC	306
Qy	101	ProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr	120
Db	307	CCCAGCAACTGGTGAAGGAGCAGCGGTGTATACCAGGAGGCCACCAAGGAGATCCCAACC	366
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<div> <div>BQ568498</div> <div>gi109c02.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA</div> <div>clone gi109c02 5', mRNA sequence.</div> <div>BQ568498.1 GI:21471815</div> <div>EST.</div> <div>Mus musculus (house mouse)</div> <div>Mus musculus</div> <div>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.</div> <div>1 (bases 1 to 514)</div> <div>Kachar, B.</div> <div>EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing</div> <div>Unpublished</div> <div>Contact: Kachar, B.</div> <div>Structural Cell Biology</div> <div>National Institute of Deafness and other Communication Disorders</div> <div>50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA</div> <div>Tel: 301-402-1599</div> <div>Fax: 301-402-1765</div> <div>Email: kacharb@nidcd.nih.gov</div> <div>Plate: 109 row: c column: 02</div> <div>Seq primer: M13RP1 reverse primer (ABI).</div> <div>Location/Qualifiers</div> <div>1. .514</div> <div>/organism="Mus musculus"</div> <div>/mol_type="mRNA"</div> <div>/strain="BALB/c"</div> <div>/db_xref="taxon:10090"</div> <div>/clone="gi109c02"</div> <div>/sex="male and female"</div> <div>/dev_stage="Post natal day 5 to 13"</div> <div>/note="Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 366 OC as follows: 102 samples from post-natal (P) day 5; 72</div> </div>			
<div> <div>FEATURES</div> <div>source</div> </div>			

from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp columns respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XLI Blue MRF<sup>+</sup> cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's EXASist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified.

BASE COUNT 147 a 85 c 143 g 139 t

#### Alignment Scores:

Pred. No.: 2,18e-81 Length: 514  
Score: 676.00 Matches: 128  
Percent Similarity: 100.00% Conservative: 0  
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Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0

US-10-019-455A-12 (1-128) x BQ568498 (1-514)

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DB 65 GTATTTATGGATAAACTTTCTTAAAGAGTTGTGTGGGATGAGGAGTGTCTATACT 124

QY 41 IleSerLeuAlaArgAlaGlnGluAspTyrrAsnAlaProAspCysArgPheIleAspVal 60  
DB 125 ATTTCTCTGGCAAGAGCAGGAGAGATTACAAATGCCAGACTGTAGGTTTCATCGATGTC 184  
QY 61 LysLysGlyGlnGlnIleTyrrValTyrrSerLysLeuValThrGluAsnGlyAlaGlyGlu 80  
DB 185 AAGAAGAGGCGCAGCAGATCTATGTTTACTTCCAAAGCTGGTAACAGAAAACCGAGCTGGAGAG 244  
QY 81 PheTTPAlaGlySerValTyrrGlyAspHisGlnAspGluMetGlyTleValGlyTyrrPhe 100  
DB 245 TTTTGGCTGGCAGGTGTTTATGTCACCAAGGATGAGATGGAAATTGTAGTTATTTC 304  
QY 101 ProSerAsnLeuValLysGluGlnArgValTyrrGlnGlnAlaThrLysGluIleProThr 120  
DB 305 CCCGCAACTTGGTGAAGGAGCAGCGTGTATACCAAGGAGGCCACCAAGGAGATCCCAACC 364  
QY 121 ThrAspIleAspPheCysGlu 128  
DB 365 ACGGATATTGACTTCTTCTGTGAA 388

#### RESULT 4

BQ564134

#### LOCUS

DEFINITION

gillid01.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA

clone gillid01 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished

Contact: Kachar, B.

Structural Cell Biology

National Institute of Deafness and other Communication Disorders

50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA

Tel: 301-402-1599

Fax: 301-402-1765

Email: kachar@nidcd.nih.gov

Plate: 11 row: d column: 01

Seq primer: M13RP1 reverse primer (ABI).

Location/Qualifiers

1. 534

/organism="Mus musculus"

/mol\_type="mRNA"

/strains="BALB/c"

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/clone="gillid01"

/sex="male and female"

/dev\_stage="Post natal day 5 to 13"

/clone\_lib="Mouse Organ of Corti cDNA pBluescript"

/note="Organ of Corti; Vector: pBluescript; The

organ of Corti (OC) was fine dissected from a total of 386

OC as follows: 102 samples from post-natal (P) day 5; 72

from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;

14 from P12 and 24 from P13. After killing animals by

cervical dislocation followed by decapitation, the bulla

was removed and opened in Leibowitz medium. The bony

capsule of the cochlea was chipped away, stria vascularis

and spiral ligament were removed and the sensory

epithelium was carefully dissected out of the modiolus.

Total RNA was extracted using the micro Fasttrack kit

(catalog # K1593-02; Invitrogen, Carlsbad, CA), according

to manufacturer's instructions. Reverse transcription and

library construction were carried out with the Uni-Zap XR

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BASE COUNT 155 a 87 c 148 g 144 t  
ORIGIN

Alignment Scores:  
Prad. No.: 2,3e-81 Length: 534  
Score: 676.00 Matches: 128  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0

US-10-019-455A-12 (1-128) x BQ564134 (1-534)

QY 1 MetAlaArgIleuLeuLeuLeuGlyLeuValValLeuValLeuValLeuGlyHisGly 20  
DB 3 ATGGCAAGGATATTGATCTTTTGTGGGGCCCTGTGTCTATGTCCCGGCATGGT 62  
QY 21 ValPheMetAspLysLeuSerSerLysLysLeuValLeuValLeuValLeuValLeuVal 40  
DB 63 GTATTATGATTAACCTTCTCTAAGAGTTGTGTGGGATGAGAGTGTCTATCT 122  
QY 41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal 60  
DB 123 ATTTCTCTGGCAAGACACAGCAAGATTAACAATGCCCAAGATGTAGGTTCATCATGTC 182  
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlnValAlaGlyGlu 80  
DB 183 AAGAAGGGCAGCAGATCTATGTTTACTCCAGCTGTGTACAGAAAACGGAGCTGAGAG 242  
QY 81 PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100  
DB 243 TTTTGGGCTGGCAGTCTTTATGTGTGACCAACCGAGATGAGATGGGAATGTAGTTATTTC 302

QY 101 ProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120  
DB 303 CCCCAACTTGTGTGAAGGAGCAGCGTGTATATACCGAGAGCCCAAGGAGATCCCAACC 362  
QY 121 ThrAspIleAspPhePheCysGlu 128  
DB 363 ACGGATATTGACTTCTTCTGTGAA 386  
RESULT 5  
LOCUS BQ569741 560 bp mRNA linear EST 19-JUN-2002  
DEFINITION g1135f01.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA  
Clone g1135f01 5', mRNA sequence.  
VERSION BQ569741  
KEYWORDS BQ569741.1 GI:21473058  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Kachar, B.  
EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing  
Unpublished  
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Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kacharbenid@nih.gov  
Plate: 135 row: f column: 01  
Seq primer: M13RPI reverse primer (ABI).  
Location/Qualifiers  
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/dev\_stage="Post natal day 5 to 13"  
/notes="Organ: Mouse Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5-72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA)

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BASE COUNT 160 a 92 c 154 g 153 t 1 others  
ORIGIN

Alignment Scores:  
Pred. No.: 2,478-81 Length: 560  
Score: 676.00 Matches: 128  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0

US-10-019-455A-12 (1-128) x BQ564941 (1-560)

QY 1 MetAlaArgIleLeuIleLeuLeuLeuGlyGlyLeuValValLeuCysAlaGlyHisGly 20  
DB 6 ATGGCAAGGATATTGATCTTTTGGCTTGGGGCCCTTGTTCTATGTCGGGGCATGGT 65  
QY 21 ValPheMetAspLysIleuSerSerLysLysLeuCysAlaAspGluCysValTyrThr 40  
DB 66 GTATTATTGGATAAACTTTCTCTAAGAAGTTGTGTGGGATGAGGAGTGTCTATACT 125  
QY 41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal 60  
DB 126 ATTTCTTGGCAAGACAGCAGAGATTACATGCCCCAGACTGTAGTTTCATCGATGTC 185  
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu 80  
DB 186 AAGAAGGGCAGCAGATCTATCTTTTACTCCAACTGGTAACAGAAAACGAGCTCGAGAG 245  
QY 81 PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100  
DB 246 TTTTGGCTGGCAGGTATTATGGTCACCACCGAGATGAGATGGGAATTTGTAGTTATTTC 305  
QY 101 ProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120  
DB 306 CCCACCACTTGGTGAAGGAGCAGCGTGTATACCGAGAGGCCACCAAGAGATCCCAACC 365  
QY 121 ThrAspIleAspPheCysGlu 128  
DB 366 ACGGATATTGACTTCTCTGTGAA 389

RESULT 6  
LOCUS BQ564944 608 bp mRNA linear EST 19-JUN-2002  
DEFINITION g127g09.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone g127g09 5', mRNA sequence.

ACCESSION BQ564944  
VERSION BQ564944.1 GI:21468261  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS 1 (bases 1 to 608)  
Kachar,B.  
TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing  
JOURNAL Unpublished  
COMMENT Contact: Kachar,B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kachar@nidcd.nih.gov  
Plate: 27 row: g column: 09  
Seq primer: M13RP1 reverse primer (ABI).  
FEATURES  
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/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapak III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp , respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on XL1 Blue MRF<sup>+</sup> cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen,

BQ564944  
BQ564944.1 GI:21468261  
EST.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
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EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing  
Unpublished  
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Tel: 301-402-1599  
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Email: kachar@nidcd.nih.gov  
Plate: 27 row: g column: 09  
Seq primer: M13RP1 reverse primer (ABI).  
FEATURES  
1..608  
Location/Qualifiers  
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/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapak III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp , respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on XL1 Blue MRF<sup>+</sup> cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen,





CONTACT: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Tel: 81-45-503-9216  
Fax: 81-45-503-9216  
Email: genome-res@gsc.riken.go.jp,  
URL: <http://genome.gsc.riken.go.jp/>

Db 144 ATTCTCTGCGACAGCAGGAGATACATGCCCCAGACTGAGGTTTCATGATGTC 203  
 Qy 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu 80  
 Db 204 AAGAAAGGCGAGCAGATCTATGTTACTCAAGCTGGTAACAGAAACGAGCTGGAGAG 263  
 Qy 81 PheTTPAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100  
 Db 264 TTTTGGGCTGGCAGTGTTTATGTCACCAAGGAGATGGGAATTTGATGTTATTTTC 323  
 Qy 101 ProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120  
 Db 324 CCCAGCAACTTGGTGAAGCAGCAGCGTGATACAGGAGGCCACCAAGAGATCCCAACC 383  
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 Db 384 ACGGATATTGACTTCTCTGTGAA 407

RESULT 9  
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 LOCUS  
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 g142903.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA  
 clone g142903 5', mRNA sequence.

ACCESSION  
 B0565637  
 VERSION  
 B0565637.1 GI:21468954  
 KEYWORDS  
 EST.

SOURCE  
 Mus musculus (house mouse)

ORGANISM  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 474)

REFERENCE  
 AUTHORS  
 TITLE  
 Kachar, B.  
 EST analysis of gene expression in the mouse Organ of Corti at the  
 onset of hearing

JOURNAL  
 COMMENT

Unpublished  
 Contact: Kachar, B.  
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 Tel: 301-402-1599  
 Fax: 301-402-1765

Email: kachar@nidcd.nih.gov  
 Plate: 42 row: 9 column: 03  
 Seq primer: M13RPI reverse primer (ABI).

Location/Qualifiers  
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FEATURES  
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 /note="Organ: Organ of Corti; Vector: pBluescript; The  
 organ of Corti (OC) was fine dissected from a total of 386  
 OC as follows: 102 samples from post-natal (P) day 5; 72  
 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;  
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 cervical dislocation followed by decapitation, the bulla  
 was removed and opened in Leibowitz medium. The bony  
 capsule of the cochlea was chipped away, stria vascularis  
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 epithelium was carefully dissected out of the modiolus.  
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 manufacturer's instructions. Briefly: 1.5 ug mRNA was

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 EcoR I adapters in the presence of ligase and digested  
 with Xho I. The cDNA was sequentially size fractionated  
 over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden)  
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 columns to enrich for cDNAs greater than 400bp and 1000 bp  
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 the 5' end of the cDNA clones were generated with the  
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 Biosystems, Foster City, CA). Sequencing reactions were  
 performed on MJ Tetrad thermal cyclers (MJ Research,  
 Waltham, MA), and analyzed on 3700 automated capillary  
 sequencers using POP5 polymer (Applied Biosystems, Foster  
 City, CA). The frequency distribution of the library is  
 as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10;  
 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of  
 genes are present in GenBank and have known function; 23%  
 have hits in GenBank, but do not have assigned function;  
 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 145 a 78 c 131 g 120 t  
 ORIGIN

Alignment Scores:

Pred. No.: 9,27e-81 Length: 474  
 Score: 671.00 Matches: 127  
 Percent Similarity: 99.22% Conservative: 0  
 Best Local Similarity: 99.22% Mismatches: 1  
 Query Match: 99.26% Indels: 0  
 DB: 13 Gaps: 0

US-10-019-455A-12 (1-128) x B0565637 (1-474)

Qy 1 MetAlaArgIleLeuIleLeuLeuLeuGlyGlyLeuValValLeuCysAlaGlyHisGly 20  
 Db 14 ATGGCAGGATATGATCTTTTGGTGGGCGCTTGTTGTTCTATGTCGGGCGATGCT 73  
 Qy 21 ValPheMetAspLysLeuSerLysLysLeuCysAlaAspGluGluCysValTyrThr 40  
 Db 74 GTATTATTGATAAATCTTCTCTTAATAAGTTGTGTGCGGATGAGGAGTGTCTCTACT 133  
 Qy 41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal 60  
 Db 134 ATTTCTTGGCAGACGACGAGGAGATTACATGCCCGAGACTGTAGGTTCTCGATGTC 193  
 Qy 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu 80  
 Db 194 AAGAAAGGCGAGCAGATCTATGTTACTCCAGCTGGTAACAGAAACGAGCTGGAGAG 253  
 Qy 81 PheTTPAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100  
 Db 254 TTTTGGGCTGGCAGTGTTTATGTCACCAAGGAGATGGGAATTTGATGTTATTTTC 313  
 Qy 101 ProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120







064: T

BASE COUNT

US-10-019-455A-12 (1-128) x B0565411 (1-490)

RESULT 13

RY232622

## DEFINITION

## ACCEPTANCE

VERSION

**SOURCE**

## REFERENCE

10









GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 29, 2003, 16:10:49 ; Search time 154.353 Seconds  
(without alignments)  
2238.558 Million cell updates/sec

Title: US-10-019-455A-12

Perfect score: 676

Sequence: 1 MARIILLGLGVLCAGHG.....RVYQEAQKPTTIDIFFCE 128

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5

Ygapop 10.0, Ygapext 0.5

Fgapop 6.0, Fgapext 7.0

Delop 6.0, Delext 7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DRV=xlh  
-O=/cgn2\_1/USPTO.spool/US10019455/runat\_29122003\_160347\_230/app\_query.fasta\_1.1770  
-DB=N\_Geneseq 19Jun03 -QFMT=fasta -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0  
-LOOPT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10019455 @CNG\_1.1.0 @runat\_29122003\_160347\_230 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N\_Geneseq 19Jun03.\*

1: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.\*  
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.\*  
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4: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.\*  
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.\*  
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.\*  
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.\*  
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.\*  
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11: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.\*  
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19: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.\*  
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21: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.\*  
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.\*  
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.\*  
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.\*  
25: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match %	Length	DB	ID	Description
1	676	100.0	384	22	AAF59068	Mouse MLP nucleoti
2	676	100.0	947	22	AAF59084	Mouse MLP nucleoti
3	655	96.9	384	22	AAF59098	Rat MLP nucleotide
4	602	89.1	384	22	AAF59065	Human MLP nucleoti
5	602	89.1	387	24	AAH17583	DNA encoding novel
6	602	89.1	426	22	AAH26341	Human growth regul
7	602	89.1	521	24	ABL95740	Human angiogenesis
8	602	89.1	521	24	ABL88251	Human PRO9873 cDNA
9	602	89.1	521	24	ABK33571	CDNA encoding huma
10	602	89.1	891	22	AAH98228	Human EST-derived
11	602	89.1	891	22	AAH26342	Human growth regul
12	602	89.1	923	22	AAF59083	Human MLP nucleoti
13	602	89.1	1201	22	AAH26343	Human growth regul
14	591	87.4	330	22	AAF59080	Mouse MLP nucleoti
15	574	84.9	330	22	AAF59099	Human MLP nucleoti
16	547	80.9	330	22	AAF59079	Human MLP nucleoti
17	515	76.2	307	22	AAF59093	Rat MLP nucleotide
18	445	65.8	261	22	AAF59092	Rat MLP nucleotide
19	277.5	41.1	459	16	AAQ84050	Sequence encoding
20	277.5	41.1	459	22	AAI70083	Melanoma inhibitor
21	277.5	41.1	459	22	AAI18732	Human antitense ol
22	275.5	40.8	433	22	AAH47783	Recombinant human
23	263	38.9	442	24	ABL63602	Breast cancer rela
24	263	38.9	442	24	ABL64012	Breast cancer rela
25	261.5	38.7	330	16	AAQ84061	Sequence encoding
26	261.5	38.7	555	23	ABV59229	Human prostate exp
27	247	36.5	581	16	AAQ84052	Sequence encoding
28	219.5	32.5	305	16	AAQ84055	Amplified fragment
29	218	32.2	1060	22	AAF92140	Human PRO19670 cDN
30	218	32.2	1060	24	ABT74460	Human cDNA encodin
31	218	32.2	1060	24	ABT95738	Human angiogenesis
32	218	32.2	1060	24	ABL88249	Human angiogenesis
33	218	32.2	1060	25	ACA57963	Human PRO19670 cDN
34	218	32.2	1060	25	ACA58892	CDNA encoding huma
35	218	32.2	1060	25	ACA60445	Novel human secret
36	218	32.2	1060	25	ACA63455	CDNA encoding huma
37	218	32.2	1060	25	ABX98433	Human cDNA encodin
38	218	32.2	1060	25	ABX98935	Novel human secret
39	218	32.2	1060	25	ACA05980	Human secreted/tra
40	218	32.2	1060	25	ABX98024	Human PRO polynucl
41	218	32.2	1060	25	ABX78808	Human PRO polynucl
42	218	32.2	1060	25	ABX75821	Human cDNA encodin
43	218	32.2	1060	25	ABX77026	Human PRO polynucl
44	218	32.2	1060	25	ABX16866	Human cDNA encodin
45	218	32.2	1061	22	AA546205	Human DNA encoding

# ALIGNMENTS

RESULT 1  
AAF59068  
ID AAF59068 standard; DNA; 384 BP.  
XX  
AC AAF59068;  
XX  
DT 23-APR-2001 (first entry)  
XX  
DE Mouse MLP nucleotide sequence SEQ ID NO:10.  
XX

MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
cardiant; gene therapy; secretory cell function regulator; promoter;  
inhibitor; ds.  
XX  
OS Mus musculus.  
XX



191 AAGAAAGGCGCAGAGATCTATGTTACTCCAGCTGGTAACAGAAAACGGAGCTGGAGAG 250  
 81 PheTrpAlaGlySerValTrpGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100  
 251 TTTTGGGCTGGCAGTGTATGCTGACCAACAGGATGAGATGGGAATTTAGGTATTATTC 310  
 101 ProSerAsnLeuValLysGlnArgValTrpGlnGluAlaThrLysGluIleProThr 120  
 311 CCAGCAACTTGGTGAGAGAGCAGGCTGTATACCGAGGAGGCCACCAAGAGATCCCAACC 370

121 ThrAspIleAspPheCysGlu 128  
 371 ACGGATATTGACTTCTCTGTGAA 394

RESULT 3  
 AAF59098  
 ID AAF59098 standard; DNA; 384 BP.  
 AC AAF59098;  
 XX  
 XX  
 DT 23-APR-2001 (first entry)  
 XX  
 DE Rat MLP nucleotide sequence SEQ ID NO:46.  
 XX  
 XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
 XX joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
 XX cardiant; gene therapy; secretory cell function regulator; promoter;  
 XX inhibitor; ds.  
 XX  
 OS Rattus sp.  
 XX  
 XX  
 PN W0200102564-A1.  
 XX  
 XX 11-JAN-2001.  
 XX  
 XX 29-JUN-2000; 2000WO-JP04278.  
 XX  
 XX 30-JUN-1999; 99JP-0186718.  
 XX  
 XX (TAKEDA ) TAKEDA CHEM IND LTD.  
 XX  
 XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
 XX Tanaka H;  
 XX WPI; 2001-159271/16.  
 XX P-PSDB; AAB69130.  
 XX  
 XX Safe, low-toxicity secretory cell function-regulatory protein and  
 XX encoded DNA, applicable as drugs, in diagnosis and development of  
 XX promoters and inhibitors for preventing or treating e.g. bone and joint  
 XX diseases -  
 XX  
 XX Claim 13; Page 105-106; 11lpp; Japanese.  
 XX  
 XX The present invention describes novel MLP proteins and their encoding  
 XX DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
 XX activities, and can be used in gene therapy and as secretory cell  
 XX function regulators. The MLP proteins and DNAs can be used in drugs, in  
 XX the diagnosis and development of promoters and inhibitors for preventing  
 XX or treating bone and joint diseases as well as pathologic angiogenesis.  
 XX AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
 XX in the exemplification of the present invention.  
 XX  
 XX SQ Sequence 384 BP; 98 A; 72 C; 109 G; 105 T; 0 other

Alignment Scores:  
 Pred. No.: 1.64e-81 Length: 384  
 Score: 655.00 Matches: 123  
 Percent Similarity: 98.4% Conservative: 3  
 Best Local Similarity: 96.09% Mismatches: 2  
 Query Match: 96.89% Indels: 0  
 Gaps: 0

US-10-019-455a-12 (1-128) x AAF59098 (1-384)

QY 1 MetAlaArgIleIleuIleLeuLeuLeuGlyGlyLeuValValLeuCysAlaGlyHisGly 20  
 DB 1 ATGGCAAGAAATATATGATCTTTTGTCTGGGGCCCTTGTGGCTCTCTGTGCCGGGTGGC 60  
 QY 21 ValPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValTyrThr 40  
 DB 61 ATGTTTATGGATAAATCTTCTTAAGAAGTTGTGTGCAGATGAGGAGTGTCTATATACC 120  
 QY 41 IleSerIleAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal 60  
 DB 121 ATTTCTCTGGCAAGACACAGGAAGACTACAAATGCCCGGACTGTAGGTTCATCAATATGC 180  
 QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu 80  
 DB 181 AAGAAAGGCGCAGCAGATCTATGTTTATCCAGCTGGTAACAGAAAATGGAGCTGGGCA 240  
 QY 81 PheTrpAlaGlySerValTrpGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100  
 DB 241 TTCTGGGCTGGCAGTGTATGCTGACCAACAGGATGAGATGGGAATTTAGGTATTATTC 300  
 QY 101 ProSerAsnLeuValLysGlnArgValTrpGlnGluAlaThrLysGluIleProThr 120  
 DB 301 CCAGCAACTTGGTGAGAGAGCAGGCTGTATACCGAGGAGGCCACCAAGAGATCCCAACC 360  
 QY 121 ThrAspIleAspPheCysGlu 128  
 DB 361 ACGGATATTGACTTCTCTGTGAA 384

RESULT 4  
 AAF59065  
 ID AAF59065 standard; DNA; 384 BP.  
 XX  
 XX AAF59065;  
 XX  
 DT 23-APR-2001 (first entry)  
 XX  
 DE Human MLP nucleotide sequence SEQ ID NO:4.  
 XX  
 XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
 XX joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
 XX cardiant; gene therapy; secretory cell function regulator; promoter;  
 XX inhibitor; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 XX W0200102564-A1.  
 XX  
 XX 11-JAN-2001.  
 XX  
 XX 29-JUN-2000; 2000WO-JP04278.  
 XX  
 XX 30-JUN-1999; 99JP-0186718.  
 XX  
 XX (TAKEDA ) TAKEDA CHEM IND LTD.  
 XX  
 XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
 XX Tanaka H;  
 XX WPI; 2001-159271/16.  
 XX P-PSDB; AAB69123.  
 XX  
 XX Safe, low-toxicity secretory cell function-regulatory protein and  
 XX encoded DNA, applicable as drugs, in diagnosis and development of  
 XX promoters and inhibitors for preventing or treating e.g. bone and joint  
 XX diseases -  
 XX  
 XX Example 1; Page 91; 11lpp; Japanese.  
 XX  
 XX The present invention describes novel MLP proteins and their encoding  
 XX DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
 XX activities, and can be used in gene therapy and as secretory cell

CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
 CC the diagnosis and development of promoters and inhibitors for preventing  
 CC or treating bone and joint diseases as well as pathologic angiogenesis.  
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
 CC in the exemplification of the present invention.

XX Sequence 384 BP; 99 A; 70 C; 106 G; 109 T; 0 other;

Alignment Scores:  
 Pred. No.: 3,79e-74 Length: 384  
 Score: 602.00 Matches: 111  
 Percent Similarity: 93.75% Conservative: 9  
 Best Local Similarity: 86.72% Mismatches: 8  
 Query Match: 89.05% Indels: 0  
 DB: 22 Gaps: 0

US-10-019-455A-12 (1-128) x AAF59065 (1-384)

Qy 1 MetAlaArgIleLeuLeuLeuLeuLeuGlyGlyLeuValValLeuCysAlaGlyHisGly 20  
 Db 1 ATGGCAAGAATATTGTTACTTTCTCCCGGCTTGTGCTGTATGCTGTGCTGATGGA 60  
 Qy 21 ValPheMetAspLysLeuSerSerLysLeuCysAlaAspGluCysValThr 40  
 Db 61 ATATTATGACCGCTGTAGCTTCAAGAGCTCTGTGCAATGATGATGCTGTATCT 120  
 Qy 41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal 60  
 Db 121 ATTTCTCTGGCTAGTGTCTCAAGAAGATTAATATGCTCCCGAGCTGTAGATTCAACGTT 180  
 Qy 61 LysIleGlyGlnGlnIleValThrValThrSerLysLeuValThrGluAsnGlyAlaGlyGlu 80  
 Db 181 AAAAAAGGGCAGCAGATCTATGTTCTCAAGAGCTGTAAAGAAATGGAGCTGAGAA 240  
 Qy 81 PheTrpAlaGlySerValThrGlyAspHisGlnAspGluMetGlyIleValGlyThrPhe 100  
 Db 241 TTTTGGGCTGGCAGTGTTATGTTGATGGCCAGCAGATGGAGTCTGGGTTATTTC 300  
 Qy 101 ProSerAsnLeuValLysGluGlnArgValThrGluAlaThrLysGluIleProThr 120  
 Db 301 CCCAGGAACTGGTCAAGGACAGCGTGTTGATCCAGAGCTACCAAGGAAGTCCACC 360  
 Qy 121 ThrAspIleAspPheCysGlu 128  
 Db 361 ACGGATATTGACTTCTCTCGAG 384

RESULT 5

AA517583  
 ID AA517583 standard; cDNA; 387 BP.

XX AC AA517583;

XX DT 26-FEB-2002 (first entry)

XX DE DNA encoding novel secreted protein #12.

XX KW Secreted protein; cytostatic; immunosuppressive; vulnary; vaccine;  
 XX KW antiinflammatory; neuroprotective; nephrotropic; cardiovascular;  
 XX KW human cancer; autoimmune disease; wound healing disorder; infection;  
 KW haematopoietic disorder; inflammatory disorder; infertility;  
 KW neurological disease; psychiatric disease; cardiovascular disease;  
 KW respiratory disease; renal; gastrointestinal; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
 XX CDS 1..387  
 FT /\*tag= a  
 FT /product= "Human secreted protein"

XX WO200179454-A1.

XX PD 25-OCT-2001.

XX 11-APR-2001; 2001WO-US11797.  
 XX 13-APR-2000; 2000US-196603P.  
 PR 24-APR-2000; 2000US-199417P.  
 XX (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.

XX Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;  
 FI WPI; 2002-061975/08.  
 XX P-PSDB; AAU09871.

PT New secreted proteins or polypeptides, useful for treating e.g. cancer,  
 PT autoimmune diseases, wound healing disorder, infections, haematopoietic  
 PT disorders, inflammatory disorders, infertility, cancer -

XX Claim 2; Page 44; 92pp; English.

XX The invention relates to an isolated novel secreted polypeptide (I) and  
 CC polynucleotide (II). (I) and (II) are useful for treating cancer,  
 CC autoimmune diseases, wound healing disorder, infections, haematopoietic  
 CC disorders, inflammatory disorders, infertility, neurological and  
 CC psychiatric diseases, cardiovascular diseases, respiratory diseases,  
 CC renal diseases, or gastrointestinal diseases. These may also be used to  
 CC treat diseases, abnormalities and disorders caused by abnormal  
 CC expression, production, function and/or metabolism of the genes, as  
 CC vaccines for inducing immunological response in a mammal, and in  
 CC screening methods for detecting the effect of added compounds on the  
 CC production of mRNA and polypeptide in cells. The polypeptides can be used  
 CC as immunogens to produce antibodies immunospecific for the polypeptides,  
 CC and to identify membrane-bound or soluble receptors. The polynucleotides,  
 CC may be used as diagnostic reagents, in chromosome localisation studies,  
 CC and in tissue expression studies. The present sequence represents the  
 CC coding sequence of novel human secreted protein #12.

XX SQ Sequence 387 BP; 101 A; 70 C; 106 G; 110 T; 0 other;

Alignment Scores:

Pred. No.: 3,83e-74 Length: 387  
 Score: 602.00 Matches: 111  
 Percent Similarity: 93.75% Conservative: 9  
 Best Local Similarity: 86.72% Mismatches: 8  
 Query Match: 89.05% Indels: 0  
 DB: 24 Gaps: 0

US-10-019-455A-12 (1-128) x AA517583 (1-387)

Qy 1 MetAlaArgIleLeuLeuLeuLeuGlyGlyLeuValValLeuCysAlaGlyHisGly 20  
 Db 1 ATGGCAAGAATATTGTTACTTTCTCCCGGCTTGTGCTGTATGCTGTGCTGATGGA 60

Qy 21 ValPheMetAspLysLeuSerSerLysLeuCysAlaAspGluCysValThr 40  
 Db 61 ATATTATGACCGCTGTAGCTTCAAGAGCTCTGTGCAATGATGATGCTGTATCT 120

Qy 41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal 60  
 Db 121 ATTTCTCTGGCTAGTGTCTCAAGAAGATTAATATGCTCCCGAGCTGTAGATTCAACGTT 180

Qy 61 LysIleGlyGlnGlnIleValThrValThrSerLysLeuValThrGluAsnGlyAlaGlyGlu 80  
 Db 181 AAAAAAGGGCAGCAGATCTATGTTGATGGCCAGGACGAGATGGAGTCTGGGTTATTTC 240

Qy 81 PheTrpAlaGlySerValThrGlyAspHisGlnAspGluMetGlyIleValGlyThrPhe 100  
 Db 241 TTTTGGGCTGGCAGTGTTATGTTGATGGCCAGGACGAGATGGAGTCTGGGTTATTTC 300

Qy 101 ProSerAsnLeuValLysGluGlnArgValThrGlnGluAlaThrLysGluIleProThr 120  
 Db 301 CCCAGGAACTGGTCAAGGACAGCGTGTTGATCCAGAGCTACCAAGGAAGTCCACC 360

QY 121 ThrAspIleAspPheCysGlu 128  
 DB 361 ACGGATATTGACTTCTCTGCGAG 384

## RESULT 6

AAH26341  
 ID AAH26341 standard; cDNA; 426 BP.

AC AAH26341;

XX 02-OCT-2001 (first entry)

DE Human growth regulatory-like polypeptide clone 16372272.

KW Growth regulatory-like polypeptide; human; cartilage; melanoma;  
 KW neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;  
 KW ss.

OS Homo sapiens.

XX WO200155332-A2.

XX 02-AUG-2001.

XX 25-JAN-2001; 2001WO-US02455.

XX 25-JAN-2000; 2000US-0491404.

XX 02-MAY-2000; 2000US-0563786.

XX (HYSE-) HYSEQ INC.

XX Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;  
 PI Drmanac RT;

XX MPI; 2001-483233/52.

XX Isolated human growth regulatory-like polypeptide useful for treating  
 PT e.g. Alzheimer's disease, cancer, autoimmune disorders,  
 PT hyperproliferative disorders, coagulation disorders, and nervous system  
 PT disorders -

XX Example 1; Page 114; 119pp; English.

XX The present sequence is that of Hyseq clone identification number  
 CC 16372272, which was obtained from a human thymus cDNA library  
 CC using standard PCR with primers specific for vector sequences  
 CC flanking the inserts, sequencing by hybridisation sequence  
 CC signature analysis, and Sanger sequencing techniques. This  
 CC expressed sequence tag was used in the assembly of a full-length  
 CC cDNA sequence (see AAH26341) encoding a novel human growth  
 CC regulatory-like polypeptide (GRP, see AAH2671). The GRP  
 CC belongs to the same protein family as growth regulatory proteins,  
 CC growth factors, human melanoma derived growth regulatory protein  
 CC precursor (64% similarity and 45% identity over 111 amino acids)  
 CC or melanoma inhibitory activity, cattle cartilage-derived  
 CC retinoic acid sensitive protein (CD-RAP, 44% identity and 64%  
 CC similarity over 126 amino acids) and other retinoic acid-sensitive  
 CC proteins. GRP polypeptides and polynucleotides of the invention  
 CC can be used in the prophylaxis, treatment (including gene therapy)  
 CC and diagnosis of disorders and diseases caused by, or involving,  
 CC cartilage development and maintenance, inhibition of melanoma cell  
 CC growth and tumours, including neuroectodermal tumours such as  
 CC gliomas. The polynucleotides can also be used to design probes  
 CC and primers, for chromosome and gene mapping, in the recombinant  
 CC production of protein, in the generation of antisense, ribozyme and  
 CC peptide-nucleic acid molecules, and to produce transgenic animals.

XX Sequence 426 BP; 119 A; 73 C; 113 G; 120 T; 1 other;

Alignment Scores:

Pred. No.: 4,39e-74 Length: 426  
 Score: 602.00 Matches: 111  
 Percent Similarity: 93.75% Conservative: 9

Best Local Similarity: 86.72% Mismatches: 8  
 Query Match: 89.05% Indels: 0  
 DB: 22 Gaps: 0

US-10-019-455A-12 (1-128) x AAH26341 (1-426)

QY 1 MetAlaAATGileLeuileLeuLeuGlyGlyLeuValValLeuCysAlaGlyHisGly 20  
 DB 19 ATGGCAAGAATATTGTTACTTTCTCCCGGCTCTTGTTGGTGTATGCTGTGCAATGA 78  
 QY 21 ValPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValThr 40  
 DB 79 ATATTATGACCGCTAGCTTCCCAAGAGCTCTGTGCAGATGATGAGTGTGTCTATACT 138  
 QY 41 IleSerLeuAlaAArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal 60  
 DB 139 ATTCTCTGGCTAGTGTCTCAAGAGATTATATGCTCCCGGACTGTAGATTATTACGTT 198  
 QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu 80  
 DB 199 AAAAAAGGCGCAGCAGATCTATGTACTCAAGCTGTGTAAGAAATAATGGAGCTGGAGAA 258  
 QY 81 PheTTPAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100  
 DB 259 TTTTGGCTGGCAGTGTATTATGTTGATGCGCAGCAGATGGGAGTCTGGGTATTTC 318  
 QY 101 ProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120  
 DB 319 CCCAGGAACCTTGGTCAAGGAAACAGCGTGTGTACCAAGGAAGCTACCAAGGAAGTCCCACC 378  
 QY 121 ThrAspIleAspPheCysGlu 128  
 DB 379 ACGGATATTGACTTCTCTGCGAG 402

## RESULT 7

ABL95740

ID ABL95740 standard; cDNA; 521 BP.

XX ABL95740;

XX 19-JUL-2002 (first entry)

XX Human angiogenesis related cDNA PRO9873 SEQ ID NO: 359.

XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
 KW cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;  
 KW antiarteriosclerotic; gene; ss.

XX Homo sapiens.

XX WO200208284-A2.

XX 31-JAN-2002.

XX 09-JUL-2001; 2001WO-US21735.

XX 20-JUL-2000; 2000US-219556P.

XX 25-JUL-2000; 2000US-220624P.

XX 25-JUL-2000; 2000US-220664P.

XX 28-JUL-2000; 2000WO-US20710.

XX 02-AUG-2000; 2000US-222695P.

XX 17-AUG-2000; 2000US-0643657.

XX 23-AUG-2000; 2000WO-US23522.

XX 24-AUG-2000; 2000US-230978P.

XX 15-SEP-2000; 2000US-000000P.

XX 18-SEP-2000; 2000US-0664610.

XX 24-SEP-2000; 2000US-0665350.

XX 24-OCT-2000; 2000US-242922P.

XX 08-NOV-2000; 2000US-0709238.

XX 08-NOV-2000; 2000WO-US30952.

XX 10-NOV-2000; 2000WO-US30873.







```
PS Claim 2; Figure 71; 359pp; English.
XX The invention relates to one hundred and twenty two nucleic acids
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
CC agonists and antagonists are useful for treating a PRO related disorder.
CC The PRO polypeptides are useful for diagnosing tumours, especially lung
CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
CC liver tumour. The PRO polypeptides are useful for stimulating the
CC proliferation of, or gene expression, in pericyte cells, for stimulating
CC the proliferation or differentiation of chondrocyte cells, for
CC stimulating the release of tumour necrosis factor-alpha from human blood,
CC for stimulating or inhibiting the proliferation of normal human dermal
CC fibroblast cells. The PRO polypeptide may also be used as molecular
CC weight markers and for tissue typing. The PRO nucleic acids have
CC applications in molecular biology, including use as hybridisation probes,
CC and in chromosome and gene mapping. ABK33536-ABK33657 represent human
CC PRO protein coding sequences of the invention.
XX
SQ Sequence 521 BP; 167 A; 86 C; 131 G; 137 T; 0 other;

Alignment Scores:
Pred. No.: 5.85e-74 Length: 521
Score: 602.00 Matches: 111
Percent Similarity: 93.75% Conservative: 9
Best Local Similarity: 86.72% Mismatches: 8
Query Match: 89.05% Indels: 0
DB: 24 Gaps: 0

US-10-019-455A-12 (1-128) x ABK33571 (1-521)
QY 1 MetAlaArgIleLeuLeuLeuLeuGlyGlyLeuValValLeuCysAlaGlyHisGly 20
DB 38 ATGGCAAGATATTGTTACTTTCTCCCGGCTCTTGTGGCTGTATGCTGTGCATGGA 97
QY 21 ValPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValThr 40
DB 98 ATATTATGGACCGTCTAGCTTCCAAAGAGCTCTGTGCAGATGATGATGCTGTACT 157
QY 41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal 60
DB 158 ATTCTCTGGCTAGTGTCTCAAGAAGATATTATATGCCCGGAGCTGTAGATTCAATACGTT 217
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu 80
DB 218 AAAAAAGGCGCAGACAGATCTATGTACTCAAAAGCTGTTAAAAAGAAATGGAGCTGAGAA 277
QY 81 PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
DB 278 TTTTGGCTGGCAGGTATTATGGTATGGCCAGGACGAGATGGAGTCTGGGTATTTC 337
QY 101 ProSerAsnLeuValLysGluGlnArgValTyrGlnGlnAlaThrLysGluIleProThr 120
DB 338 CCCAGGAACCTTGGTCAAGGACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTCCACC 397
QY 121 ThrAspIleAspPheCysGlu 128
DB 398 ACGGATATTGACTTCTTCTGCGAG 421

RESULT 10
AAH98228
ID AAH98228 standard; cDNA; 891 BP.
XX
AC AAH98228;
XX
AC AAH98228;
XX
DT 12-OCT-2001 (first entry)
XX
DE Human EST-derived coding sequence SEQ ID NO: 85.
XX
XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder;
KW biodiversity; gene therapy; nutrition; ss.

XX OS Homo sapiens.
XX PN WO200154477-A2.
XX PD 02-AUG-2001.
XX PF 25-JAN-2001; 2001WO-US02687.
XX PR 25-JAN-2000; 2000US-0491404.
XX PR 17-JUL-2000; 2000US-0617746.
XX PR 03-AUG-2000; 2000US-0631451.
XX PR 15-SEP-2000; 2000US-0663870.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX PI
XX DR WPI; 2001-476164/51.
XX DR P-PSDB; AAM23569.
XX PT Isolated polypeptide for treatment of diseases, diagnostics, raising
XX antibodies and research use -
XX PS Claim 1; Page 236; 1275pp; English.
XX
CC The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a cDNA
CC of the invention.
XX
SQ Sequence 891 BP; 272 A; 146 C; 214 G; 259 T; 0 other;

Alignment Scores:
Pred. No.: 1.25e-73 Length: 891
Score: 602.00 Matches: 111
Percent Similarity: 93.75% Conservative: 9
Best Local Similarity: 86.72% Mismatches: 8
Query Match: 89.05% Indels: 0
DB: 22 Gaps: 0

US-10-019-455A-12 (1-128) x AAH98228 (1-891)
QY 1 MetAlaArgIleLeuLeuLeuLeuGlyGlyLeuValValLeuCysAlaGlyHisGly 20
DB 19 ATGGCAAGATATTGTTACTTTCTCCCGGCTCTTGTGGCTGTATGCTGTGCATGGA 78
QY 21 ValPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValThr 40
DB 79 ATATTATGGACCGTCTAGCTTCCAAAGAGCTCTGTGCAGATGATGATGCTGTACT 138
QY 41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal 60
DB 139 ATTTCTTGGCTAGTGTCTCAAGAAGATATTATATGCCCGGAGCTGTAGATTCAATACGTT 198
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu 80
DB 199 AAAAAAGGCGCAGACAGATCTATGTACTCAAAAGCTGTTAAAAAGAAATGGAGCTGAGAA 258
QY 81 PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
DB 259 TTTTGGCTGGCAGGTATTATGGTATGGCCAGGACGAGATGGAGTCTGGGTATTTC 318
QY 101 ProSerAsnLeuValLysGluGlnArgValTyrGlnGlnAlaThrLysGluIleProThr 120
DB 319 CCCAGGAACCTTGGTCAAGGACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTCCACC 378
QY 121 ThrAspIleAspPheCysGlu 128
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[illegible]



Tue Dec 30 10:20:37 2003

Db 93 ATATTTATGACCGCTCTAGCTTCCAGAGAGCTCTGTGCAGATGATGATGTGTCTACT 152  
Qy 41 lIeSerleuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal 60  
Db 153 ATTTCCTCGCTAGTCTCAGAGATATTAATGCGCCGACTGTAGATTCATTAAGTT 212  
Qy 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAenGlyAlaGlyGlu 80  
Db 213 AAAAAAGGCGAGAGATCTATGTCTCAAGCTGGTAAAGAAATGGAGCTGGAGAA 272  
Qy 81 PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100  
Db 273 TTTTGGGCTGCGAGTGTATGCTGATGGCGAGACGAGATGGAGTGGGATGCTGTTATTC 332  
Qy 101 ProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120  
Db 333 CCCAGGAACTTGGTCAAGGAACACGGTGTGTACCAAGAGTACCAGGAAGTCCCAACC 392  
Qy 121 ThrAspIleAspPheCysGlu 128  
Db 393 ACGGATATTGACTTCTTCGCGAG 416  
RESULT 14  
ID AAF59080 standard; DNA; 330 BP.  
XX AAF59080;  
XX AC AAF59080;  
XX DT 23-APR-2001 (first entry)  
XX DE Mouse MLP nucleotide sequence SEQ ID NO:25.  
XX KW MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
XX KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
XX KW cardiant; gene therapy; secretory cell function regulator; promoter;  
XX KW inhibitor; ds.  
XX OS Mus musculus.  
XX PN WO200102564-A1.  
XX PD 11-JAN-2001.  
XX PF 29-JUN-2000; 2000WO-JP04278.  
XX PR 30-JUN-1999; 99JP-0186718.  
XX PA (TAKE ) TAKEDA CHEM IND LTD.  
XX PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
XX PI Tanaka H;  
XX DR WPI; 2001-159271/16.  
XX DR P-PSDB; AAB69127.  
XX PT Safe, low-toxicity secretory cell function-regulatory protein and  
XX PT encoded DNA, applicable as drugs, in diagnosis and development of  
XX PT promoters and inhibitors for preventing or treating e.g. bone and joint  
XX PT diseases -  
XX PS Claim 10; Page 98; 111pp; Japanese.  
XX CC The present invention describes novel MLP proteins and their encoding  
XX CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
XX CC activities, and can be used in gene therapy and as secretory cell  
XX CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
XX CC the diagnosis and development of promoters and inhibitors for preventing  
XX CC or treating bone and joint diseases as well as pathologic angiogenesis.  
XX CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
XX CC in the exemplification of the present invention.  
XX SQ Sequence 330 BP; 91 A; 60 C; 92 G; 87 T; 0 other;

Alignment Scores: 1.03e-72 Length: 330  
Pred. No.: 591.00 Matches: 110  
Score: 591.00 Conservatives: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 87.43% Gaps: 0  
DB: 22  
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Qy 19 HisGlyValPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysVal 38  
Db 1 CATGGTGTATTTATGGATAAACITTTCTTAAGAAGTTGTGCGGATGAGGAGTGTCTC 60  
Qy 39 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 58  
Db 61 TATACTATTTCTTCGCAAGAGCACAGCAAGATTACAAATGCCCAGACTGTAGGTTCATC 120  
Qy 59 AspValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 78  
Db 121 GATGTCAGAAAGGCGACAGATCTATGTTTCTCCAGCTGCTTAACAGAAACGAGCT 180  
Qy 79 GlyGluPheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 98  
Db 181 GGAGAGTTTGGGCTGGCAGTGTATGTTGTCACCCAGGATGAGATGGGAATTGTAGGT 240  
Qy 99 TyrPheProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIle 118  
Db 241 TATTTCCCAACAACCTTGGTGAAGGAGCAGCGTGTATACCAGGAGGCCCAAGAGATC 300  
Qy 119 ProThrThrAspIleAspPheCysGlu 128  
Db 301 CCAACCAAGGATATGACTTCTTCGTGAA 330  
RESULT 15  
ID AAF59099 standard; DNA; 330 BP.  
XX AAF59099  
XX AC AAF59099;  
XX DT 23-APR-2001 (first entry)  
XX DE Rat MLP nucleotide sequence SEQ ID NO:48.  
XX KW MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
XX KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
XX KW cardiant; gene therapy; secretory cell function regulator; promoter;  
XX KW inhibitor; ds.  
XX OS Rattus sp.  
XX PN WO200102564-A1.  
XX PD 11-JAN-2001.  
XX PF 29-JUN-2000; 2000WO-JP04278.  
XX PR 30-JUN-1999; 99JP-0186718.  
XX PA (TAKE ) TAKEDA CHEM IND LTD.  
XX PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
XX PI Tanaka H;  
XX DR WPI; 2001-159271/16.  
XX DR P-PSDB; AAB69131.  
XX PT Safe, low-toxicity secretory cell function-regulatory protein and  
XX PT encoded DNA, applicable as drugs, in diagnosis and development of  
XX PT promoters and inhibitors for preventing or treating e.g. bone and joint  
XX PT diseases -  
XX PS Claim 12; Page 107; 111pp; Japanese.

XX

The present invention describes novel MLP proteins and their encoding DNAs. The MLP proteins and DNAs have antiinflammatory and cardiac activities, and can be used in gene therapy and as secretory cell function regulators. The MLP proteins and DNAs can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing or treating bone and joint diseases as well as pathologic angiogenesis. CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used in the exemplification of the present invention.

XX SQ Sequence 330 BP; 91 A; 62 C; 91 G; 86 T; 0 other;

## Alignment Scores:

Pred. No.:	2,37e-70	Length:	330
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Best Local Similarity:	96.36%	Mismatches:	1
Query Match:	84.91%	Indels:	0
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Qy	39	TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle	58
Db	61	TATACCAATTTCTCTGGCAAGAGCACAGGAAGACTACATGCCCCGGACTGTAGGTTTCATC	120
Qy	59	AspValIysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla	78
Db	121	AATGTCAGAAAGAGGCGAGCATCTATGTTTATTCCAAGCTGGTAAACAGAAATGGAGCT	180
Qy	79	GlyGluPheThrAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly	98
Db	181	GGGGCATTCCTGGGCTGGCACTGTTTATGGTGACCAACAGATGAGATGGGAATTTGGGCT	240
Qy	99	TyrPheProSerAsnLeuValLysGluGlnArgValTyrGlnGluIleThrLysGluIle	118
Db	241	TATTTCCCAAGCAACTGGTTAGAGAGCAACGAGTGTACAGAGGGCCCAAGAGGATT	300
Qy	119	ProThrThrAspIleAspPhePheCysGlu	128
Db	301	CCAACCAACGGATATTGACTTCTTCTGTGAA	330

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Job time : 161.353 secs



GenCore version 5.1.6  
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Run on: December 29, 2003, 19:57:30 ; Search time 287.193 Seconds  
(without alignments)  
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Title: US-10-019-455a-12

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2244575 seqs, 1713117285 residues

Total number of hits satisfying chosen parameters: 4489150

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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No.	Score	Query	Length	ID	Description

ALIGNMENTS

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; Publication No. US20030124573A1  
; GENERAL INFORMATION:  
; APPLICANT: Mize, Nancy K  
; APPLICANT: Boyle, Bryan J  
; APPLICANT: Ford, John E  
; APPLICANT: Atterburn, Matthew C  
; APPLICANT: Tang, Y Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Drmanac, Radoje T  
; APPLICANT: Song, Yong  
; APPLICANT: Sjaastad, Michael  
; TITLE OF INVENTION: Methods and Materials Relating to No. US20030124573A1e1 Growth R  
; TITLE OF INVENTION: Polypeptides and Polynucleotides  
; FILE REFERENCE: HVS-7CIP  
; CURRENT APPLICATION NUMBER: US/10/216,038  
; CURRENT FILING DATE: 2002-08-08  
; PRIOR APPLICATION NUMBER: US 09/563,786  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: US 09/491,404  
; PRIOR FILING DATE: 2000-01-25  
; NUMBER OF SEQ ID NOS: 8

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12	602	89.1	521	13	US-10-219-483-71	Sequence 71, Appl
13	602	89.1	521	13	US-10-219-525-71	Sequence 71, Appl
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25	602	89.1	521	15	US-10-230-338-71	Sequence 71, Appl
26	602	89.1	521	15	US-10-218-631-71	Sequence 71, Appl
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32	602	89.1	521	15	US-10-219-076-71	Sequence 71, Appl
33	602	89.1	521	15	US-10-230-434-71	Sequence 71, Appl
34	602	89.1	521	15	US-10-219-075-71	Sequence 71, Appl
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36	602	89.1	521	15	US-10-219-466-71	Sequence 71, Appl
37	602	89.1	521	15	US-10-219-479-71	Sequence 71, Appl
38	602	89.1	521	15	US-10-219-481-71	Sequence 71, Appl
39	602	89.1	521	15	US-10-230-260-71	Sequence 71, Appl
40	602	89.1	521	15	US-10-232-231-71	Sequence 71, Appl
41	602	89.1	521	15	US-10-232-233-71	Sequence 71, Appl
42	602	89.1	521	15	US-10-216-163-71	Sequence 71, Appl
43	602	89.1	521	15	US-10-218-956-71	Sequence 71, Appl
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 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (426)..(426)  
 ; OTHER INFORMATION: n = A, T, G, or C  
 US-10-216-038-1

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 Query Match: 89.05% Indels: 0  
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US-10-019-455A-12 (1-128) x US-10-216-038-1 (1-426)

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 DB 139 ATTTCTCTGGCTAGTGTCTCAAGAAATATTATATGCCCGGAGCTGTAGATTCAATTAACGTT 198  
 QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyValAlaGlyGlu 80  
 DB 199 AAAAAAGGCGCAGCAGATCTATGTGTACTCAAGCTGGTAAAAAGAAATGGAGCTGGAGAA 258  
 QY 81 PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyThrPhe 100  
 DB 259 TTTTGGCTGGCAGGTATTATGGTGTATGGCAGGACGAGATGGAGTCTGGGTATTATTC 318  
 QY 101 ProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120  
 DB 319 CCCAGGAACCTTGGTCAAGACAGCGTGTATCCAGGAGTACCAGGAGATGCCAGG 378  
 QY 121 ThrAspIleAspPheCysGlu 128  
 DB 379 ACGGATATTGACTTCTTCTCGCAG 402

# RESULT 2

US-10-216-163-71  
 ; Sequence 71, Application US/10216163  
 ; Publication No. US20030149239A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Gerritsen, Mary  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Goddard, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stephan, Jean-Philippe F.  
 ; APPLICANT: Watanabe, Colin L.  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
 ; FILE REFERENCE: P3530PIC3  
 ; CURRENT APPLICATION NUMBER: US/10/216,163  
 ; CURRENT FILING DATE: 2002-08-09  
 ; PRIOR APPLICATION NUMBER: 10/119,480  
 ; PRIOR FILING DATE: 2002-04-09  
 ; PRIOR APPLICATION NUMBER: 60/059113

; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/062287  
 ; PRIOR FILING DATE: 1997-10-17  
 ; PRIOR APPLICATION NUMBER: 60/063549  
 ; PRIOR FILING DATE: 1997-10-28  
 ; PRIOR APPLICATION NUMBER: 60/064103  
 ; PRIOR FILING DATE: 1997-10-31  
 ; PRIOR APPLICATION NUMBER: 60/069873  
 ; PRIOR FILING DATE: 1997-12-17  
 ; PRIOR APPLICATION NUMBER: 60/078910  
 ; PRIOR FILING DATE: 1998-03-20  
 ; PRIOR APPLICATION NUMBER: 60/079294  
 ; PRIOR FILING DATE: 1998-03-25  
 ; PRIOR APPLICATION NUMBER: 60/079656  
 ; PRIOR FILING DATE: 1998-03-26  
 ; PRIOR APPLICATION NUMBER: 60/079728  
 ; PRIOR FILING DATE: 1998-03-27  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 246  
 ; SEQ ID NO 71  
 ; LENGTH: 521  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 US-10-216-163-71

Alignment Scores:  
 Pred. No.: 3.11e-83 Length: 521  
 Score: 602.00 Matches: 111  
 Percent Similarity: 93.75% Conservative: 9  
 Best Local Similarity: 86.72% Mismatches: 8  
 Query Match: 89.05% Indels: 0  
 DB: 13 Gaps: 0

US-10-019-455A-12 (1-128) x US-10-216-163-71 (1-521)

QY 1 MetAlaArgIleLeuIleLeuLeuGlyGlyLeuValValLeuCysAlaGlyHisGly 20  
 DB 38 ATGGCAAGAAATATTGTTACTTTCTCCCGGCTCTGTGGCTGTATGCTGTGCATGGA 97  
 QY 21 ValPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValThr 40  
 DB 98 ATATTATTGACCGCTAGCTTCCCAAGAAAGCTCTGTGCAGATGATGATGTCTATACT 157  
 QY 41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal 60  
 DB 158 ATTTCTCTGGCTAGTGTCTCAAGAAATATTATATGCCCGGAGCTGTAGATTCAATTAACGTT 217  
 QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyValAlaGlyGlu 80  
 DB 218 AAAAAAGGCGCAGCAGATCTATGTGTACTCAAGCTGGTAAAAAGAAATGGAGCTGGAGAA 277  
 QY 81 PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyThrPhe 100  
 DB 278 TTTTGGCTGGCAGGTATTATGGTGTATGGCAGGACGAGATGGAGTCTGGGTATTATTC 337  
 QY 101 ProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120  
 DB 338 CCCAGGAACCTTGGTCAAGACAGCGTGTATCCAGGAGTACCAGGAGATGCCAGG 397  
 QY 121 ThrAspIleAspPheCysGlu 128  
 DB 398 ACGGATATTGACTTCTTCTCGCAG 421

# RESULT 3

US-10-218-765-71  
 ; Sequence 71, Application US/10218765  
 ; Publication No. US20030187201A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Gerritsen, Mary  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3530P1C19  
CURRENT APPLICATION NUMBER: US/10/218,765  
CURRENT FILING DATE: 2002-08-12  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/081819  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081955  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/082804  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/084441  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/085323  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/086392  
PRIOR FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 60/089532  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089538  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089905  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/090472  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090557  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090691  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090695  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/095302  
PRIOR FILING DATE: 1998-08-04  
PRIOR APPLICATION NUMBER: 60/095318  
PRIOR FILING DATE: 1998-08-04  
PRIOR APPLICATION NUMBER: 60/095916  
PRIOR FILING DATE: 1998-08-10  
PRIOR APPLICATION NUMBER: 60/096146  
PRIOR FILING DATE: 1998-08-11  
PRIOR APPLICATION NUMBER: 60/096791  
PRIOR FILING DATE: 1998-08-17  
PRIOR APPLICATION NUMBER: 60/097986  
PRIOR FILING DATE: 1998-08-26  
PRIOR APPLICATION NUMBER: 60/098544  
PRIOR FILING DATE: 1998-08-31  
PRIOR APPLICATION NUMBER: 60/099596  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099598  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099803  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099811  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099812  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099816  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/100038  
PRIOR FILING DATE: 1998-09-11  
PRIOR APPLICATION NUMBER: 60/100385  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100390  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100627  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100848  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/100919  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/101477  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101738  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101741  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101786  
PRIOR FILING DATE: 1998-09-25  
PRIOR APPLICATION NUMBER: 60/101916  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101922  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/106178  
PRIOR FILING DATE: 1998-10-28  
PRIOR APPLICATION NUMBER: 60/106248  
PRIOR FILING DATE: 1998-10-29  
PRIOR APPLICATION NUMBER: 60/106464  
PRIOR FILING DATE: 1998-10-30  
PRIOR APPLICATION NUMBER: 60/106905  
PRIOR FILING DATE: 1998-11-03  
PRIOR APPLICATION NUMBER: 60/108787  
PRIOR FILING DATE: 1998-11-17  
PRIOR APPLICATION NUMBER: 60/108801  
PRIOR FILING DATE: 1998-11-17  
PRIOR APPLICATION NUMBER: 60/108849  
PRIOR FILING DATE: 1998-11-18  
PRIOR APPLICATION NUMBER: 60/112422  
PRIOR FILING DATE: 1998-12-15  
PRIOR APPLICATION NUMBER: 60/113296  
PRIOR FILING DATE: 1998-12-22  
PRIOR APPLICATION NUMBER: 60/113605  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: 60/113621  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: 60/115558  
PRIOR FILING DATE: 1999-01-12  
PRIOR APPLICATION NUMBER: 60/115565  
PRIOR FILING DATE: 1999-01-12  
PRIOR APPLICATION NUMBER: 60/115733  
PRIOR FILING DATE: 1999-01-12  
PRIOR APPLICATION NUMBER: 60/119549  
PRIOR FILING DATE: 1999-02-10  
PRIOR APPLICATION NUMBER: 60/123618  
PRIOR FILING DATE: 1999-03-10  
PRIOR APPLICATION NUMBER: 60/125259  
PRIOR FILING DATE: 1999-03-19  
PRIOR APPLICATION NUMBER: 60/125775

```

QY      81 PheTpaLaGlySerValTYrGLyAspHisGlnAspGluMetGlyIleValGlyTYrPhe 100
Db      278 TTTTGCGCTGCAGGTGGATGTTATGGTGATGCCAGACGAGATGGAGTCGTGGGTATTTC 337

QY     101 ProSerAnLeuVAllysGluInAtqValTYrClnGlulaThrlLysGluIleProThr 120
Db     338 CCCAGGAACAATTGGTCAGGAACACGCGTGTACTCCAGGAAGCTACCRAAGAGAgtTCCCacc 397

QY    121 ThrAspileAaspPhcCysGlu 128
Db   398 ACGGATAATTgacttcttcTTCGGAG 421


RESULT 4
US-10-219--063-71
; Sequence 71, Application US/10219063
; Publication No. US20030187202A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Garney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC24
; CURRENT APPLICATION NUMBER: US/10/219_063
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119_480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-219-063-71


Alignment Scores:
Pred. No.:          3,11E+83             Length:           521
Score:              602.00               Matches:         111
Percent Similarity: 93.75%                Conservative:       9
Best Local Similarity: 86.72%            Mismatches:        8
Query Match:       89.05%                 Indels:           0
DB:                  13                   Gaps:             0


US-10-019-455A-12 (1-128) x US-10-219-063-71 (1-521)
QY      1 MetalaArglieLeulleLeuLeuLeuGlyLeuValLeuCysalaGlyHISgly 120
```

[illegible]



```
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-067-71

Alignment Scores:
Pred. No.: 3,11e-83 Length: 521
Score: 602.00 Matches: 111
Percent Similarity: 93.75% Conservative: 9
Best Local Similarity: 86.72% Mismatches: 8
Query Match: 89.05% Indels: 0
DB: 13 Gaps: 0

US-10-019-455a-12 (1-128) x US-10-219-067-71 (1-521)
QY 1 MetAlaArgIleLeuLeuLeuGlyGlyLeuValValLeuCysAlaGlyHisGly 20
Db 38 ATGGCAAGATATTTCTCTCCCGGCTCTTGGCTGTATGCTGTCATGGA 97
QY 21 ValPheMetAspLysLeuSerSerLysLeuCysAlaAspGluGluCysValThr 40
Db 98 ATATTTATGGACCGTCTAGCTTCCAAAGAGCTCTGTGCAGATGATGATGCTATACT 157
QY 41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal 60
Db 158 ATTTCTCTGGCTAGTCTCAAGAGNTATATATGCCCCGACTGTAGATTCATTAACGTT 217
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu 80
Db 218 AAAAAAGGCGCAGCAGATCTATGTGTACTCAAGAGTAAAGAGAAATGGAGCTGGAGAA 277
QY 81 PheTyrAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyThrPhe 100
Db 278 TTTTGGCTGGCAGTGTATTTATGGTATGCCAGGACGAGATGGAGTGGTGGTATTTTC 337
QY 101 ProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120
Db 338 CCCAGGAACCTTGGTCAAGGAACAGCGGTGTGTACCAAGAGCTACCAAGGAAGTCCCAACC 397
QY 121 ThrAspIleAspPheCysGlu 128
Db 398 ACGGATATTGACTTCTTCTGCGAG 421

RESULT 7
US-10-219-068-71
; Sequence 71, Application US/10219068
; Publication No. US20030187205A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P35530PIC31
```

```
; CURRENT APPLICATION NUMBER: US/10/219,068
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-068-71

Alignment Scores:
Pred. No.: 3,11e-83 Length: 521
Score: 602.00 Matches: 111
Percent Similarity: 93.75% Conservative: 9
Best Local Similarity: 86.72% Mismatches: 8
Query Match: 89.05% Indels: 0
DB: 13 Gaps: 0

US-10-019-455a-12 (1-128) x US-10-219-068-71 (1-521)
QY 1 MetAlaArgIleLeuLeuLeuGlyGlyLeuValValLeuCysAlaGlyHisGly 20
Db 38 ATGGCAAGATATTTCTCTCCCGGCTCTTGGCTGTATGCTGTCATGGA 97
QY 21 ValPheMetAspLysLeuSerSerLysLeuCysAlaAspGluGluCysValThr 40
Db 98 ATATTTATGGACCGTCTAGCTTCCAAAGAGCTCTGTGCAGATGATGATGCTATACT 157
QY 41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal 60
Db 158 ATTTCTCTGGCTAGTCTCAAGAGNTATATATGCCCCGACTGTAGATTCATTAACGTT 217
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu 80
Db 218 AAAAAAGGCGCAGCAGATCTATGTGTACTCAAGAGTAAAGAGAAATGGAGCTGGAGAA 277
QY 81 PheTyrAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyThrPhe 100
Db 278 TTTTGGCTGGCAGTGTATTTATGGTATGCCAGGACGAGATGGAGTGGTGGTATTTTC 337
QY 101 ProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120
Db 338 CCCAGGAACCTTGGTCAAGGAACAGCGGTGTGTACCAAGAGCTACCAAGGAAGTCCCAACC 397
QY 121 ThrAspIleAspPheCysGlu 128
Db 398 ACGGATATTGACTTCTTCTGCGAG 421

RESULT 8
US-10-219-069-71
; Sequence 71, Application US/10219069
; Publication No. US20030187206A1
; GENERAL INFORMATION:
```





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Db 98 ATATTATGACCGTCTAGCTTCAAGAAAGCTCTGTGCAGATGATGAGTGCTATACT 157
Qy 41 IleserLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal 60
Db 158 ATTTCTCTGGCTAGTGTCTCAAGAAGATTATTAATGCCCGGAGCTGTAGATTCAATTAACGTT 217
Qy 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu 80
Db 218 AAAAAAGGCGCAGCAGATCTATGTGTACTCAAAAGCTGTGTAAGAAATGGAGCTGGAGAA 277
Qy 81 PheTyrAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
Db 278 TTTTGGCTGCGAGTGTATGTTGATGATGCCAGAGATGGAGTCTGGGTATTTC 337
Qy 101 ProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120
Db 338 CCCAGGAACCTTGGTCAAGGAACACGCTGTGTACCAAGGAGCTACCAAGGAAGTCCCAACC 397
Qy 121 ThrAspIleAspPheCysGlu 128
Db 398 ACGGATATTGACTTCTCTGGGAG 421

```

## RESULT 10

```

US-10-219-475-71
; Sequence 71, Application US/10219475
; Publication No. US20030187208A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

```

```

; FILE OF INVENTION: ACIDS ENCODING THE SAME

```

```

; FILE REFERENCE: P3530PIC49

```

```

; CURRENT FILING DATE: 2002-08-13

```

```

; PRIOR FILING DATE: 2002-04-09

```

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; PRIOR FILING DATE: 1997-10-31

```

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; PRIOR FILING DATE: 1997-09-17

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; PRIOR FILING DATE: 1997-10-17

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; PRIOR FILING DATE: 1997-10-28

```

```

; PRIOR FILING DATE: 1997-10-31

```

```

; PRIOR FILING DATE: 1997-12-17

```

```

; PRIOR FILING DATE: 1998-03-20

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```

; PRIOR FILING DATE: 1998-03-25

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; PRIOR FILING DATE: 1998-03-26

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```

; PRIOR FILING DATE: 1998-03-27

```

```

; PRIOR FILING DATE: 1998-03-27

```

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; Remaining Prior Application data removed - See File Wrapper or PALM.

```

```

; NUMBER OF SEQ ID NOS: 246

```

```

; SEQ ID NO 71

```

```

; TYPE: DNA

```

```

; LENGTH: 521

```

```

; ORGANISM: Homo Sapien

```

```

US-10-219-475-71

```

```

Alignment Scores:

```

```

Pred. No.: 3,11e-83 Length: 521
Score: 602.00 Matches: 111
Percent Similarity: 93.75% Conservative: 9
Best Local Similarity: 86.72% Mismatches: 8
Query Match: 89.05% Indels: 0
DB: 13 Gaps: 0

```

```

US-10-019-455A-12 (1-128) x US-10-219-475-71 (1-521)

```

```

Qy 1 MetAlaArgIleLeuIleLeuLeuLeuGlyGlyLeuValValLeuCysAlaGlyHisGly 20
Db 38 ATGGCAAGAAATATGTTTCTTCTCCCGGCTCTGTGGCTGTATGCTGTGCTGATGGA 97
Qy 21 ValPheMetAspLysLeuSerLysLysLeuCysAlaAspGluGluCysValTyrThr 40
Db 98 ATATTATGGACCGTCTAGCTTCCAAAGAAGCTCTGTGCAGATGATGAGTGTCTATACT 157
Qy 41 IleserLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal 60
Db 158 ATTTCTCTGGCTAGTGTCTCAAGAAGATTATTAATGCCCGGAGCTGTAGATTCAATTAACGTT 217
Qy 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu 80
Db 218 AAAAAAGGCGCAGCAGATCTATGTGTACTCAAAAGCTGTGTAAGAAATGGAGCTGGAGAA 277
Qy 81 PheTyrAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
Db 278 TTTTGGCTGCGAGTGTATGTTGATGATGCCAGAGATGGAGTCTGGGTATTTC 337
Qy 101 ProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120
Db 338 CCCAGGAACCTTGGTCAAGGAACACGCTGTGTACCAAGGAGCTACCAAGGAAGTCCCAACC 397
Qy 121 ThrAspIleAspPheCysGlu 128
Db 398 ACGGATATTGACTTCTCTGGGAG 421

```

## RESULT 11

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US-10-219-480-71

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; Sequence 71, Application US/10219480

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; Publication No. US20030187209A1

```

```

; GENERAL INFORMATION:

```

```

; APPLICANT: Baker, Kevin P.

```

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; APPLICANT: Desnoyers, Luc

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; APPLICANT: Gerritsen, Mary

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; APPLICANT: Goddard, Audrey

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; APPLICANT: Godowski, Paul J.

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; APPLICANT: Grimaldi, J. Christopher

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; APPLICANT: Gurney, Austin L.

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; APPLICANT: Smith, Victoria

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; APPLICANT: Stephan, Jean-Philippe F.

```

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; APPLICANT: Watanabe, Colin L.

```

```

; APPLICANT: Wood, William I.

```

```

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

```

```

; FILE OF INVENTION: ACIDS ENCODING THE SAME

```

```

; FILE REFERENCE: P3530PIC38

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; CURRENT FILING DATE: 2002-08-13

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; PRIOR FILING DATE: 2002-08-13

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; PRIOR FILING DATE: 2002-04-09

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```

; PRIOR FILING DATE: 1997-09-17

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; PRIOR FILING DATE: 1997-09-17

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; PRIOR FILING DATE: 1997-10-17

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; PRIOR FILING DATE: 1997-10-17

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; PRIOR FILING DATE: 1997-10-28

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; PRIOR FILING DATE: 1997-10-31

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; PRIOR FILING DATE: 1997-10-31

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; PRIOR FILING DATE: 1997-12-17

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; PRIOR FILING DATE: 1997-12-17

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; PRIOR FILING DATE: 1998-03-20

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; PRIOR FILING DATE: 2002-08-13

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; PRIOR FILING DATE: 2002-08-13

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; PRIOR FILING DATE: 2002-08-13

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; PRIOR FILING DATE: 2002-08-13

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; PRIOR FILING DATE: 2002-08-13

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; PRIOR FILING DATE: 2002-08-13

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; PRIOR FILING DATE: 2002-08-13

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; PRIOR FILING DATE: 2002-08-13

```

```

; PRIOR FILING DATE: 2002-08-13

```



	Db	338	CCAGGAACTTGGTCAAGGAACAGCGTGTTGTATCACGGAAGCTACCAAGGAGTTGCCACC	397
	Qy	121	ThrAspIleAaspPheCysGlu	128
	Db	398	ACGGATAATTGACTTCTTCGCGAG	421
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	US-10-219-526-71			
	; Sequence 71, Application US/10219526			
	; Publication No. US20030187212A1			
	; GENERAL INFORMATION:			
	; APPLICANT: Baker, Kevin P.			
	; APPLICANT: Desnoyers, Luc			
	; APPLICANT: Gerritsen, Mary			
	; APPLICANT: Goddard, Audrey			
	; APPLICANT: Godowski, Paul J.			
	; APPLICANT: Grimaldi, J. Christopher			
	; APPLICANT: Gurney, Austin L.			
	; APPLICANT: Smith, Victoria			
	; APPLICANT: Stephan, Jean-Philippe F.			
	; APPLICANT: Watanabe, Colin L.			
	; APPLICANT: Wood, William I.			
	; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC			
	; FILE REFERENCE: P3530P1C41			
	; CURRENT APPLICATION NUMBER: US/10/219,526			
	; CURRENT FILING DATE: 2002-08-13			
	; PRIOR APPLICATION NUMBER: 10/119,480			
	; PRIOR FILING DATE: 2002-04-09			
	; PRIOR APPLICATION NUMBER: 60/059113			
	; PRIOR FILING DATE: 1997-09-17			
	; PRIOR APPLICATION NUMBER: 60/062287			
	; PRIOR FILING DATE: 1997-10-17			
	; PRIOR APPLICATION NUMBER: 60/063549			
	; PRIOR FILING DATE: 1997-10-28			
	; PRIOR APPLICATION NUMBER: 60/064103			
	; PRIOR FILING DATE: 1997-10-31			
	; PRIOR APPLICATION NUMBER: 60/069873			
	; PRIOR FILING DATE: 1997-12-17			
	; PRIOR APPLICATION NUMBER: 60/078910			
	; PRIOR FILING DATE: 1998-03-20			
	; PRIOR APPLICATION NUMBER: 60/079294			
	; PRIOR FILING DATE: 1998-03-25			
	; PRIOR APPLICATION NUMBER: 60/079656			
	; PRIOR FILING DATE: 1998-03-26			
	; PRIOR APPLICATION NUMBER: 60/079728			
	; PRIOR FILING DATE: 1998-03-27			
	; Remaining Prior Application data removed - See File Wrapper or PALM.			
	; NUMBER OF SEQ ID NOS: 246			
	; SEQ ID NO 71			
	; LENGTH: 521			
	; TYPE: DNA			
	; ORGANISM: Homo Sapien			
	US-10-219-525-71			
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	Score: 602.00	Matches:	111	
	Percent Similarity: 93.75%	Conservative:	9	
	Best Local Similarity: 86.72%	Mismatches:	8	
	Query Match: 89.05%	Indels:	0	
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	Qy	21	ValPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluCysValTyrrThr	40
	Db	98	ATATTATGACCGCTAGCTTCCAAGAAGCTCTGTGCAGATGATGATGCTCTACT	157
	Qy	41	IleSerLeuAlaArgAlaGlnGluAspTyrrAsnAlaProAspCysArgPheIleAspVal	60
	Db	158	ATTTCCTCTGGCTAGTGCTCAAGAAGATTATATGCCCGGACTGTAGATTCATTACGTT	217
	Qy	61	LysLysGlyGlnGlnIleTyrrValTyrrSerLysLeuValThrGluAsnGlyAlaGlyGlu	80
	Db	218	AAAAAAGGCGACGATCTATGTTGTTCTCAAAGCTGGTAAAAGAAAAATGGAGCTGGAGAA	277
	Qy	81	PheTrpAlaGlySerValTyrrGlyAspHisGlnAspGluMetGlyIleValGlyTyrrPhe	100
	Db	278	TTTTGGGCTGGCAGTGTTTATGGTGATGCCAGGACGAGATGGGAGTCTGGGGTTATTC	337
	Qy	101	ProSerAsnLeuValLysGluGlnArgValTyrrGlnGluAlaThrLysGluIleProThr	120

41	QY	IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal	60
158	Db	ATTTCCTCGGCTAGTGCTCAAGAAAGATTATAATGCCCGGACTGTAGATTCAATACGTT	217
61	QY	LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu	80
218	Db	AAAAAGGGCAGCAGATCTATGTCTACTCAAGCTGTTAAAGAAATGGAGCTGGAGAA	277
81	QY	PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe	100
278	Db	TTTTTGGGCTGGCAGGTATTATGGTGATGGCCAGACAGATGGGAGTCGTGGGGTTATTTC	337
101	QY	ProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr	120
338	Db	CCGAGAACTTGGTCAAGACACAGCGTGTGTACCAAGAACTACCAAGAGTTCCACCC	397
121	QY	ThrAspIleAspPhePheCysGlu	128
398	Db	ACGGATATTGACTTCTCTGGCGAG	421

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RESULT 15
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/ Sequence 71, Application US/10219530
/ Publication No. US20030187213A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Gerritsen, Mary
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe F.
/ APPLICANT: Watanabe, Colin L.
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P35301C34
/ CURRENT APPLICATION NUMBER: US/10/219,530
/ CURRENT FILING DATE: 2003-08-14
/ PRIOR APPLICATION NUMBER: 10/119,480
/ PRIOR FILING DATE: 2002-04-09
/ PRIOR APPLICATION NUMBER: 60/059113
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/062287
/ PRIOR FILING DATE: 1997-10-17
/ PRIOR APPLICATION NUMBER: 60/063549
/ PRIOR FILING DATE: 1997-10-28
/ PRIOR APPLICATION NUMBER: 60/064103
/ PRIOR FILING DATE: 1997-10-31
/ PRIOR APPLICATION NUMBER: 60/069873
/ PRIOR FILING DATE: 1997-12-17
/ PRIOR APPLICATION NUMBER: 60/078910
/ PRIOR FILING DATE: 1998-03-20
/ PRIOR APPLICATION NUMBER: 60/079294
/ PRIOR FILING DATE: 1998-03-25
/ PRIOR APPLICATION NUMBER: 60/079656
/ PRIOR FILING DATE: 1998-03-26
/ PRIOR APPLICATION NUMBER: 60/079728
/ PRIOR FILING DATE: 1998-03-27
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 246
/ SEQ ID NO 71
/ LENGTH: 521
/ TYPE: DNA
/ ORGANISM: Homo Sapien
US-10-219-530-71

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Query Match:	89.05%	Indels:	0
DB:	13	Gaps:	0
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DB	38	ATGGCAAGAATATTGTACTTCTCCCGGGTCTGTGGCTGTATGTCTGTGCATAGA	97
QY	21	ValPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValTyrThr	40
DB	98	ATATTATTGACCGCTAGCTTCCAAGAAGCTCTGTGCAGATCATGATGTGTCTACT	157
QY	41	IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal	60
DB	158	ATTTCTCTGGCTAGTGCTCAAGAAGATTATAATGCCCGGACTGTATAGATTCAATTACGTT	217
QY	61	LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu	80
DB	218	AAAAAAGGCACGACATCTATGTCTACTCAAGCTGGTAAAGAAATGGAGCTGAGAA	277
QY	81	PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe	100
DB	278	TTTTTGGGTGGCAGTGTTTATGTGTATGGTCAGACGAGATGGGAGTCGTGGGTATTATTC	337
QY	101	ProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr	120
DB	338	CCCGAGACTTGGTCAGGAACACGGTGTGTACCAAGAGCTACCAAGGAAGTTCACC	397
QY	121	ThrAspIleAspPheCysGlu	128
DB	398	ACGGATATTGACTTCTTCTGCGAG	421

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Job time : 289.193 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

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(without alignments)  
1388.315 Million cell updates/sec

Title: US-10-019-455A-12

Perfect score: 676

Sequence: 1 MARILLILLGLLVILCAGH.....RVYQATKEIPTTIDIFFCE 128

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Ygapop 10.0, Ygapext 0.5

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Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

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Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	277.5	41.1	459	1	US-08-578-649-1 Sequence 1, Appl
2	261.5	38.7	330	1	US-08-578-649-18 Sequence 18, Appl
3	247	36.5	581	1	US-08-578-649-4 Sequence 4, Appl
4	219.5	32.5	305	1	US-08-578-649-8 Sequence 8, Appl
5	210	31.1	596	1	US-08-578-649-24 Sequence 24, Appl
6	177.5	26.3	3565	1	US-08-578-649-3 Sequence 3, Appl
7	91.5	13.5	2793	1	US-07-646-537B-1 Sequence 1, Appl
8	89.5	13.2	2757	1	US-08-306-691B-48 Sequence 48, Appl
9	89.5	13.2	2757	5	PCT-US93-06251-79 Sequence 79, Appl
10	89.5	13.2	4762	4	US-09-300-958A-30 Sequence 30, Appl
11	82	12.1	467	4	US-09-300-958A-28 Sequence 28, Appl
12	78.5	11.6	5398	3	US-09-356-952-11 Sequence 11, Appl

13	77	11.4	2085	1	US-08-164-839-3 Sequence 3, Appl
14	77	11.4	2085	1	US-08-583-799-3 Sequence 3, Appl
15	77	11.4	2520	1	US-08-164-839-5 Sequence 5, Appl
16	77	11.4	2520	1	US-08-583-799-5 Sequence 5, Appl
17	76	11.2	1664976	4	US-08-916-421B-1 Sequence 1, Appl
18	75	11.1	2873	4	US-08-630-915A-193 Sequence 193, Appl
19	75	11.1	11864	4	US-08-961-527-61 Sequence 61, Appl
20	74.5	11.0	3981	4	US-09-328-352-760 Sequence 760, Appl
21	71.5	10.6	747	4	US-08-630-915A-39 Sequence 39, Appl
22	71.5	10.6	2064	1	US-08-164-839-30 Sequence 30, Appl
23	71.5	10.6	2064	1	US-08-164-839-32 Sequence 32, Appl
24	71.5	10.6	2064	1	US-08-583-799-30 Sequence 30, Appl
25	71.5	10.6	2064	1	US-08-583-799-32 Sequence 32, Appl
26	71.5	10.6	2148	1	US-08-164-839-69 Sequence 69, Appl
27	71.5	10.6	2148	1	US-08-164-839-71 Sequence 71, Appl
28	71.5	10.6	2148	1	US-08-583-799-69 Sequence 69, Appl
29	71.5	10.6	2148	1	US-08-583-799-71 Sequence 71, Appl
30	71	10.5	3398	5	PCT-US95-08493-12 Sequence 12, Appl
31	68	10.1	999	4	US-09-830-217-15 Sequence 15, Appl
32	67.5	10.0	1170	4	US-09-252-991A-2073 Sequence 2073, Appl
33	67.5	10.0	1593	4	US-09-252-991A-5394 Sequence 5394, Appl
34	67	9.9	3345	4	US-08-630-915A-29 Sequence 29, Appl
35	66.5	9.8	4119	4	US-09-076-259-1 Sequence 1, Appl
36	66	9.8	971	4	US-08-630-915A-197 Sequence 197, Appl
37	66	9.8	1457	3	US-09-444-053-3 Sequence 3, Appl
38	66	9.8	1878	3	US-08-996-139-14 Sequence 14, Appl
39	66	9.8	1878	3	US-08-995-659-14 Sequence 14, Appl
40	66	9.8	1878	3	US-09-215-649A-14 Sequence 14, Appl
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42	66	9.8	1878	4	US-09-577-800-14 Sequence 14, Appl
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44	66	9.8	1878	4	US-09-871-856-14 Sequence 14, Appl
45	66	9.8	1878	4	US-09-871-291-14 Sequence 14, Appl

#### ALIGNMENTS

#### RESULT 1

US-08-578-649-1  
; Patent 1, Application US/08578649  
; Sequence No. 5770366  
; GENERAL INFORMATION:  
; APPLICANT: Ulrich Bogdan  
; APPLICANT: Reinhard Buttner  
; APPLICANT: Brigitte Kaluza  
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felfe & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: Wordperfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/578,649  
; FILING DATE: 29-July-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE P 43 24 247.2  
; FILING DATE: 20-July-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Andrew L. Tiajloff  
; REGISTRATION NUMBER: 31,575  
; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 688-3200  
; TELEFAX: (212) 838-3884

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; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 459 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 40..432
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 40..111
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 112..432
; US-08-578-649-1

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Score: 277.50 Matches: 59
Percent Similarity: 64.71% Conservative: 29
Best Local Similarity: 43.38% Mismatches: 35
Query Match: 41.05% Indels: 13
DB: 1 Gaps: 6

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QY 18 GlyHisGlyValPhe-----MetAspLysLeuSerSerLysLysLeuCysAlaAsp 34
DB 94 GGACCTGTGTGTCAGGGTGTGCTTATGCCAAGCTGCTGACCGGAAGCTGTGTGGGAC 153
QY 35 GluGluCysValThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAsp 54
DB 154 CAGGAGTACAGCCCTTATCTCCATGCTGTGGCCCTTCAGGACTACATGGCCCGGAC 213
QY 55 CysArgPheIleAspValLysGlyGlnGlnIleTyrValTyrSerLysLeuValThr 74
DB 214 TGCCGATTCCTGACCAITACCGGGGCCAAGTGTGTATGTTCTTCTCAAGCTG----- 267
QY 75 GluAsnGlyAlaGlyGlu---PheTrpAlaGlySerValTyrGlyAspHisGlnAspGlu 93
DB 268 ---AAGGGCCGTGGCGGCTCTTCTGGGGAGGCGCTTCAGGAGATTACTATGGAGAT 324
QY 94 MetGlyIle---ValGlyTyrPheProSerAsnLeuValLysGluGlnArgValTyrGln 112
DB 325 CTGGCTGTGCTCGCTGGCTATTTCCCCAGTAGCATTTGCCAGAGGACGACCCCTGAAA 384
QY 113 GluAlaThrLysGluIleProThrThrAspIleAspPheCysGlu 128
DB 385 CTGGCAAAAGTCGATGTGAAGACACACAAATGGGATTCTTACTGCCAG 432

RESULT 2
US-08-578-649-18
; Sequence 18, Application US/08578649
; Patent No. 5770366
; GENERAL INFORMATION:
; APPLICANT: Ulrich Bogdan
; APPLICANT: Reinhard Buttner
; APPLICANT: Brigitte Kaluza
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESS: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/578,649
; FILING DATE: 29-July-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 24 247.2
; FILING DATE: 20-July-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Andrew L. Tajoloff
; REGISTRATION NUMBER: 31,575
; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 330 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 7..327
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: 4..6
; OTHER INFORMATION: /function= "Startcodon Met"
; US-08-578-649-18

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Pred. No.: 7,49e-29 Length: 330
Score: 261.50 Matches: 49
Percent Similarity: 67.59% Conservative: 24
Best Local Similarity: 45.37% Mismatches: 30
Query Match: 38.68% Indels: 5
DB: 1 Gaps: 3

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QY 43 LeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspValLysLys 62
DB 73 ATGGCTGTGGCCCTTCAGGACTACATGCCCCGACTGCGGATTCCTGACCATTCACCGG 132
QY 63 GlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu---Phe 81
DB 133 GCGCAAGTGTGTATGTCTCTCTCCAAAGCTG-----AAGGGCCGTGGCGGCTCTTC 183
QY 82 TrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIle---ValcIlyTyrPhe 100
DB 184 TGGGAGGCGCGCTTCAGGAGATTACTATGGAGATCTGGCTGCTCGCTGCGCTATCTTC 243
QY 101 ProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120
DB 244 CCCAGTAGCATTTGCCGAGGACGACCCCTGGAACCTGGCAAAAGTCGATGTGAAGACA 303
QY 121 ThrAspIleAspPheCysGlu 128
DB 304 GACAAATGGGATTCTTACTGCCAG 327

RESULT 3
US-08-578-649-4
; Sequence 4, Application US/08578649
; Patent No. 5770366
```

Db	305	GGCCCAAGTGTGATCTCTCTCCTCAAGTTG-----AAGGGCGCGTGCGGCCTTTTC	355
Qy	82	TtpAlaGlySerValTyrcGlyAspHisGlnaspGluMetGlyIle---ValglyTyrrPhe	100
Db	356	TGGGGAGGCGAGTGTTCAGGGAGGTTACTATGAGACCTGGCAGCGCGCTGGGCTATTTC	415
Qy	101	ProSerAsnLeuValLysGluGlnargValTyrgInGluAlaThrLysGluIleProthr	120
Db	416	CCAGTAGCATYGTTCGGGAGGACCTGAACCTCGAAACCTGGCAAATTCATATGAAGACC	475
Qy	121	ThrAspIleAspPheCysGlu	128
Db	476	GATCAATGGGATTCTTACTGCCAG	499
<b>RESULT 4</b>			
US-08-578-649-8			
; Sequence 8, Application US/08578649			
; Patent No. 5770366			
; GENERAL INFORMATION:			
; APPLICANT: Ulrich Bogdan			
; APPLICANT: Reinhard Buttner			
; APPLICANT: Brigitte Kaluza			
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN			
; NUMBER OF SEQUENCES: 24			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Felfe & Lynch			
; STREET: 805 Third Avenue			
; CITY: New York			
; STATE: New York			
; COUNTRY: USA			
; ZIP: 10022			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette			
; COMPUTER: IBM PS/2			
; OPERATING SYSTEM: PC-DOS			
; SOFTWARE: Wordperfect			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/578,649			
; FILING DATE: 29-July-1994			
; CLASSIFICATION: 435			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: DE P 43 24 247.2			
; FILING DATE: 20-July-1993			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Andrew L. Tiajoloiff			
; REGISTRATION NUMBER: 31,575			
; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (212) 688-9200			
; TELEFAX: (212) 838-3884			
; INFORMATION FOR SEQ ID NO: 8:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 305 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
; MOLECULE TYPE: cDNA			
; FEATURE:			
; NAME/KEY: misc RNA			
; LOCATION: join(1..29, 277..305)			
; OTHER INFORMATION: /function= "Primer"			
US-08-578-649-8			
<b>Alignment Scores:</b>			
Pred. No.:	7,64e-23	Length:	305
Score:	219.50	Matches:	44
Percent Similarity:	64.6%	Conservative:	20
Best Local Similarity:	44.4%	Mismatches:	30
Query Match:	32.4%	Indels:	5
DB:	1	Gaps:	3
US-10-019-455A-12 (1-128) x US-08-578-649-8 (1-305)			



```

Qy 30 LysLeuCysAlaLeuGluGluCysValTyrThrIleSerLeuAlaArgAlaGlnGluAsp 49
Db 7 AAGTTTCGGCGGATGAGGAGTGCAGCCACCTTATCTCCATGGCTGTGGCCCTTCAGGAC 66
Qy 50 TyrAsnAlaProAspCysArgPheIleAspValTyrLysGlyGlnGlnIleTyrValTyr 69
Db 67 TACATGGCCCCCGACTGCGGATTCCTGACCATTCACCGGGGCCAAGTGGTGTATGCTTC 126
Qy 70 SerLysLeuValThrGluAsnGlyAlaGlyGlu---PheTrpAlaGlySerValTyrGly 88
Db 127 TCCAAAGCTG-----AAGGGCCGTGGCGGCTCTCTGGGAGGCGGTCACAGGA 177
Qy 89 AspHisGln---AspGluMetGlyIleValGlyTyrPheProSerAsnLeuValLysGlu 107
Db 178 GATTACTATGAGATCTGTCGCTCGCTGGCTATTTCCCGATGACATGTCAGAG 237
Qy 108 GlnArgValTyrGlnGluAlaThrLysGluIleProThrAspIleAspPhe 126
Db 238 GACCAGACCTGAAACCTGGCAAGTCGATGTGAAGACAGATAAATGGGATTCTTAC 294

RESULT 5
US-08-578-649-24
; Sequence 24, Application US/08578649
; Patent No. 5770366
; GENERAL INFORMATION:
; APPLICANT: Ulrich Bogdan
; APPLICANT: Reinhard Buttner
; APPLICANT: Brigitte Kaluza
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/578,649
; FILING DATE: 29-July-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 24 247.2
; FILING DATE: 20-July-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Andrew L. Tiajolloff
; REGISTRATION NUMBER: 31,575
; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 596 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(40..111, 40..166, 214..347, 393..503, 549
; LOCATION: ..569)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 40..111
; FEATURE:
; NAME/KEY: exon

```

```

; LOCATION: 40..166
; FEATURE:
; NAME/KEY: exon
; LOCATION: 214..347
; FEATURE:
; NAME/KEY: exon
; LOCATION: 393..503
; FEATURE:
; NAME/KEY: exon
; LOCATION: 549..569
; FEATURE:
; NAME/KEY:
; LOCATION: one of (194, 369, 527)
; OTHER INFORMATION: /note= "N in positions 194, 369
; OTHER INFORMATION: and 527 denotes an indefinite number and sequence
; OTHER INFORMATION: of nucleotides "
US-08-578-649-24

Alignment Scores:
Pred. No.: 4.72e-21 Length: 596
Score: 210.00 Matches: 60
Percent Similarity: 48.63% Conservative: 29
Best Local Similarity: 32.79% Mismatches: 33
Query Match: 21.07% Indels: 62
DB: 1 Gaps: 10

US-10-019-455A-12 (1-128) x US-08-578-649-24 (1-596)

Qy 1 MetAlaArgIleLeuIleLeuLeuGlyGlyValValValCys-----Ala 17
Db 40 ATGGCCCGGTCCCTGGTGGCTT-----GGTGCATCATCTGTGTCTCTCTCC 93
Qy 18 GlyHisGlyValPhe-----MetAspLysLeuSerSerLysLeuValCysAlaAsp 34
Db 94 GGACCTGGTGTGAGGGGTGGTCTATGCCAAGCTGGCTGACCGGAGCTGTGTGGGAC 153
Qy 35 GluGluCysValTyr----- 39
Db 154 CAGGAGTGCAGCCG-TAAGATGGGAGGGTAGAATTGGGNCCTTCTATTCTTCCCTA 212
Qy 40 ---ThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 58
Db 213 GACCCATATCTCCATGGCTGTGGCTTCCAGGACTACATGGCCCGGACTGCGGATTCTG 272
Qy 59 AspValLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 78
Db 273 ACCATTACCGGGGCCAAGTGGTGTATGTCTTCTCCAGCTG-----AAGGGCGGT 323
Qy 79 GlyGlu---PheTrpAlaGlySer----- 85
Db 324 GGGCGGCTCTTCTGGGAGGCGCAGCTGGTCTTGGAGAGTGAAGAGCTTTTAACCTCT 383
Qy 86 -----ValTyrGlyAspHisGlnAspGluMetGlyIle---ValGlyTyrPhePro 101
Db 384 CTTCCCGAGGTTCAGGAGATTACTATGGAGATCTGTGCTGCTGCGCTATTTCTCCC 443
Qy 102 SerAsnLeuValLysGlnArgValTyrGlnGluAlaThrLysGluIleProThrThr 121
Db 444 ACTAGCATTTGCCGAGAGACCAGACCTGAAACCTGCGAAAGTCGATGTG---AAGACA 500
Qy 122 AspIle----- 125
Db 501 GAGTGGAGTGTATGGGGGTGGGCTTCCCTTTCTCTTTTCAGAAATGGGATTTC 560
Qy 126 PheCysGlu 128
Db 561 TACTGCCAG 569

RESULT 6
US-08-578-649-3
; Sequence 3, Application US/08578649
; Patent No. 5770366
; GENERAL INFORMATION:

```



Alignment Scores:  
 Pred. No.: 0.00544 Length: 2793  
 Score: 91.50 Matches: 23  
 Percent Similarity: 52.86% Conservative: 14  
 Best Local Similarity: 32.86% Mismatches: 20  
 Query Match: 13.54% Indels: 13  
 DB: 3

US-10-019-455A-12 (1-128) x US-07-646-537B-1 (1-2793)

QY 44 AlaAraGAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVallyLysGly 63  
 DB 2369 GCCAAGCCCGCTACGACTTCTGCGCCGACAGGTGCGAACTGTCCTTAAGGAGGT 2428  
 QY 64 GlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGluPheTrpAla 83  
 DB 2429 GATATCATC-----AAGATCCTCAATAGAAGGACAGCAAGCGTGGTGGCGT 2476  
 QY 84 GlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPheProSerAsn 103  
 DB 2477 GGGGAGATCTACGCGCG-----ATCGGTGGTTCCTTCTTAAC 2515  
 QY 104 LeuVallyysGluGlnArgValTyrGlnGlu 113  
 DB 2516 TATGTGGAGGAAGAC-----TATTCGAA 2539

## RESULT 8

US-08-306-691B-48  
 ; Sequence 48, Application US/08306691B  
 ; Patent No. 5734039  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Calabretta, Bruno  
 ; APPLICANT: Skorski, Tomasz  
 ; TITLE OF INVENTION: ANTIGENSE  
 ; TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES  
 ; NUMBER OF SEQUENCES: 55  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.  
 ; STREET: Two Penn Center, Suite 1800  
 ; CITY: Philadelphia  
 ; STATE: Pennsylvania  
 ; COUNTRY: U.S.A.  
 ; ZIP: 19102  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
 ; COMPUTER: IBM PS/2  
 ; OPERATING SYSTEM: MS-DOS  
 ; SOFTWARE: WordPerfect 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/306,691B  
 ; FILING DATE: September 15, 1994  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Monaco, Daniel A.  
 ; REGISTRATION NUMBER: 30,480  
 ; REFERENCE/DOCKET NUMBER: 8321-8  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (215) 568-8383  
 ; TELEFAX: (215) 568-5549  
 ; TELEX: No. 5734039e  
 ; INFORMATION FOR SEQ ID NO: 48:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 2757 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; US-08-306-691B-48

## Alignment Scores:

Pred. No.: 0.0104 Length: 2757  
 Score: 89.50 Matches: 23  
 Percent Similarity: 52.86% Conservative: 14  
 Best Local Similarity: 32.86% Mismatches: 20  
 Query Match: 13.24% Indels: 13  
 DB: 3

US-10-019-455A-12 (1-128) x US-08-306-691B-48 (1-2757)

QY 44 AlaAraGAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVallyLysGly 63  
 DB 2325 GCCAAGCCCGCTACGACTTCTGCGCCGACAGGTGCGAACTGTCCTTAAGGAGGT 2384  
 QY 64 GlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGluPheTrpAla 83  
 DB 2385 GACATCATC-----AAGATCCTTAACAAGAAGGCACAGCAAGCGTGGTGGCGA 2432  
 QY 84 GlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPheProSerAsn 103  
 DB 2433 GGGGAGATCTATGCGCG-----GTTGGCTGGTTCCTTCTTCCGCAAC 2471  
 QY 104 LeuVallyysGluGlnArgValTyrGlnGlu 113  
 DB 2472 TACGTGGAGGAAGAT-----TATTCGAA 2495

## RESULT 9

PCT-US93-06251-79  
 ; Sequence 79, Application PC/TUS9306251  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wickstrom, Eric and Rife, Jason P.  
 ; TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing  
 ; TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates  
 ; NUMBER OF SEQUENCES: 93  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER  
 ; STREET: 400 Garden City Plaza  
 ; CITY: Garden City  
 ; STATE: NY  
 ; COUNTRY: USA  
 ; ZIP: 11530  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US93/06251  
 ; FILING DATE: 19930630  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Digiglio, Frank S.  
 ; REGISTRATION NUMBER: 31,345  
 ; REFERENCE/DOCKET NUMBER: 8586  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 516-742-4343  
 ; TELEFAX: 516-742-4366  
 ; TELEX: 230 901 SANS UR  
 ; INFORMATION FOR SEQ ID NO: 79:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 2757 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; PCT-US93-06251-79

Alignment Scores:  
 Pred. No.: 0.0104 Length: 2757  
 Score: 89.50 Matches: 23  
 Percent Similarity: 52.86% Conservative: 14  
 Best Local Similarity: 32.86% Mismatches: 20  
 Query Match: 13.24% Indels: 13  
 DB: 3

US-10-019-455A-12 (1-128) x PCT-US93-06251-79 (1-2757)

QY 44 AlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspValIleAspGly 63  
Db 2325 GCAAAAGCCGCTATGACTTCTGCGCCCTGACCGTTCAGACTGCTCCAGAGGGT 2384  
QY 64 GlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGluPheTrpAla 83  
Db 2385 GACATCATC-----AAGATCCTTAAACAAGAGGACCAAGGCTGTGGCGA 2432  
QY 84 GlycerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPheProSerAsn 103  
Db 2433 GGGGAGATCATGCGCGG-----GTTGGTGGTTCCCTGCCAAC 2471  
QY 104 LeuValLysGlnGlnArgValTyrGlnGlu 113  
Db 2472 TACGTGAGGAGAT-----TATTCTGAA 2495

## RESULT 10

US-09-300-958A-30  
; Sequence 30, Application US/09300958A  
; Patent No. 6495319  
; GENERAL INFORMATION:  
; APPLICANT: McClelland, Michael  
; APPLICANT: Welsh, John  
; APPLICANT: Trenkle, Thomas  
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of  
; FILE REFERENCE: P-PH 3457  
; CURRENT APPLICATION NUMBER: US/09/300,958A  
; CURRENT FILING DATE: 1999-04-27  
; PRIOR APPLICATION NUMBER: 60/083,331  
; PRIOR FILING DATE: 1998-04-27  
; PRIOR APPLICATION NUMBER: 60/098,070  
; PRIOR FILING DATE: 1998-08-27  
; PRIOR APPLICATION NUMBER: 60/118,624  
; PRIOR FILING DATE: 1999-02-04  
; NUMBER OF SEQ ID NOS: 85  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 30  
; LENGTH: 4762  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-300-958A-30

Alignment Scores:  
Pred. No.: 0.0229 Length: 4762  
Score: 89.50 Matches: 22  
Percent Similarity: 52.24% Conservative: 13  
Best Local Similarity: 32.84% Mismatches: 21  
Query Match: 13.24% Indels: 11  
Gaps: 2  
DB:

US-10-019-455A-12 (1-128) x US-09-300-958A-30 (1-4762)

QY 41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal 60  
Db 2405 CTGGCATTGCCATCGCTCGGTATGACTTCTGTGCAAGAGATATGAGAGATTGTCTGTG 2464  
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu 80  
Db 2465 TTGAAGAGAGATGTGGTGAAGATTACAAAGATG-----AGTGCAAATGGC 2512  
QY 81 PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100  
Db 2513 TGGTGGAGAGAGAGAGATTAAATGGCAGG-----GTGGGCTGGTTT 2551  
QY 101 ProSerAsnLeuValLysGlu 107  
Db 2552 CCATCCACATATGTGAAGAG 2572

## RESULT 11

US-09-300-958A-28  
; Sequence 28, Application US/09300958A  
; Patent No. 6495319  
; GENERAL INFORMATION:  
; APPLICANT: McClelland, Michael  
; APPLICANT: Welsh, John  
; APPLICANT: Trenkle, Thomas  
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of  
; FILE REFERENCE: P-PH 3457  
; CURRENT APPLICATION NUMBER: US/09/300,958A  
; CURRENT FILING DATE: 1999-04-27  
; PRIOR APPLICATION NUMBER: 60/083,331  
; PRIOR FILING DATE: 1998-04-27  
; PRIOR APPLICATION NUMBER: 60/098,070  
; PRIOR FILING DATE: 1998-08-27  
; PRIOR APPLICATION NUMBER: 60/118,624  
; PRIOR FILING DATE: 1999-02-04  
; NUMBER OF SEQ ID NOS: 85  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 28  
; LENGTH: 467  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (428)  
; NAME/KEY: unsure  
; LOCATION: (462)  
US-09-300-958A-28

Alignment Scores:  
Pred. No.: 0.00961 Length: 467  
Score: 82.00 Matches: 24  
Percent Similarity: 50.00% Conservative: 15  
Best Local Similarity: 30.77% Mismatches: 27  
Query Match: 12.13% Indels: 12  
Gaps: 3  
DB:

US-10-019-455A-12 (1-128) x US-09-300-958A-28 (1-467)

QY 46 AlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspValLysGlyGlnGln 65  
Db 152 GCTCGGTATGACTTCTGTGCAAGAGATATGAGAGATTGTCTGTGTTGAAAGGAGATGTG 211  
QY 66 IleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGluPheTrpAlaGlySer 85  
Db 212 GTGAAGATTACAAAGATG-----AGTCAAATGGCTGTGGAGGGAGAA 259  
QY 86 ValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPheProSerAsnLeuVal 105  
Db 260 GTAAATGGCAGG-----GTGGGCTGGTTTCCATCCACATATGTG 298  
QY 106 LysGlnGlnArgValTyrGlnGluAlaThrLysGluIleProThrThrAspIle 123  
Db 299 ---GGAAGGAGGATGAATAATTCAAATCCCGTGTTCACCCCTGCACCAAAATT 349  
RESULT 12  
US-09-356-952-11  
; Sequence 11, Application US/09356952  
; Patent No. 6117663  
; GENERAL INFORMATION:  
; APPLICANT: Borlack-Sjodin, Ann  
; APPLICANT: Margaret, S. M.  
; APPLICANT: Bor-Sogli, Dafna  
; APPLICANT: Cole, Philip  
; APPLICANT: Kuriyan, John  
; TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE  
; FILE REFERENCE: 600-1-228N  
; CURRENT APPLICATION NUMBER: US/09/356,952  
; CURRENT FILING DATE: 1999-07-19  
; EARLIER APPLICATION NUMBER: 60/093,631

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; EARLIER FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 5398
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-356-952-11

Alignment Scores:
Pred. No.: 1.06 Length: 5398
Score: 78.50 Matches: 24
Percent Similarity: 47.19% Conservatives: 18
Best Local Similarity: 26.97% Mismatches: 36
Query Match: 11.61% Indels: 11
DB: 3 Gaps: 4

US-10-019-455A-12 (1-128) x US-09-356-952-11 (1-5398)
QY 26 LeuSerSerLysLysLeuCysAlaAspGluGluCysValTyrThrIleSerLeuAlaArg 45
Db 445 CTTCTCTTCTCCCTCCAGAGTGAGTTCACCGAGTTCGTCCTCAATGGAATAGTATC 504
QY 46 AlaGlnGluAspTyrAsnAlaPro-----AspCysArgPheIleAspVal 60
Db 505 GCTGCTTATGACTTTTAAATTATCCCAATTAAAAAGACAGAGTTCTTCGCAACTTTTGTCTGTA 564
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu 80
Db 565 CAACAGGGGGAACCACTTATATCTACTTAACAAA-----AACTCATCTGGG--- 609
QY 81 PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
Db 610 TGGTGGGATGGATTAGTTATTGACGACAGTAATGGAAAGTTAAC---AGAGGCTGGTTT 666
QY 101 ProSerAsnLeuValLysGluGlnArg 109
Db 667 CTTCAAAACTTCGGTAGACCTTTAAGA 693

RESULT 13
US-08-164-839-3
; Sequence 3, Application US/08164839
; Patent No. 5514573
; GENERAL INFORMATION:
; APPLICANT: YASUEDA, HISASHI
; APPLICANT: NAKANISHI, KAZUO
; APPLICANT: MOTOKI, MASAO
; APPLICANT: NAGASE, KAZUO
; APPLICANT: MATSUI, HIROSHI
; TITLE OF INVENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED
; FROM FISH
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/164,839
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/004,729
; FILING DATE: 14-JAN-1993
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Oblon, No. 5514573man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-599-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)412-3000
; TELEFAX: (703)412-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2085 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:
; ORGANISM: Pagrus major
; TISSUE TYPE: liver
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2082
US-08-164-839-3

Alignment Scores:
Pred. No.: 0.44 Length: 2085
Score: 77.00 Matches: 22
Percent Similarity: 52.50% Conservatives: 20
Best Local Similarity: 27.50% Mismatches: 28
Query Match: 11.39% Indels: 10
DB: 1 Gaps: 3

US-10-019-455A-12 (1-128) x US-08-164-839-3 (1-2085)
QY 49 AspTyrAsnAlaProAspCysArgPheIleAspValLysLysGlyGlnIleTyrVal 68
Db 1174 GAGGTGAACGCTGACACCATCTACTGATCTGTCACAAAGATGCGCAACGA----- 1224
QY 69 TyrSerLysLeuValThrGluAsnGlyAlaGly-----GluPheTrpAlaGlySer 85
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Db 1279 GTTTACGGCAACCCACAGAGAGATGTCATCTGCTACATAAATATCTGAAGGCTCCAG 1338
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RESULT 14
US-08-583-799-3
; Sequence 3, Application US/08583799
; Patent No. 5607849
; GENERAL INFORMATION:
; APPLICANT: YASUEDA, HISASHI
; APPLICANT: NAKANISHI, KAZUO
; APPLICANT: MOTOKI, MASAO
; APPLICANT: NAGASE, KAZUO
; APPLICANT: MATSUI, HIROSHI
; TITLE OF INVENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED
; FROM FISH
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: IBM PC compatible
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PC-DOS/MS-DOS

```

SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/583,799  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/004,729  
FILING DATE: 14-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Oblon, No. 5607849man F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 10-599-0  
TELEPHONE: (703)412-3000  
TELEFAX: (703)413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2085 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
ORIGINAL SOURCE:  
ORGANISM: Pagrus major  
TISSUE TYPE: liver  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..2082  
US-08-583-799-3

Alignment Scores:  
Pred. No.: 0.44 Length: 2085  
Score: 77.00 Matches: 22  
Percent Similarity: 52.50% Conservative: 20  
Best Local Similarity: 27.50% Mismatches: 28  
Query Match: 11.39% Indels: 10  
DB: 1 Gaps: 3

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## RESULT 15

US-08-164-839-5  
Sequence 5, Application US/08164839  
Patent No. 5514573  
GENERAL INFORMATION:  
APPLICANT: YASUEDA, HISASHI  
APPLICANT: NAKANISHI, KAZUO  
APPLICANT: MOTOKI, MASAO  
APPLICANT: NAGASE, KAZUO  
APPLICANT: MATSUI, HIROSHI  
TITLE OF INVENTION: GENE ENCODING TRANSGLUAMINASE DERIVED FROM FISH  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
ADDRESSEE: P.C.

STREET: 1755 Jefferson Davis Highway, Fourth Floor  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/164,839  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/004,729  
FILING DATE: 14-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Oblon, No. 5514573man F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 10-599-0  
TELEPHONE: (703)412-3000  
TELEFAX: (703)413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2520 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
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ORGANISM: Pagrus major  
TISSUE TYPE: liver  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 34..2121  
US-08-164-839-5

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US-10-019-455A-12 (1-128) x US-08-164-839-5 (1-2520)

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Db 1315 GTTTACGGCAACACAGAGAGATGTCCTCTGCCTACATCAATATCTGAAGGCTCCAG 1374  
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Search completed: December 29, 2003, 22:05:04  
Job time : 46.6947 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 22:08:26 ; Search time 1045 Seconds  
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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 5777422

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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41: em.htgo.other.\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

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2	330	100.0	330	6	BD093117	BD093117 Novel pol
3	330	100.0	384	6	BD010802	BD010802 Novel pol
4	330	100.0	384	6	BD093103	BD093103 Novel pol
5	330	100.0	521	6	AX358818	AX358818 Sequence
6	330	100.0	521	6	AX362311	AX362311 Sequence
7	330	100.0	521	6	AX454774	AX454774 Sequence
8	330	100.0	521	6	AX491252	AX491252 Sequence
9	330	100.0	846	9	AF233261	AF233261 Homo sapi
10	330	100.0	865	9	AF243505	AF243505 Homo sapi
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24	249	75.5	384	6	BD010835	BD010835 Novel pol
25	249	75.5	384	6	BD093136	BD093136 Novel pol
26	249	75.5	384	6	BD093131	BD093131 Novel pol
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ALIGNMENTS

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LOCUS

Novel polypeptide and DNA thereof.

BD010816

DEFINITION

BD010816.1 GI:19639189

ACCESSION

VERSION

JP 2001069994-A/17.

KEYWORDS

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 330)

Yoshimura, K. and Tanaka, H.

Novel polypeptide and DNA thereof

Pred. No. is the number of results predicted by chance to have a



JOURNAL Patent: JP 2001069994-A 17 21-MAR-2001;  
TAKEDA CHEMICAL INDUSTRIES LTD  
COMMENT OS Homo sapiens (human)  
PN JP 2001069994-A/17  
PD 21-MAR-2001  
PF 29-JUN-2000 JP 2000195911  
PR YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI  
SHINICHI MOGI,  
HIDEYUKI TANAKA  
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA  
PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P19/02, PC  
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PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC  
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Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 CATGGAATATTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGATGTC 60  
QY 61 TATACTATTTCTCTGGCTAGTGTCTCAAGAGATTATTAATGCCCGGACTGTAGATTCATT 120  
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LOCUS Novel polypeptide and its DNA.  
DEFINITION BD093117  
ACCESSION BD093117  
VERSION BD093117.1 GI:22638705  
KEYWORDS WO 0102564-A/17.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 330)  
AUTHORS Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,  
Yoshimura, K. and Tanaka, H.  
TITLE Novel polypeptide and its DNA  
JOURNAL Patent: JP 2001069994-A 17 21-JAN-2001;  
TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO  
COMMENT OS Homo sapiens (human)  
PN JP 2001069994-A/3

JOURNAL Patent: JP 2001069994-A 17 21-MAR-2001;  
TAKEDA CHEMICAL INDUSTRIES LTD  
COMMENT OS Homo sapiens (human)  
PN WO 0102564-A/17  
PD 11-JAN-2001  
PF 29-JUN-2000 WO 2000JP004278  
PF 30-JUN-1999 JP 99P 186718  
PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI  
MOGI,  
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA  
PC C12N15/12, C12N5/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC  
A61K38/17,  
PC A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7088// (C12P21/  
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BASE COUNT 91 a 60 c 91 g 88 t  
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Best Local Similarity 100.0%; Pred. No. 6.7e-90;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CATGGAATATTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGATGTC 60  
DB 1 CATGGAATATTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGATGTC 60  
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DB 301 CCCACCCAGGATATTGACTTCTCTGCGAG 330  
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LOCUS Novel polypeptide and DNA thereof.  
DEFINITION BD010802  
ACCESSION BD010802  
VERSION BD010802.1 GI:18639175  
KEYWORDS JP 2001069994-A/3.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 384)  
AUTHORS Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,  
Yoshimura, K. and Tanaka, H.  
TITLE Novel polypeptide and DNA thereof  
JOURNAL Patent: JP 2001069994-A 3 21-MAR-2001;  
TAKEDA CHEMICAL INDUSTRIES LTD  
COMMENT OS Homo sapiens (human)  
PN JP 2001069994-A/3

PD 11-JAN-2001  
PF 29-JUN-2000 WO 2000JP004278  
PR 30-JUN-1999 JP 99P 186718  
PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI MOGI,  
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA  
PC C12N15/12, C12N5/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC  
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Best Local Similarity 100.0%; Pred. No. 6.9e-90;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Qy 61 TATACATTTCTCTGGCTAGTCTCAAGAAATATATATGCCCCGGAGCTAGATTCAAT 120  
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RESULT 5  
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LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
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Sequence 71 from Patent WO0193983.  
AX358818  
AX358818.1 GI:18675310  
Homo sapiens (human)  
Homo sapiens  
Homo sapiens  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
Baker, K.P., Desnovers, L., Gerritsen, M.E., Goddard, A.,  
Godowski, J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,  
Watanabe, C.K. and Wood, W.I.  
Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
Patent: WO 0193983-A 71 13-DEC-2001;  
Genentech Inc. (US)  
Location/Qualifiers  
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PF 29-JUN-2000 JP 2000195911  
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SHINICHI MOGI,  
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA  
PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC  
A61P19/08, C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC  
G01N33/53//  
PC C12P21/08, C12N15/00, A61K37/02, C12N5/00  
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FH source 1..384  
FT /organism="Homo sapiens (human)"  
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Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 355 CCCACACGGATATTGACTTCTCTCGCGAG 384

RESULT 4  
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LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
BD093103  
Novel polypeptide and its DNA.  
BD093103  
BD093103.1 GI:22638691  
WO 0102564-A/3.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 384)  
Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,  
Yoshimura, K. and Tanaka, H.  
Novel polypeptide and its DNA  
Patent: WO 0102564-A 3 11-JAN-2001;  
TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO  
OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,  
HIDEYUKI TANAKA  
OS Homo sapiens (human)  
PN WO 0102564-A/3

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Best Local Similarity 100.0%; Pred. No. 7.1e-90;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 301 CCCACCAAGGATATTGACTTCTTCTGCGAG 330
DB 392 CCCACCAAGGATATTGACTTCTTCTGCGAG 421

RESULT 7
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LOCUS      AX454774
DEFINITION Sequence 359 from Patent WO0208284.
ACCESSION  AX454774
VERSION     AX454774.1 GI:21714011
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
and Ye,W.
TITLE       Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
JOURNAL     Patent: WO 0208284-A 359 31-JAN-2002;
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone
(US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,
Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;
Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US)
Hillan, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William
I. (US)
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BASE COUNT  167 a      86 c      131 g      137 t
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Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATGGAATATTATGACCGCTAGCTTCCAAAGAGCTCTGTGACAGATGATGAGTGTGC 60
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DB 392 CCCACCAAGGATATTGACTTCTTCTGCGAG 421

RESULT 6
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DEFINITION Sequence 71 from Patent WO0208288.
ACCESSION  AX362311
VERSION     AX362311.1 GI:18694613
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,
Watanabe,C.K. and Wood,W.I.
TITLE       Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL     Patent: WO 0208288-A 71 31-JAN-2002;
Genentech, Inc. (US)
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BASE COUNT  167 a      86 c      131 g      137 t
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Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 TATACTATTCTCTGGCTAGTGTCAAGAAAGCTCTGTGACAGATGATGAGTGTGC 120
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 392 CCCACCGGATATTGACTTCTCTCGCGAG 421

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 LOCUS Sequence 359 from Patent WO0200690.  
 DEFINITION AX491252  
 ACCESSION AX491252.1 GI:223223963  
 VERSION  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
 1  
 AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gertitsen, M.E., Goddard, A.,  
 Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,  
 Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.  
 and Ye, W.  
 TITLE Compositions and methods for the diagnosis and treatment of  
 disorders involving angiogenesis  
 JOURNAL Patent: WO 0200690-A 359 03-JAN-2002;  
 Genentech, Inc. (US)

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 392 CCCACCGGATATTGACTTCTCTCGCGAG 421

RESULT 9  
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 LOCUS Homo sapiens otoraplin (OTOR) mRNA, complete cds.  
 DEFINITION AF233261  
 ACCESSION AF233261.1 GI:8927427  
 VERSION  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 846)  
 Robertson, N.G., Heller, S., Lin, J.S., Resendes, B.L., Weremowicz, S.,  
 Denis, C.S., Bell, A.M., Hudspeth, A.J., and Morton, C.C.  
 TITLE A novel conserved cochlear gene, OTOR: identification, expression  
 analysis, and chromosomal mapping  
 JOURNAL Genomics 66 (3), 242-248 (2000)  
 MEDLINE 20334619  
 PUBMED 10873378  
 2 (bases 1 to 846)  
 Robertson, N.G., Heller, S., Lin, J.S., Resendes, B.L., Weremowicz, S.,  
 Denis, C.S., Bell, A.M., Hudspeth, A.J., and Morton, C.C.  
 AUTHORS Direct Submission  
 TITLE Submitted (09-FEB-2000) Pathology, Brigham and Women's Hospital, 75  
 JOURNAL Francis Street, Boston, MA 02115, USA

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QY 301 CCCACCGGATATTGACTTCTCTCGCGAG 330  
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RESULT 10  
 AF243505 865 bp mRNA linear PRI 26-DEC-2000  
 LOCUS Homo sapiens fibrocyte-derived protein (FDP) mRNA, complete cds.  
 DEFINITION AF243505  
 ACCESSION AF243505

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VERSION      AF243505.1 GI:11991843
KEYWORDS
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 865)
AUTHORS      Cohen-Salmon, M., Frenz, D., Liu, W., Verpy, E., Voegelting, S. and
TITLE        Fdp, a new fibrocyte-derived protein related to MIA/CD-RAP, has an
              in vitro effect on the early differentiation of the inner ear
              mesenchyme
JOURNAL      J. Biol. Chem. 275 (51), 40036-40041 (2000)
MEDLINE      20568254
PUBMED       10998416
REFERENCE    2 (bases 1 to 865)
AUTHORS      Cohen-Salmon, M., Frenz, D., Verpy, E., Voegelting, S. and Petit, C.
TITLE        Direct Submission
JOURNAL      Submitted (09-MAR-2000) Biotechnologies, Institut Pasteur, 25 rue
              du Dr. Roux, Paris 75015, France
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BASE COUNT   258 a 145 c 207 g 255 t
ORIGIN
Query Match      100.0%; Score 330; DB 9; Length 865;
Best Local Similarity 100.0%; Pred. No. 7.6e-90;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 301 CCCACCGAGATATTGACTTCTTCTCGGAG 330
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LOCUS       BD010820
DEFINITION Novel polypeptide and its DNA.
ACCESSION   BD010820
VERSION     1
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 923)
AUTHORS      Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
              Yoshimura, K. and Tanaka, H.
TITLE        Novel polypeptide and DNA thereof
JOURNAL      TAKEDA CHEMICAL INDUSTRIES LTD
COMMENT      OS Homo sapiens (human)
              PN JP 2001069994-A/21
              PD 21-MAR-2001
              PF 29-JUN-2000 JP 2000195911
              PR YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI
              SHINICHI MOGI,
              PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
              PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC
              A61P19/08,
              PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC
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Query Match      100.0%; Score 330; DB 6; Length 923;
Best Local Similarity 100.0%; Pred. No. 7.6e-90;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CATGGAATATTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTGC 60
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RESULT 12
BD093121
LOCUS       BD093121
DEFINITION Novel polypeptide and its DNA.
ACCESSION   BD093121

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KEYWORDS melanoma inhibitory activity like protein; Mial gene.  
SOURCE Homo sapiens (human)  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 Rendtorff,N.D., Frodin,M., Attie-Bitach,T., Vekemans,M. and Tommerup,N.  
AUTHORS Identification and characterization of an inner ear-expressed human melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent polymorphism that abolishes translation  
TITLE Genomics 71 (1), 40-52 (2001)  
JOURNAL 21100875  
MEDLINE 11161796  
PUBMED 2 (bases 1 to 1422)  
REFERENCE Rendtorff,N.D.  
AUTHORS Direct Submission  
TITLE Submitted (21-MAY-1999) Rendtorff N.D., Department of Medical Genetics, Institute of Medical Biochemistry and Genetics, Blegdamsvej 3, 2200 Copenhagen N, DENMARK  
JOURNAL Revised by author 03-AUG-1999  
REMARK Related sequences: AJ245339 (Mus musculus mRNA)  
COMMENT Related sequences: AJ252324 to AJ252327 (genomic sequence).  
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BD093121.1 GI:22638709  
WO 0102564-A/21  
Homo sapiens (human)  
Homo sapiens  
REFERENCE 1 (bases 1 to 923)  
AUTHORS Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y., Yoshimura,K. and Tanaka,H.  
TITLE Novel polypeptide and its DNA  
JOURNAL Patent: WO 0102564-A 21 11-JAN-2001;  
TAKEDA CHEMICAL INDUSTRIES LTD, YASUKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA  
COMMENT OS Homo sapiens (human)  
PN WO 0102564-A/21  
PD 11-JAN-2001  
PF 29-JUN-2000 WO 2000JP004278  
PR 30-JUN-1999 JP 99P 186718  
PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI MOGI,  
YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA  
PC C12N15/12, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC A61K38/17,  
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PC 02, C12R1.19)  
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DEFINITION (MIAL gene).  
ACCESSION AJ242552  
VERSION AJ242552.1 GI:12619172



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ACCESSION      BD010817
VERSION      BD010817.1 GI:18639190
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SOURCE      Mus sp.
ORGANISM      Mus sp.
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE      Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
JOURNAL      Yoshimura, K. and Tanaka, H.
COMMENT      Novel polypeptide and DNA thereof
PATENT: JP 2001069994-A 18 21-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD
OS Mus sp. (mouse)
PN JP 2001069994-A/18
PD 21-MAR-2001
PF 29-JUN-2000 JP 2000195911
PR
PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI
SHINICHI MOGI,
YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
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DEFINITION      Novel polypeptide and its DNA.
ACCESSION      BD093118
VERSION      BD093118.1 GI:22638706
KEYWORDS      WO 0102564-A/18.
SOURCE      Mus sp.
ORGANISM      Mus sp.
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE      Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
JOURNAL      Yoshimura, K. and Tanaka, H.
COMMENT      Novel polypeptide and its DNA
PATENT: WO 0102564-A 18 11-JAN-2001;
TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO
OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,
HIDEYUKI TANAKA
OS Mus sp. (mouse)
PN WO 0102564-A/18
PD 11-JAN-2001
PF 29-JUN-2000 WO 2000JP004278
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PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
MOGI,
YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/12, C12N5/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC
A61K38/17,
PC A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7088// (C12P21/
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us-10-019-455a-23.rge

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 30, 2003, 01:02:37 ; Search time 1098.31 Seconds  
(without alignments)  
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Scoring table: IDENTITY\_NUC  
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8: em\_hic:\*  
9: gb\_est1:\*  
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17: em\_gss\_hum:\*  
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29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	252.2	76.4	534	13 BQ564134	BQ564134 g11d01.y

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6	252.2	76.4	608	13 BQ564944	BQ564944 g127g09.y
7	252.2	76.4	630	13 BQ568471	BQ568471 g1108g04.
8	252.2	76.4	684	13 BQ563768	BQ563768 g106c09.y
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10	250.6	75.9	474	13 BQ565637	BQ565637 g142g03.y
11	238.6	72.3	409	13 BQ566932	BQ566932 g173g09.y
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13	236.2	71.6	490	13 BQ565411	BQ565411 g137b12.y
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19	158	47.9	280	13 BQ568785	BQ568785 g1114f04.
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21	131.6	39.9	338	9 AW021345	AW021345 df21c01.y
22	129	39.1	1201	13 BX418941	BX418941 BX418941
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24	118	35.8	533	9 AL925854	AL925854 AL925854
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27	110	33.3	678	10 BB647928	BB647928 BB647928
28	109	33.0	593	9 AL717905	AL717905 AL717905
29	109	33.0	615	9 AL717964	AL717964 AL717964
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ALIGNMENTS

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LOCUS  
DEFINITION  
ACCESSION  
VERSION  
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SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BQ570035 398 bp mRNA linear EST 19-JUN-2002  
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BQ570035  
BQ570035  
EST.

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 398)

EST analysis of gene expression in the mouse Organ of Corti at the

onset of hearing

Unpublished

Contact: Kachar, B.

Structural Cell Biology

National Institute of Deafness and other Communication Disorders

50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA

Tel: 301-402-1599

Fax: 301-402-1765

Email: kachar@nidcd.nih.gov

Plate: 143 row: b column: 10

Seq primer: M13RPI reverse primer (ABI).

Location/Qualifiers

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/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMuLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp , respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been pre-digested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACACGATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."
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Best Local Similarity 85.4%; Pred. No. 9.5e-64;
Matches 281; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
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## RESULT 2

BQ564607

LOCUS

DEFINITION

clone gi19h02 5', mRNA sequence.

ACCESSION

BQ564607

VERSION

BQ564607.1

KEYWORDS

EST.

SOURCE

Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 488)

AUTHORS

Kachar,B.S.

TITLE

EST analysis of gene expression in the mouse Organ of Corti at the

onset of hearing

JOURNAL

Unpublished

COMMENT

Structural Cell Biology

National Institute of Deafness and other Communication Disorders

50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA

Tel: 301-402-1599

Fax: 301-402-1765

Email: kachar@nidcd.nih.gov

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Seq primer: M13RP1 reverse primer (ABI).

Location/Qualifiers

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/dev\_stage="Post natal day 5 to 13"

/clone\_lib="Mouse Organ of Corti cDNA pBluescript"

/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and





ORIGIN	Query Match	76.4%;	Score 252.2;	DB 13;	Length 534;	
	Best Local Similarity	85.4%;	Pred. No. 1.1e-63;			
	Matches 281;	Conservative 0;	Mismatches 48;	Indels 0;	Gaps 0;	
QY	1	CATGAATATTATGACCGCTAGCTTCCAGAGCTCTGTGCAGATGATGAGTGTGC	60			
DB	57	CATGGTGATTATGATAAATCTTCTTAAGAAGTTGTGTGCGATGAGAGTGTGC	116			
QY	61	TATACTATTCTCTGCTAGTCTCAGAGATTATAATGCCCGGACTGTAGATTCATT	120			
DB	117	TATACTATTCTCTGCAAGACACAGGAAGATTACAATGCCCGGACTGTAGTTCATC	176			
QY	121	AACGTTAAAAAGCGCAGCAGATCTATGTGTACTCAAGCTGTGTAAGAAATGAGCT	180			
DB	177	GATGTCAGAAAGGCGCAGCATCTATGTTTACTCAAGCTGTAAACAGAAACGGAGCT	236			
QY	181	GGAGAAATTTGGCTGGCAGTGTATGTGTATGGCCAGCAGATGGGAGTCGTGGGT	240			
DB	237	GGAGAGTTTTGGCTGGCAGTGTATGTGTATGGCCAGCAGATGGGAAATTTGAGGT	296			
QY	241	TATTTCCCGAGCACTTGTCAAGGACACGCTGTGTACCAAGAACTACCAAGGAAGTT	300			
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QY	301	CCACACGAGATATTGACTTCTTCTGCGA	329			
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RESULT 5	B0569741	560 bp	mRNA	linear	EST 19-JUN-2002	
LOCUS	g1135f01.y1	Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA				
DEFINITION	clone g1135f01 5', mRNA sequence.					
ACCESSION	B0569741					
VERSION	B0569741.1	GI:21473058				
KEYWORDS	EST.					
SOURCE	Mus musculus (house mouse)					
ORGANISM	Mus musculus					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
TITLE	1 (bases 1 to 560)					
JOURNAL	Kachar, B.					
COMMENT	EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing					
	Unpublished					
	Contact: Kachar, B.					
	Structural Cell Biology					
	National Institute of Deafness and other Communication Disorders					
	50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA					
	Tel: 301-402-1599					
	Fax: 301-402-1765					
	Email: kachar@nidcd.nih.gov					
	Plate: 135 row: f column: 01					
	Seg primer: M13RP1 reverse primer (ABI).					
FEATURES	Location/Qualifiers					
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	/sex="male and female"					
	/dev_stage="Post natal day 5 to 13"					
	/clone_lib="Mouse Organ of Corti cDNA pBluescript"					
	/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla					

BASE COUNT	160 a	92 c	154 g	153 t	
ORIGIN					
Query Match	76.4%;	Score 252.2;	DB 13;	Length 560;	
Best Local Similarity	85.4%;	Pred. No. 1.1e-63;			
Matches 281;	Conservative 0;	Mismatches 48;	Indels 0;	Gaps 0;	
QY	1	CATGCAATATTATGACCGCTAGCTTCCAGAGCTCTGTGCAGATGATGAGTGTGC	60		
DB	60	CATGGTGATTATGAGATAAATCTTCTTAAGAAGTTGTGTGCGATGAGAGTGTGC	119		
QY	61	TATACTATTCTCTGCGCTAGTCTCAGAGATTATAATGCCCGGACTGTAGATTCATT	120		
DB	120	TATACTATTCTCTGCAAGACACAGGAAGATTACAATGCCCGGACTGTAGTTCATC	179		
QY	121	AACGTTAAAAAGCGCAGCAGATCTATGTGTACTCAAGCTGTGTAAGAAATGAGCT	180		
DB	180	GATGTCAGAAAGGCGCAGCATCTATGTTTACTCAAGCTGTAAACAGAAACGGAGCT	239		
QY	181	GGAGAAATTTGGCTGGCAGTGTATGTGTATGGCCAGCAGATGGGAGTCGTGGGT	240		
DB	240	GGAGAGTTTTGGCTGGCAGTGTATGTGTATGGCCAGCAGATGGGAAATTTGAGGT	299		

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241 TATTTCCTCCAGGAATGGTTCAGGAACACGGTGTGTACCGAGGAGCTACCAAGGAGTT 300  
 300 TATTTCCTCCAGGAATGGTTCAGGAACACGGTGTGTATACCGAGGAGCCACCAAGGAGATC 359  
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 360 CCAACCAAGGATATGACTTCTTCTGTGA 388

RESULT 6  
 BQ564944  
 LOCUS  
 DEFINITION  
 g127g09.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA  
 clone g127g09 5', mRNA sequence.  
 ACCSSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 1 (bases 1 to 608)  
 EST analysis of gene expression in the mouse Organ of Corti at the  
 onset of hearing  
 Unpublished  
 Contact: Kachar, B.  
 Structural Cell Biology  
 National Institute of Deafness and other Communication Disorders  
 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
 Tel: 301-402-1599  
 Fax: 301-402-1765  
 Email: kachar@nidcd.nih.gov  
 Plate: 27 row: G Column: 09  
 Seq primer: M13RPA reverse primer (ABI).  
 Location/Qualifiers  
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 /organism="Mus musculus"  
 /mol\_type="mRNA"  
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 /sex="male and female"  
 /dev\_stage="Post natal day 5 to 13"  
 /clone\_lib="Mouse Organ of Corti cDNA pBluescript"  
 /note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden)

and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XL1 Blue MRP<sup>+</sup> cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGAAACGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 169 a 107 c 166 g 166 t  
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Query Match 76.4%; Score 252.2; DB 13; Length 608;  
 Best Local Similarity 85.4%; Pred. No. 1.2e-63;  
 Matches 281; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 CATGGATATTTATGGACCGTCTAGCTTCCAGAGCTCTGTGAGATGATGAGTGTCTC 60

DB 67 CATGGTATTTATGGATAAACTTCTTCTAAGAAGTTGTGTGCGATGAGAGTGTCTC 126

QY 61 TATCTATTTCTCGGCTAGTCTCAAGAGATATATATGCCCGACTGTAGATTTCATT 120

1 127 TATCTATTTCTCGGCAAGAGCACAGAGATTTACAAATGCCCGAGCTGTAGTTTCATC 186

QY 121 AACGTAAAAAGGCGACAGATCTATGTGTACTCAAAAGCTGGTAAAAAGAAATGGAGCT 180

DB 187 GATGTCAAGAAGGCGACAGATCTATGTGTACTCAAGCTGGTAAACAGAAACCGAGCT 246

QY 181 GGAGAAATTTGGGCTGGCAGTGTATGTGTATGCGCAGGACGAGATGGGAGTCTGGGT 240

DB 247 GGAGAGTTTGGGCTGGCAGTGTATGTGTATGCGCAGGATGAGATGGGAAATTGTAGGT 306

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RESULT 7

BQ568471

LOCUS

DEFINITION

g1108g04.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA

clone g1108g04 5', mRNA sequence.

ACCESSION

BQ568471

VERSION

BQ568471.1

GI:21471788

KEYWORDS

EST.

SOURCE

ORGANISM

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

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BQ568471 630 bp mRNA linear EST 19-JUN-2002

g1108g04.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA

clone g1108g04 5', mRNA sequence.

ACCESSION

BQ568471

VERSION

BQ568471.1

GI:21471788

KEYWORDS

EST.

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

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Kachar, B.  
EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing  
Unpublished  
Contact: Kachar, B.  
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National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kachar@nidcd.nih.gov  
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Seq primer: M13RPI reverse primer (ABI).  
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/clone\_lib="Mouse Organ of Corti: Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on Xl1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTATGACC) and 25' strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster

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178 a 111 c 167 g 174 t

BASE COUNT  
ORIGIN

Query Match 76.4%; Score 252.2; DB 13; Length 630;  
Best Local Similarity 85.4%; Pred. No. 1.2e-63;  
Matches 281; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 CATGGAATTTATGACCGCTCTAGCTTCCAAAGCTCTGTCCAGATGATGATGTC 60  
DB 67 CATGGGTATTTATGGATAAATCTTCTTAAAGATTGTGTCGATGAGGATGTC 126  
QY 61 TATACCTATTTCTGGCTAGTGTCTCAAGAGATTATTAATGCCCGGACTGTAGATTCATT 120  
DB 127 TATACCTATTTCTGGCAAGAGCACAGGAAGATTACATGCCCGGACTGTAGGTTTCATC 186  
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QY 181 GGGAATTTTGGCTGGCAGTGTATGTGTATGATGGCCAGGACAGATGGGAGTCGGGT 240  
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DB 307 TATTTCCCAAGAACTTGGTCAAGGAACAGCGTGTGTATACCAAGGAGCCACCAAGGAGATC 366  
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DB 367 CCAACCAAGGATATGACTTCTTCTGGA 395

RESULT 8  
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LOCUS  
DEFINITION BQ563768.1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone gi06c09 5', mRNA sequence.  
ACCESSION BQ563768  
VERSION BQ563768.1 GI:21466749  
KEYWORDS EST...  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 684)  
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EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing  
Unpublished  
Contact: Kachar, B.  
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Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kachar@nidcd.nih.gov  
Plate: 06 row: c column: 09  
Seq primer: M13RPI reverse primer (ABI).  
Location/Qualifiers  
1. 684  
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/clone="gi06c09"  
/sex="male and female"  
/dev\_stage="Post natal day 5 to 13"

FEATURES  
source

AUTHORS Kachar, B.  
TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing  
JOURNAL Unpublished  
COMMENT Contact: Kachar, B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
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Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kachar@nidcd.nih.gov  
Plate: 108 row: g column: 04  
Seq primer: M13RPI reverse primer (ABI).  
Location/Qualifiers  
1. 630  
/organism="Mus musculus"  
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/clone="g108g04"  
/sex="male and female"  
/dev\_stage="Post natal day 5 to 13"  
/clone\_lib="Mouse Organ of Corti: Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on Xl1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTATGACC) and 25' strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster

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BASE COUNT 194 a 120 c 178 g 192 t  
 ORIGIN  
 Query Match 76.4%; Score 252.2; DB 13; Length 684;  
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 DEFINITION musculus cDNA clone 3110083012 5', mRNA sequence.  
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 SOURCE Mus musculus (house mouse)  
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 1 (bases 1 to 696)  
 REFERENCE Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,  
 Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,  
 M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,  
 Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,  
 D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,  
 Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,  
 Muramatsu,M. and Hayashizaki,Y.  
 RIKEN Mouse ESTs (Arakawa,T., et al. 2001)  
 Unpublished  
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 Sciences Center(GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
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 Fax: 81-45-503-9216  
 Email: genome-res@gsr.riken.go.jp,  
 URL:http://genome.gsc.riken.go.jp/  
 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh  
 M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new  
 genes. Genome Res. 10 (10), 1617-1630 (2000)  
 wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,  
 Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura  
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 Hayashizaki,Y.  
 RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
 10 (11), 1757-1771 (2000)  
 Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara  
 Y. and Hayashizaki,Y.  
 Computer-based methods for the mouse full-length cDNA  
 encyclopedia: real-time sequence clustering for construction of a  
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 Yamanaka,I., Kiyosawa,H., Kondo,S., Saito,T., Shinagawa,A., Aizawa  
 K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K., Arakawa,T.,  
 Ishii,Y. and Hayashizaki,Y.  
 Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.  
 Func. Genomics 2 pre, L72-L86 (2001)  
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for  
 further details.  
 e mouse tissues.  
 Location/Qualifiers

FEATURES

JOURNAL  
COMMENT

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Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5',
GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was
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cap-trapper. cDNA went through one round of normalization
to Rot = 10.0 and subtraction to Rot = 50.0. Second strand
cDNA was prepared with the primer adapter of sequence [5',
GAGAGAGAGATCTCGAGTTAATTAATTAATTCCTCCCCCCCC 3']. cDNA
was cleaved with XhoI and SstI."
204 a 122 c 176 g 194 t
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ORIGIN
Query Match 76.4%; Score 252.2; DB 10; Length 696;
Best Local Similarity 85.4%; Pred. No. 1.2e-63;
Matches 281; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

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QY 301 CCCACCAAGGATATTGACTTCTTCTGCGA 329
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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RESULT 10
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DEFINITION gi42903.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
clone gi42903.5', mRNA sequence.
ACCESSION B0565637
VERSION B0565637.1 GI:21468954
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 474)
AUTHORS Kachar,B.
TITLE EST analysis of gene expression in the mouse Organ of Corti at the
onset of hearing

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## Unpublished

Contact: Kachar, B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kachar@nidcd.nih.gov  
Plate: 42 row: 9 column: 03  
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Location/Qualifiers  
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FEATURES  
source

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organ of Corti (OC) was fine dissected from a total of 386
OC as follows: 102 samples from post-natal (P) day 5; 72
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
14 from P12 and 24 from P13. After killing animals by
cervical dislocation followed by decapitation, the bulla
was removed and opened in Leibowitz medium. The bony
capsule of the cochlea was chipped away, stria vascularis
and spiral ligament were removed and the sensory
epithelium was carefully dissected out of the modiolus.
Total RNA was extracted using the micro Fasttrack kit
(catalog # K1593-02; Invitrogen, Carlsbad, CA), according
to manufacturer's instructions. Reverse transcription and
library construction were carried out with the Uni-Zap XR
vector kit (catalog # 237211, Stratagene) and Uni-Zap XR
Gigapack III Gold Cloning kit (catalog # 237612), both
from Stratagene (La Jolla, CA, USA), according to
manufacturer's instructions. Briefly: 1.5 ug mRNA was
reverse transcribed using a hybrid oligo(dT) linker-primer
primed with the linker- primer and transcribed using
that contains an Xho I site. First strand synthesis was
Moloney murine leukemia virus reverse transcriptase
(MMLV-RT) and 5-methyl dCTP. The second strand was
synthesized with DNA polymerase and RNase H. Complementary
DNA was blunt ended with Pfu DNA polymerase, ligated with
EcoR I adapters in the presence of ligase and digested
with Xho I. The cDNA was sequentially size fractionated
over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden)
and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA)
columns to enrich for cDNAs greater than 400bp and 1000 bp
, respectively. The cDNA was then directionally ligated to
the Uni-ZAP XR vector, which had been predigested with
EcoR I and Xho I. The phagemid was packaged with Gigapack
III Gold and, upon titration on XL1 Blue MRF' cells, the
yield of the phage library was estimated to be 11,100,000
recombinants. Stratagene's ExAssist Interference
resistance helper phage (catalogue # 211203) was adopted
to rescue plasmid DNA from the phages. Upon plating of the
rescued library, individual cDNA clones were selected and
grown in 96-well, 2 ml growth plate. Plasmid DNA was
purified from 200 ul of saturated culture with the
Concert96(TM) plasmid purification kit (Invitrogen,
Carlsbad, CA) as instructed by the manufacturer. ESTs from
the 5' end of the cDNA clones were generated with the
universal M13 reverse primer (CAGGAACAGCTATGACC) and 25%
strength BigDye terminator sequencing chemistry (Applied
Biosystems, Foster City, CA). Sequencing reactions were
performed on MJ Tetrad thermal cyclers (MJ Research,
Waltham, MA), and analyzed on 3700 automated capillary
sequencers using POPs polymer (Applied Biosystems, Foster
City, CA). The frequency distribution of the library is
as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10;
1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of

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genes are present in GenBank and have know function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

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BASE COUNT      145 a   78 c   131 g   120 t
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Query Match      75.9%; Score 250.6; DB 13; Length 474;
Best Local Similarity 85.1%; Pred. No. 3.1e-63;
Matches 280; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
QY 1 CATGGAATTTATGACCGCTAGCTTCCAGAGAGCTGTGCGAGATGATGAGTGTGC 60
Db 68 CATGGTATTATGATGAATACTTTCTTATATAGTTGTGCGGATGAGAGTGTGC 127
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ACCESSION BQ566932
VERSION   BQ566932.1 GI:21470249
KEYWORDS  EST.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 409)
Kachar.B.
EST analysis of gene expression in the mouse Organ of Corti at the
onset of hearing
Unpublished
Contact: Kachar.B.
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: kacharbenidcd.nih.gov
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Seq primer: M13RPl reverse primer (ABI).
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ACCESSION BQ567343
VERSION BQ567343.1 GI:21470660
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

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REFERENCE
AUTHORS Kachar,B.
TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
JOURNAL Unpublished
COMMENT Contact: Kachar,B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: kachar@nidcd.nih.gov
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FEATURES
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```

DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on Xli Blue MRF<sup>+</sup> cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

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VERSION BQ565411.1 GI:21468728
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SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 490)
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Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.  
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)  
 22354683  
 12466851  
 Contact: Yoshitake Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-res@gsc.riken.go.jp/  
 URL: http://genome.gsc.riken.go.jp/  
 Arizawa, K., Akimura, T., Akakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, I., Togami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)  
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Kirk W. Beisel ( Boys Town National Research Hospital 555 North 30th Street Omaha, NE 68131 USA ) whose assistance we gratefully acknowledge. Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

#### FEATURES

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 Matches 244; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 1 CATGGAATATTTTGGACCGCTCTAGCTTCCAGAGCTGTGCAGATGATGAGTGTGTC 60  
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QY 181 GGAGAAATTTTGGCTCGCAGTGTATGCTGATGGCCAGGACGAGATGGGAGTCGTGGCT 240  
 DB 258 GGAGAGTTTGGGGCTGGCAGTGTATGCTGACCCAGGATGAGATGGGAATGTAGGT 317  
 QY 241 TATTTCCCGAGGAAGTGTGTCAAGAACAGCGTGTACAGGAAGC 287  
 DB 318 TATTTCCCGAGCAACTTGGTGAAGGAGCAGCGTGTATACAGGAGGC 364

#### RESULT 15

BU748241 795 bp mRNA linear EST 10-OCT-2002  
 CH3#018 G05T7 Canine heart normalized cDNA Library in pBluescript  
 Canis familiaris cDNA clone CH3#018\_G05 5', mRNA sequence.  
 ACCESSION BU748241 GI:23700286  
 VERSION BU748241.1  
 KEYWORDS EST.  
 SOURCE Canis familiaris (dog)  
 ORGANISM Canis familiaris  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 1 (bases 1 to 795)  
 YI, Y., Desai, R., Olarte, M., Henthorn, P. and George A.L.  
 Expressed sequence tags from Canine heart  
 Unpublished  
 Other ESTs: CH3#018\_G05T3  
 Contact: George A.L.  
 Division of Genetic Medicine  
 Vanderbilt University  
 529 Light Hall, 2215 Garland Avenue, Nashville, TN 37232-0275, USA  
 Tel: 615 936 2660  
 Fax: 615 936 2661  
 Email: al.george@vanderbilt.edu  
 Insert Length: 1892 Std Error: 0.00  
 Seq primer: T7: TAATACGACTCACTATAGG  
 High quality sequence start: 39  
 High quality sequence stop: 559.

#### REFERENCE

#### AUTHORS

#### TITLE

#### JOURNAL

#### COMMENT

#### FEATURES

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 /db\_xref="taxon:9615"  
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 /tissue\_type="heart"  
 /cell\_type="heart"  
 /dev\_stage="mixed developmental stages (adult, 30 day - 40 day fetal)"  
 /clone\_lib="Canine heart normalized cDNA Library in pBluescript"  
 /note="Organ: heart; Vector: pBluescript; Site 1: 5' of vector NotI; Site 2: 3' of vector EcoRI; Tissue source: dog heart (adult, 30 day - 40 day fetal), right and left atria and ventricle. Dog breed - mixed (beagle, German shepherd, pointer, Irish setter). Library construction: oligo-dT primed"  
 199 a 176 c 195 g 225 t

#### BASE COUNT

#### ORIGIN

Query Match 60.2%; Score 198.6; DB 13; Length 795;  
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 Matches 232; Conservative 0; Mismatches 34; Indels 3; Gaps 1;  
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 DB 256 ATACTATTTCTTGGCCAGAGCTCAAAAAGATTACAAATGCCCGGAGCTAGTTCATTA 315  
 QY 122 ACCTTAAAAAGGGCAGCAGATCTATGTCTACTCAAGCTGTGTAAAGAAATGGAGCTG 181  
 DB 316 ATGTGAAAAAGGACAGCAGATTTACGTTTACTCGAGCTGTGTAAAGAAATGGAGCTG 375  
 QY 182 GAGAATTTTGGCTGGCAGTGTATGCTGATGGCC---AGGACGAGATGGGAGTGTGG 238  
 DB 376 GAAAATTTTGGCTGGCAGTGTATGAGATGACCAACGAGGATGAGATGGGAACCGGG 435



Qy	239	GTTATTTC	CCCCAGGAACTTGGTCAAGGAACAGCGTGTGTACCAAGGAAGCTACCAAGGAAG	298
Db	436	GCTATTTC	CCCCAGCAGCTTGGTGGAGGAGCAACACGTTGTACCAAGGAAGCCACCAGGAAG	495
Qy	299	TTCCCA	CCAGGATATTGACTTCTTCGTC	327
Db	496	TCCCCA	CTACGGACATTGACTTCTTCGTC	524

Search completed: December 30, 2003, 06:07:15  
Job time : 1098.64 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 22:01:01 ; Search time 109.538 Seconds  
(without alignments)  
8132.484 Million cell updates/sec

Title: US-10-019-455A-23  
Perfect score: 330  
Sequence: 1 catggaatattatgacgcg.....attatgacttttttgcgag 330

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq 19Jun03:\*

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- 2: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:\*
- 3: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:\*
- 4: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:\*
- 5: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:\*
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- 13: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:\*
- 14: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:\*
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- 23: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*
- 24: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*
- 25: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query % Match	Length	ID	Description
1	330	100.0	330	22	AAF59079 Human MLP nucleoti
2	330	100.0	384	22	AAF59065 Human MLP nucleoti
3	330	100.0	387	24	AA517583 DNA encoding novel
4	330	100.0	426	22	AAH26341 Human growth regul
5	330	100.0	521	24	ABL95740 Human growth regul
6	330	100.0	521	24	ABL88251 Human angiogenesis
7	330	100.0	521	24	ABL88251 Human PRO9873 cDNA
8	330	100.0	891	22	AAH98228 cDNA encoding huma
					Human EST-derived

9	330	100.0	891	22	AAH26342 Human MLP nucleoti
10	330	100.0	923	22	AAF59083 Human growth regul
11	330	100.0	1201	22	AAH26343 Human growth regul
12	252.2	76.4	330	22	AAF59080 Mouse MLP nucleoti
13	252.2	76.4	384	22	AAF59068 Mouse MLP nucleoti
14	252.2	76.4	947	22	AAF59084 Mouse MLP nucleoti
15	249	75.5	330	22	AAF59099 Rat MLP nucleotide
16	249	75.5	384	22	AAF59098 Rat MLP nucleotide
17	214.6	65.0	307	22	AAF59093 Rat MLP nucleotide
18	193.8	58.7	261	22	AAF59092 Rat MLP nucleotide
19	63.4	19.2	433	22	AAH47783 Recombinant human
20	63.4	19.2	459	16	AAQ84050 Sequence encoding
21	63.4	19.2	459	16	AAI70083 Melanoma inhibitor
22	63.4	19.2	459	22	AAI18732 Human antisense ol
23	63.4	19.2	555	23	ABV59229 Human prostate exp
24	63.2	19.2	581	16	AAQ84052 Sequence encoding
25	61.8	18.7	442	24	ABL63602 Breast cancer rela
26	61.8	18.7	442	24	ABL64012 Breast cancer rela
27	57.4	17.4	330	16	AAQ84061 Sequence encoding
28	54.2	16.4	305	16	AAQ84055 Amplified fragment
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30	53.6	16.2	429	22	AA522695 Human cDNA encodin
31	53.6	16.2	884	22	AA522459 Human TANGO 130 pa
32	53.6	16.2	1230	24	ABQ79850 Human TANGO 130 CD
33	53.6	16.2	1263	21	AAZ51245 Human TANGO 130 po
34	53.6	16.2	1263	24	ABQ79849 Human prostate exp
35	53.6	16.2	4409	23	ABV21035 Human prostate exp
36	53.6	16.2	4409	23	ABV21751 Human prostate exp
37	53.6	16.2	4409	23	ABV26878 Human prostate exp
38	53.6	16.2	4409	23	ABV29625 Human prostate exp
39	53.6	16.2	5724	24	ABQ79852 Human TANGO 130 po
40	53.6	16.2	8121	24	ABQ79851 Human TANGO 130 po
41	52	15.8	417	22	AAH93775 Human protein enco
42	46	13.9	1060	22	AAF92140 Human PRO19670 cDN
43	46	13.9	1060	24	AB574460 Human cDNA encodin
44	46	13.9	1060	24	ABL95738 Human angiogenesis
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ALIGNMENTS

RESULT 1  
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ID AAF59079 standard; DNA; 330 BP.

XX AAF59079;

XX 23-APR-2001 (first entry)

DT Human MLP nucleotide sequence SEQ ID NO:23.

DE MLP; MTA; melanoma inhibitory activity; cancer; bone disease;

XX joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;

KW cardiant; gene therapy; secretory cell function regulator; promoter;

KW inhibitor; ds.

XX OS Homo sapiens.

XX WO200102564-A1.

XX 11-JAN-2001.

XX 29-JUN-2000; 2000WO-JP04278.

XX 30-JUN-1999; 99JP-0186718.

XX (TAKE ) TAKEDA CHEM IND LTD.

PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;

PI Tanaka H;

XX WPI; 2001-159271/16.

; PRIOR FILING DATE: 1999-08-17  
 ; PRIOR APPLICATION NUMBER: 60/149638  
 ; PRIOR FILING DATE: 1999-08-17  
 ; PRIOR APPLICATION NUMBER: 60/151733  
 ; PRIOR FILING DATE: 1999-08-31  
 ; PRIOR APPLICATION NUMBER: 60/164418  
 ; PRIOR FILING DATE: 1999-11-09  
 ; PRIOR APPLICATION NUMBER: 60/166361  
 ; PRIOR FILING DATE: 1999-11-16  
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 ; PRIOR APPLICATION NUMBER: 60/169835

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DB	92	CATGGAATATTATGGACCGTCTAGCTTCCAAAGAACTCTGTGCAGATGATGAGTGTGC	151
QY	61	TATACATTTCTGTGGCTAGTGTCTCAAGAGATTATATGCCCCGGACTGTAGATTCATT	120
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QY	121	AACGTTAAAGAAAGGCGACAGATCTATGTGTACTCAAGAGCTGTGTAAGAAATGGAGCT	180
DB	212	AACGTTAAAGAAAGGCGACAGATCTATGTGTACTCAAGAGCTGTGTAAGAAATGGAGCT	271
QY	181	GGAGAAATTTGGCTGGCAGTGTGTTATGTTGATGCGCAGACAGATGGAGTGTGGGT	240
DB	272	GGAGAAATTTGGCTGGCAGTGTGTTATGTTGATGCGCAGACAGATGGAGTGTGGGT	331
QY	241	TATTTCCCGAGAACTTGGTCAAGAACAGAGCTGTGTACCAAGAGCTTACCAAGAAATG	300
DB	332	TATTTCCCGAGAACTTGGTCAAGAACAGAGCTGTGTGTACCAAGAGCTTACCAAGAAATG	391
QY	301	CCACACCGATATTGACTTCTTCTGCGAG	330
DB	392	CCACACCGATATTGACTTCTTCTGCGAG	421

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 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Gerritsen, Mary  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stephan, Jean-Philippe F.  
 ; APPLICANT: Watanabe, Colin L.  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P3530PIC24  
 ; CURRENT APPLICATION NUMBER: US/10/219,063  
 ; CURRENT FILING DATE: 2002-08-13  
 ; PRIOR APPLICATION NUMBER: 10/119,480  
 ; PRIOR FILING DATE: 2002-04-09  
 ; PRIOR APPLICATION NUMBER: 60/059113  
 ; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/062287  
 ; PRIOR FILING DATE: 1997-10-17  
 ; PRIOR APPLICATION NUMBER: 60/063549  
 ; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/064103  
 ; PRIOR FILING DATE: 1997-10-31  
 ; PRIOR APPLICATION NUMBER: 60/069873  
 ; PRIOR FILING DATE: 1997-12-17  
 ; PRIOR APPLICATION NUMBER: 60/078910  
 ; PRIOR FILING DATE: 1998-03-20  
 ; PRIOR APPLICATION NUMBER: 60/079294  
 ; PRIOR FILING DATE: 1998-03-25  
 ; PRIOR APPLICATION NUMBER: 60/079656  
 ; PRIOR FILING DATE: 1998-03-26  
 ; PRIOR APPLICATION NUMBER: 60/079728  
 ; PRIOR FILING DATE: 1998-03-27  
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 ; LENGTH: 521  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 US-10-219-063-71

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QY	181	GGAGAAATTTGGCTGGCAGTGTGTTATGTTGATGCGCAGACAGATGGAGTGTGGGT	240
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QY	241	TATTTCCCGAGAACTTGGTCAAGAACAGAGCTGTGTACCAAGAGCTTACCAAGAAATG	300
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DB	392	CCACACCGATATTGACTTCTTCTGCGAG	421

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 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Gerritsen, Mary  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stephan, Jean-Philippe F.  
 ; APPLICANT: Watanabe, Colin L.  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P3530PIC27  
 ; CURRENT APPLICATION NUMBER: US/10/219,066  
 ; CURRENT FILING DATE: 2002-08-13  
 ; PRIOR APPLICATION NUMBER: 10/119,480  
 ; PRIOR FILING DATE: 2002-04-09  
 ; PRIOR APPLICATION NUMBER: 60/059113

; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
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; PRIOR FILING DATE: 1998-03-25
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; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-066-71

Query Match 100.0%; Score 330; DB 13; Length 521;
Best Local Similarity 100.0%; Pred. No. 7.2e-100;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATGGATATTATTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTGTC 60
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QY 61 TATACATTTCTCTGGCTAGTGTCTCAAGAAATATATAATGCCCGGAGCTGTAGATTCATT 120
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; Publication No. US20030187204A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC51

; CURRENT APPLICATION NUMBER: US/10/219,067
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-067-71

Query Match 100.0%; Score 330; DB 13; Length 521;
Best Local Similarity 100.0%; Pred. No. 7.2e-100;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATGGATATTATTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTGTC 60
DB 92 CATGGATATTATTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTGTC 151

QY 61 TATACATTTCTCTGGCTAGTGTCTCAAGAAATATATAATGCCCGGAGCTGTAGATTCATT 120
DB 152 TATACATTTCTCTGGCTAGTGTCTCAAGAAATATATAATGCCCGGAGCTGTAGATTCATT 211

QY 121 AACGTTAAAAAGGCGACAGATCTATGTGTACTCAAGAGCTGGTAAAGAAAATCGAGCT 180
DB 212 AACGTTAAAAAGGCGACAGATCTATGTGTACTCAAGAGCTGGTAAAGAAAATCGAGCT 271

QY 181 GGAGAAATTTTGGGCTGGCAGTGTATTATGGTATGTCAGGAGCGAGATGGGAGTCTGGGT 240
DB 272 GGAGAAATTTTGGGCTGGCAGTGTATTATGGTATGTCAGGAGCGAGATGGGAGTCTGGGT 331

QY 241 TATTTCCCGAGAACTTGGTCAAGAAACAGCGTGTGTACCCAGAAAGCTACCAAGGAAGTT 300
DB 332 TATTTCCCGAGAACTTGGTCAAGAAACAGCGTGTGTACCCAGAAAGCTACCAAGGAAGTT 391

QY 301 CCCACACGGATATTGACTTCTTCTGCGAG 330
DB 392 CCCACACGGATATTGACTTCTTCTGCGAG 421

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; Publication No. US20030187205A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.

Tue Dec 30 10:20:39 2003

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; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C31
; CURRENT APPLICATION NUMBER: US/10/219,068
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-219-068-71

```

```

Query Match 100.0%; Score 330; DB 13; Length 521;
Best Local Similarity 100.0%; Pred. No. 7.2e-100;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATGGAATATTTATGACCGCTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGTGTGC 60
Db 92 CATGGAATATTTATGACCGCTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGTGTGC 151

QY 61 TATACTATTTCTCTGGCTAGTGTCTCAAGAAGATTAATAATCCCGGAGCTGTAGATTCATT 120
Db 152 TATACTATTTCTCTGGCTAGTGTCTCAAGAAGATTAATAATCCCGGAGCTGTAGATTCATT 211

QY 121 AACGTTAAAAAGGCGAGCAGATCTATGTGTACTCAAGCTGGTAAAGAAATGGAGCT 180
Db 212 AACGTTAAAAAGGCGAGCAGATCTATGTGTACTCAAGCTGGTAAAGAAATGGAGCT 271

QY 181 GGAGAAATTTGGGCTGGCAGTGTATTTATGGTATGGCCAGGACGAGATGGAGTCGTGGGT 240
Db 272 GGAGAAATTTGGGCTGGCAGTGTATTTATGGTATGGCCAGGACGAGATGGAGTCGTGGGT 331

QY 241 TATTTCCCAAGGAACCTTGGTCAAGAACAGCTGTGTACCAAGGAGCTACCAAGGAAGTT 300
Db 332 TATTTCCCAAGGAACCTTGGTCAAGAACAGCTGTGTACCAAGGAGCTACCAAGGAAGTT 391

QY 301 CCCACCACGGATATTGACTTCTTCTCGGAG 330
Db 392 CCCACCACGGATATTGACTTCTTCTCGGAG 421

```

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RESULT 8
US-10-219-069-71
; Sequence 71, Application US/10219069
; Publication No. US20030187206A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey

```

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; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C40
; CURRENT APPLICATION NUMBER: US/10/219,069
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-219-069-71

```

```

Query Match 100.0%; Score 330; DB 13; Length 521;
Best Local Similarity 100.0%; Pred. No. 7.2e-100;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATGGAATATTTATGACCGCTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGTGTGC 60
Db 92 CATGGAATATTTATGACCGCTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGTGTGC 151

QY 61 TATACTATTTCTCTGGCTAGTGTCTCAAGAAGATTAATAATCCCGGAGCTGTAGATTCATT 120
Db 152 TATACTATTTCTCTGGCTAGTGTCTCAAGAAGATTAATAATCCCGGAGCTGTAGATTCATT 211

QY 121 AACGTTAAAAAGGCGAGCAGATCTATGTGTACTCAAGCTGGTAAAGAAATGGAGCT 180
Db 212 AACGTTAAAAAGGCGAGCAGATCTATGTGTACTCAAGCTGGTAAAGAAATGGAGCT 271

QY 181 GGAGAAATTTGGGCTGGCAGTGTATTTATGGTATGGCCAGGACGAGATGGAGTCGTGGGT 240
Db 272 GGAGAAATTTGGGCTGGCAGTGTATTTATGGTATGGCCAGGACGAGATGGAGTCGTGGGT 331

QY 241 TATTTCCCAAGGAACCTTGGTCAAGGAACAGCTGTGTGTACCAAGGAGCTACCAAGGAAGTT 300
Db 332 TATTTCCCAAGGAACCTTGGTCAAGGAACAGCTGTGTGTACCAAGGAGCTACCAAGGAAGTT 391

QY 301 CCCACCACGGATATTGACTTCTTCTCGGAG 330
Db 392 CCCACCACGGATATTGACTTCTTCTCGGAG 421

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RESULT 9
US-10-219-073-71
; Sequence 71, Application US/10219073
; Publication No. US20030187207A1

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```

; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C52
; CURRENT APPLICATION NUMBER: US/10/219,073
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-219-073-71

Query Match      100.0%; Score 330; DB 13; Length 521;
Best Local Similarity 100.0%; Pred. No. 7.2e-100;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATGGAATATTTATGGACCGTCTAGCTTCCAGAGAGCTCTGTGCAGATGATGAGTGTGTC 60
Db 92 CATGGAATATTTATGGACCGTCTAGCTTCCAGAGAGCTCTGTGCAGATGATGAGTGTGTC 151

QY 61 TATACATATTTCTCGGTAGTGTCTCAAGAAGATTATATGCCCCGGACTGTAGATTCATT 120
Db 152 TATACATATTTCTCGGTAGTGTCTCAAGAAGATTATATGCCCCGGACTGTAGATTCATT 211

QY 121 AACGTTAAAAAGGCGCAGACATCTATGTGTACTCAAGAGCTGTGTAAAGAAAATCGAGCT 180
Db 212 AACGTTAAAAAGGCGCAGACATCTATGTGTACTCAAGAGCTGTGTAAAGAAAATCGAGCT 271

QY 181 GGAGAAATTTTGGGCTGGCAGTGTATGTTGTTATGTTGATGTCAGGAGCGAGATCGGTGGGT 240
Db 272 GGAGAAATTTTGGGCTGGCAGTGTATGTTGTTATGTTGATGTCAGGAGCGAGATCGGTGGGT 331

QY 241 TATTTCCCGAGAACTTGGTCAAGGAAACAGCGTGTGTACCGAGAAAGCTTACCAAGGAAGTT 300
Db 332 TATTTCCCGAGAACTTGGTCAAGGAAACAGCGTGTGTACCGAGAAAGCTTACCAAGGAAGTT 391

; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C49
; CURRENT APPLICATION NUMBER: US/10/219,475
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-219-475-71

Query Match      100.0%; Score 330; DB 13; Length 521;
Best Local Similarity 100.0%; Pred. No. 7.2e-100;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATGGAATATTTATGGACCGTCTAGCTTCCAGAGAGCTCTGTGCAGATGATGAGTGTGTC 60
Db 92 CATGGAATATTTATGGACCGTCTAGCTTCCAGAGAGCTCTGTGCAGATGATGAGTGTGTC 151

QY 61 TATACATATTTCTCGGTAGTGTCTCAAGAAGATTATATGCCCCGGACTGTAGATTCATT 120
Db 152 TATACATATTTCTCGGTAGTGTCTCAAGAAGATTATATGCCCCGGACTGTAGATTCATT 211

QY 121 AACGTTAAAAAGGCGCAGACATCTATGTGTACTCAAGAGCTGTGTAAAGAAAATCGAGCT 180
Db 212 AACGTTAAAAAGGCGCAGACATCTATGTGTACTCAAGAGCTGTGTAAAGAAAATCGAGCT 271

QY 181 GGAGAAATTTTGGGCTGGCAGTGTATGTTGTTATGTTGATGTCAGGAGCGAGATCGGTGGGT 240
Db 272 GGAGAAATTTTGGGCTGGCAGTGTATGTTGTTATGTTGATGTCAGGAGCGAGATCGGTGGGT 331

QY 241 TATTTCCCGAGAACTTGGTCAAGGAAACAGCGTGTGTACCGAGAAAGCTTACCAAGGAAGTT 300
Db 332 TATTTCCCGAGAACTTGGTCAAGGAAACAGCGTGTGTACCGAGAAAGCTTACCAAGGAAGTT 391

; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C49
; CURRENT APPLICATION NUMBER: US/10/219,475
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-219-475-71

Query Match      100.0%; Score 330; DB 13; Length 521;
Best Local Similarity 100.0%; Pred. No. 7.2e-100;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATGGAATATTTATGGACCGTCTAGCTTCCAGAGAGCTCTGTGCAGATGATGAGTGTGTC 60
Db 92 CATGGAATATTTATGGACCGTCTAGCTTCCAGAGAGCTCTGTGCAGATGATGAGTGTGTC 151

QY 61 TATACATATTTCTCGGTAGTGTCTCAAGAAGATTATATGCCCCGGACTGTAGATTCATT 120
Db 152 TATACATATTTCTCGGTAGTGTCTCAAGAAGATTATATGCCCCGGACTGTAGATTCATT 211

QY 121 AACGTTAAAAAGGCGCAGACATCTATGTGTACTCAAGAGCTGTGTAAAGAAAATCGAGCT 180
Db 212 AACGTTAAAAAGGCGCAGACATCTATGTGTACTCAAGAGCTGTGTAAAGAAAATCGAGCT 271

QY 181 GGAGAAATTTTGGGCTGGCAGTGTATGTTGTTATGTTGATGTCAGGAGCGAGATCGGTGGGT 240
Db 272 GGAGAAATTTTGGGCTGGCAGTGTATGTTGTTATGTTGATGTCAGGAGCGAGATCGGTGGGT 331

QY 241 TATTTCCCGAGAACTTGGTCAAGGAAACAGCGTGTGTACCGAGAAAGCTTACCAAGGAAGTT 300
Db 332 TATTTCCCGAGAACTTGGTCAAGGAAACAGCGTGTGTACCGAGAAAGCTTACCAAGGAAGTT 391

; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C49
; CURRENT APPLICATION NUMBER: US/10/219,475
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-219-475-71

Query Match      100.0%; Score 330; DB 13; Length 521;
Best Local Similarity 100.0%; Pred. No. 7.2e-100;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATGGAATATTTATGGACCGTCTAGCTTCCAGAGAGCTCTGTGCAGATGATGAGTGTGTC 60
Db 92 CATGGAATATTTATGGACCGTCTAGCTTCCAGAGAGCTCTGTGCAGATGATGAGTGTGTC 151

QY 61 TATACATATTTCTCGGTAGTGTCTCAAGAAGATTATATGCCCCGGACTGTAGATTCATT 120
Db 152 TATACATATTTCTCGGTAGTGTCTCAAGAAGATTATATGCCCCGGACTGTAGATTCATT 211

QY 121 AACGTTAAAAAGGCGCAGACATCTATGTGTACTCAAGAGCTGTGTAAAGAAAATCGAGCT 180
Db 212 AACGTTAAAAAGGCGCAGACATCTATGTGTACTCAAGAGCTGTGTAAAGAAAATCGAGCT 271

QY 181 GGAGAAATTTTGGGCTGGCAGTGTATGTTGTTATGTTGATGTCAGGAGCGAGATCGGTGGGT 240
Db 272 GGAGAAATTTTGGGCTGGCAGTGTATGTTGTTATGTTGATGTCAGGAGCGAGATCGGTGGGT 331

QY 241 TATTTCCCGAGAACTTGGTCAAGGAAACAGCGTGTGTACCGAGAAAGCTTACCAAGGAAGTT 300
Db 332 TATTTCCCGAGAACTTGGTCAAGGAAACAGCGTGTGTACCGAGAAAGCTTACCAAGGAAGTT 391
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Tue Dec 30 10:20:39 2003

Db 272 GGAGAAATTTTGGGCTGGCAGTGTATTATGTTGATGGCCAGGACGAGATGGGAGTGTGGGT 331  
 Qy 241 TATTTCCCAAGGACTTGGTCAAGGAACAGCGTGTGTACCAAGGAGCTTACCAAGGAGCTT 300  
 Db 332 TATTTCCCAAGGAACTTGGTCAAGGAACAGCGTGTGTACCAAGGAGCTTACCAAGGAGCTT 391  
 Qy 301 CCACACGAGATATTGACTTCTTCTGCGAG 330  
 Db 392 CCCACACGAGATATTGACTTCTTCTGCGAG 421

RESULT 12  
 US-10-219-483-71  
 ; Sequence 71, Application US/10219483  
 ; Publication No. US20030187210A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Gerritsen, Mary  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stephan, Jean-Philippe F.  
 ; APPLICANT: Watanabe, Colin L.  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P3530PIC43  
 ; CURRENT APPLICATION NUMBER: US/10/219,483  
 ; CURRENT FILING DATE: 2002-08-13  
 ; PRIOR APPLICATION NUMBER: 10/119,480  
 ; PRIOR FILING DATE: 2002-04-09  
 ; PRIOR APPLICATION NUMBER: 60/059113  
 ; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/062287  
 ; PRIOR FILING DATE: 1997-10-17  
 ; PRIOR APPLICATION NUMBER: 60/063549  
 ; PRIOR FILING DATE: 1997-10-28  
 ; PRIOR APPLICATION NUMBER: 60/064103  
 ; PRIOR FILING DATE: 1997-10-31  
 ; PRIOR APPLICATION NUMBER: 60/069873  
 ; PRIOR FILING DATE: 1997-12-17  
 ; PRIOR APPLICATION NUMBER: 60/078910  
 ; PRIOR FILING DATE: 1998-03-20  
 ; PRIOR APPLICATION NUMBER: 60/079656  
 ; PRIOR FILING DATE: 1998-03-26  
 ; PRIOR APPLICATION NUMBER: 60/079728  
 ; PRIOR FILING DATE: 1998-03-27  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 246  
 ; SEQ ID NO 71  
 ; LENGTH: 521  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 ; US-10-219-483-71

Query Match 100.0%; Score 330; DB 13; Length 521;  
 Best Local Similarity 100.0%; Pred. No. 7.2e-100;  
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATGGAATATTTATGGACCGTCTAGCTTCCAAGAGCTCTGTGCAGATGATGATGTC 60  
 Db 92 CATGGAATATTTATGGACCGTCTAGCTTCCAAGAGCTCTGTGCAGATGATGATGTC 151  
 Qy 61 TATACTATTTCTCTGGCTAGTGTCTCAAGAGATTAATAATGCCCGGACTGTAGATTCATT 120  
 Db 152 TATACTATTTCTCTGGCTAGTGTCTCAAGAGATTAATAATGCCCGGACTGTAGATTCATT 211  
 Qy 121 AACGTTAAAAAGGGCAGCAGATCTATGTGTACTCAAGCTGTGTAAAGAAATGGAGCT 180

Qy 301 CCCACACGAGATATTGACTTCTTCTGCGAG 330  
 Db 392 CCCACACGAGATATTGACTTCTTCTGCGAG 421

RESULT 11  
 US-10-219-480-71  
 ; Sequence 71, Application US/10219480  
 ; Publication No. US20030187209A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Gerritsen, Mary  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stephan, Jean-Philippe F.  
 ; APPLICANT: Watanabe, Colin L.  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P3530PIC38  
 ; CURRENT APPLICATION NUMBER: US/10/219,480  
 ; CURRENT FILING DATE: 2002-08-13  
 ; PRIOR APPLICATION NUMBER: 10/119,480  
 ; PRIOR FILING DATE: 2002-04-09  
 ; PRIOR APPLICATION NUMBER: 60/059113  
 ; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/062287  
 ; PRIOR FILING DATE: 1997-10-17  
 ; PRIOR APPLICATION NUMBER: 60/063549  
 ; PRIOR FILING DATE: 1997-10-28  
 ; PRIOR APPLICATION NUMBER: 60/064103  
 ; PRIOR FILING DATE: 1997-10-31  
 ; PRIOR APPLICATION NUMBER: 60/069873  
 ; PRIOR FILING DATE: 1997-12-17  
 ; PRIOR APPLICATION NUMBER: 60/078910  
 ; PRIOR FILING DATE: 1998-03-20  
 ; PRIOR APPLICATION NUMBER: 60/079294  
 ; PRIOR FILING DATE: 1998-03-25  
 ; PRIOR APPLICATION NUMBER: 60/079656  
 ; PRIOR FILING DATE: 1998-03-26  
 ; PRIOR APPLICATION NUMBER: 60/079728  
 ; PRIOR FILING DATE: 1998-03-27  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 246  
 ; SEQ ID NO 71  
 ; LENGTH: 521  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 ; US-10-219-480-71

Query Match 100.0%; Score 330; DB 13; Length 521;  
 Best Local Similarity 100.0%; Pred. No. 7.2e-100;  
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATGGAATATTTATGGACCGTCTAGCTTCCAAGAGCTCTGTGCAGATGATGATGTC 60  
 Db 92 CATGGAATATTTATGGACCGTCTAGCTTCCAAGAGCTCTGTGCAGATGATGATGTC 151  
 Qy 61 TATACTATTTCTCTGGCTAGTGTCTCAAGAGATTAATAATGCCCGGACTGTAGATTCATT 120  
 Db 152 TATACTATTTCTCTGGCTAGTGTCTCAAGAGATTAATAATGCCCGGACTGTAGATTCATT 211  
 Qy 121 AACGTTAAAAAGGGCAGCAGATCTATGTGTACTCAAGCTGTGTAAAGAAATGGAGCT 180  
 Db 212 AACGTTAAAAAGGGCAGCAGATCTATGTGTACTCAAGCTGTGTAAAGAAATGGAGCT 271  
 Qy 181 GGAGAAATTTGGGCTGGCAGTGTATTATGTTGATGGCCAGGACGAGATGGGAGTCGTGGGT 240



```

Db 212 AACGTTAAAAAGGCGCAGAGATCTATGTGTCTCAAGAGCTGGTAAAGAAATGGAGCT 271
Qy 181 GGAGAAATTTTGGGCTGCGAGTGTATGTGTATGCGGCGAGCAGAGATGGAGTGGTGGT 240
Db 272 GGAGAAATTTTGGGCTGCGAGTGTATGTGTATGCGGCGAGCAGAGATGGAGTGGTGGT 331
Qy 241 TATTTCCCGGAGAACTTGGTCAAGAAACAGCGTGTGTACCAAGAAAGTGTACCAAGAAAGTT 300
Db 332 TATTTCCCGGAGAACTTGGTCAAGAAACAGCGTGTGTACCAAGAAAGTGTACCAAGAAAGTT 391
Qy 301 CCCACCGAGATATTGACTTCTCTGCGAG 330
Db 392 CCCACCGAGATATTGACTTCTCTGCGAG 421

RESULT 13
US-10-219-525-71
; Sequence 71, Application US/10219525
; Publication No. US20030187211A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC29
; CURRENT APPLICATION NUMBER: US/10/219,525
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-525-71
Query Match 100.0%; Score 330; DB 13; Length 521;
Best Local Similarity 100.0%; Pred. No. 7.2e-100;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 61 TATCTATTCTCTGGCTAGTGTCAAGAAAGATTTATATGCCCCGGAGTCTGTAGATTCATT 120
Db 152 TATCTATTCTCTGGCTAGTGTCAAGAAAGATTTATATGCCCCGGAGTCTGTAGATTCATT 211
Qy 121 AACGTTAAAAAGGCGCAGAGATCTATGTGTCTCAAGAGCTGGTAAAGAAATGGAGCT 180
Db 212 AACGTTAAAAAGGCGCAGAGATCTATGTGTCTCAAGAGCTGGTAAAGAAATGGAGCT 271
Qy 181 GGAGAAATTTTGGGCTGCGAGTGTATGTGTATGCGGCGAGCAGAGATGGAGTGGTGGT 240
Db 272 GGAGAAATTTTGGGCTGCGAGTGTATGTGTATGCGGCGAGCAGAGATGGAGTGGTGGT 331
Qy 241 TATTTCCCGGAGAACTTGGTCAAGAAACAGCGTGTGTACCAAGAAAGTGTACCAAGAAAGTT 300
Db 332 TATTTCCCGGAGAACTTGGTCAAGAAACAGCGTGTGTACCAAGAAAGTGTACCAAGAAAGTT 391
Qy 301 CCCACCGAGATATTGACTTCTCTGCGAG 330
Db 392 CCCACCGAGATATTGACTTCTCTGCGAG 421

RESULT 14
US-10-219-526-71
; Sequence 71, Application US/10219526
; Publication No. US20030187212A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC41
; CURRENT APPLICATION NUMBER: US/10/219,526
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-526-71
Query Match 100.0%; Score 330; DB 13; Length 521;
Best Local Similarity 100.0%; Pred. No. 7.2e-100;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 CATGGAATATTATGACCGCTCTAGCTTCCAGAGCTCTGTGCAGATGATGAGTGTGTC 60
Db 92 CATGGAATATTATGACCGCTCTAGCTTCCAGAGCTCTGTGCAGATGATGAGTGTGTC 151
Qy 61 TATACTATTCTCTGGCTAGTGTCAAGAAGATTATAATGCCCGGACTGTAGATTCAAT 120
Db 152 TATACTATTCTCTGGCTAGTGTCAAGAAGATTATAATGCCCGGACTGTAGATTCAAT 211
Qy 121 AAGCTTAAAAAGGCGACGAGATCTATGTGTACTCAAGCTGGTAAAGAAAATGGAGCT 180
Db 212 AAGCTTAAAAAGGCGACGAGATCTATGTGTACTCAAGCTGGTAAAGAAAATGGAGCT 271
Qy 181 GGAGAAATTTTGGGCTGGCAGTGTATGTGTGATGGCCAGGACGAGATGGGAGTCTGGGT 240
Db 272 GGAGAAATTTTGGGCTGGCAGTGTATGTGTGATGGCCAGGACGAGATGGGAGTCTGGGT 331
Qy 241 TATTTCGCCAGGAACCTTGGTCAAGAACAGCGTGTGTACAGGAAGCTACCAAGGAAGTT 300
Db 332 TATTTCGCCAGGAACCTTGGTCAAGAACAGCGTGTGTACAGGAAGCTACCAAGGAAGTT 391
Qy 301 CCCACCAAGGATATTGACTTCTTCTGCGAG 330
Db 392 CCCACCAAGGATATTGACTTCTTCTGCGAG 421
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## RESULT 15

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US-10-219-530-71
; Sequence 71, Application US/10219530
; Publication No. US20030187213A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C54
; CURRENT APPLICATION NUMBER: US/10/219,530
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
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## US-10-219-530-71

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Query Match 100.0%; Score 330; DB 13; Length 521;
Best Local Similarity 100.0%; Pred. No. 7.2e-100; Indels 0; Gaps 0;
Matches 330; Conservative 0; Mismatches 0;

Qy 1 CATGGAATATTATGACCGCTCTAGCTTCCAGAGCTCTGTGCAGATGATGAGTGTGTC 60
Db 92 CATGGAATATTATGACCGCTCTAGCTTCCAGAGCTCTGTGCAGATGATGAGTGTGTC 151
Qy 61 TATACTATTCTCTGGCTAGTGTCAAGAAGATTATAATGCCCGGACTGTAGATTCAAT 120
Db 152 TATACTATTCTCTGGCTAGTGTCAAGAAGATTATAATGCCCGGACTGTAGATTCAAT 211
Qy 121 AAGCTTAAAAAGGCGACGAGATCTATGTGTACTCAAGCTGGTAAAGAAAATGGAGCT 180
Db 212 AAGCTTAAAAAGGCGACGAGATCTATGTGTACTCAAGCTGGTAAAGAAAATGGAGCT 271
Qy 181 GGAGAAATTTTGGGCTGGCAGTGTATGTGTGATGGCCAGGACGAGATGGGAGTCTGGGT 240
Db 272 GGAGAAATTTTGGGCTGGCAGTGTATGTGTGATGGCCAGGACGAGATGGGAGTCTGGGT 331
Qy 241 TATTTCGCCAGGAACCTTGGTCAAGAACAGCGTGTGTACAGGAAGCTACCAAGGAAGTT 300
Db 332 TATTTCGCCAGGAACCTTGGTCAAGAACAGCGTGTGTACAGGAAGCTACCAAGGAAGTT 391
Qy 301 CCCACCAAGGATATTGACTTCTTCTGCGAG 330
Db 392 CCCACCAAGGATATTGACTTCTTCTGCGAG 421
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Search completed: December 30, 2003, 10:03:02  
Job time : 271.994 secs

Tue Dec 30 10:20:39 2003

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 30, 2003, 01:34:27 ; Search time 26.6527 Seconds  
(without alignments)  
5464.987 Million cell updates/sec

Title: US-10-019-455A-23

Perfect score: 330

Sequence: 1 catggaatatttgagccg.....atattgactttcttgcgag 330

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.\*

- 1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq.\*
- 2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq.\*
- 3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/2/ina/PCFUS\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63.4	19.2	459	1	US-08-578-649-1
2	63.2	19.2	581	1	US-08-578-649-4
3	57.4	17.4	330	1	US-08-578-649-18
4	54.2	16.4	305	1	US-08-578-649-8
5	40.4	12.2	596	1	US-08-578-649-24
6	40.4	12.2	3565	1	US-08-578-649-3
7	34	10.3	7218	1	US-08-232-463-14
8	33.6	10.2	1136	3	US-08-860-820-1
9	33.6	10.2	1929	4	US-09-359-161-4
10	33.6	10.2	2159	3	US-08-286-870A-7
11	32.8	9.9	6501	4	US-09-767-515-1
12	32.8	9.9	6501	4	US-09-767-515-2
13	32.2	9.8	202001	4	US-09-734-674-3
14	31.4	9.5	1944	4	US-09-252-991A-889
15	31.2	9.5	4403765	3	US-09-103-840A-2
16	31.2	9.5	4411529	3	US-09-103-840A-1
17	30.8	9.3	1736	3	US-09-360-197-13
18	30.4	9.2	289	3	US-09-007-008-17
19	30.4	9.2	289	3	US-09-244-798-17
20	29.8	9.0	1830121	4	US-09-557-884-1
21	29.8	9.0	1830121	4	US-09-643-990A-1
22	29.6	9.0	1000	3	US-09-018-584A-38
23	29.6	9.0	319608	4	US-09-539-333D-1
24	29.6	9.0	319608	4	US-09-679-409-1
25	29.4	8.9	1497	4	US-09-220-132-94
26	29.4	8.9	2718	4	US-09-651-656-14
27	29.4	8.9	2718	4	US-09-650-855-14

28	29.2	8.8	876	4	US-09-107-532A-3486
29	29.2	8.8	1718	4	US-09-620-312D-161
30	29.2	8.8	3101	2	US-08-868-786-1
31	29.2	8.8	3489	4	US-09-134-001C-1171
32	29	8.8	810	4	US-09-252-991A-10933
C 33	29	8.8	10357	4	US-08-961-527-191
C 34	29	8.8	45175	4	US-09-453-702B-116
35	28.8	8.7	1497	4	US-09-220-132-94
36	28.8	8.7	1941	4	US-09-107-532A-2654
37	28.6	8.7	849	4	US-09-252-991A-1103
C 38	28.6	8.7	1518	2	US-08-929-501-4
39	28.6	8.7	1518	2	US-08-929-501-5
C 40	28.6	8.7	1518	3	US-09-140-177-4
41	28.6	8.7	1518	3	US-09-140-177-5
C 42	28.6	8.7	1518	3	US-09-397-979-4
C 43	28.6	8.7	1518	3	US-09-397-979-5
C 44	28.6	8.7	1753	2	US-08-929-501-1
45	28.6	8.7	1753	2	US-08-929-501-3

ALIGNMENTS

RESULT 1  
US-08-578-649-1  
; Sequence 1, Application US/08578649  
; Patent No. 5770366  
; GENERAL INFORMATION:  
; APPLICANT: Ulrich Bogdan  
; APPLICANT: Reinhard Buttner  
; APPLICANT: Brigitte Kaluza  
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felfe & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/578,649  
FILING DATE: 29-July-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P 43 24 247.2  
FILING DATE: 20-July-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Andrew L. Tiajoloiff  
REGISTRATION NUMBER: 31,575  
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 459 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 40..432  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 40..111  
FEATURE:

Sequence 3486, Ap  
Sequence 161, App  
Sequence 1, Appli  
Sequence 1171, Ap  
Sequence 10933, A  
Sequence 131, App  
Sequence 116, App  
Sequence 94, Appl  
Sequence 2654, Ap  
Sequence 1103, Ap  
Sequence 4, Appli  
Sequence 5, Appli  
Sequence 4, Appli  
Sequence 5, Appli  
Sequence 4, Appli  
Sequence 5, Appli  
Sequence 1, Appli  
Sequence 3, Appli

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; NAME/KEY: mat_peptide
; LOCATION: 112...432
US-08-578-649-1

Query Match      19.2%; Score 63.4; DB 1; Length 459;
Best Local Similarity 58.2%; Pred. No. 5e-11;
Matches 153; Conservative 0; Mismatches 101; Indels 9; Gaps 2;

QY 12 TATGACCGTCTAGCTTCCAAAGAGCTCTGTCAGATGATGCTGTCTATATCTTTC 71
DB 117 TATGCCCAAGCTGGCTGACCGAGAGCTGTGCGACCGAGGAGTGACGCCACCTATCTC 176
QY 72 TCTGCTAGTCTCAAGAGATTAAATGCCCCGAGCTGTAGATTCATTAACGTTAAAAA 131
DB 177 CATGCTGTGGCCCTTCAGGACTACATGCCCCGAGCTGCCGATTCCTGACCATTCACCG 236
QY 132 AGGCAGCAGATCTATGTCTACTCAAGCTGTTAAAGAAATGAGCTGGAGATTTTG 191
DB 237 GGGCCCAAGTGGTGTATGCTCTTCTCAAGCTG-----AAGGCCGTGGCGGCTCTTCTG 290
QY 192 GGCTGGCAGTGTATTATGGTGTATGGCCAGGACGAGATGGGAG---TCGTGGGTTATTTCC 248
DB 291 GGGAGGCGAGCTTCAGGAGATTACTATGAGATCTGGGTCTGCGCCTGGGCTATTTCCC 350
QY 249 CAGGAACCTGGTCAAGGAAACAGC 271
DB 351 CAGTAGCATTGTCGAGAGGACC 373

RESULT 2
US-08-578-649-4
; Sequence 4, Application US/08578649
; Patent No. 5770366
; GENERAL INFORMATION:
; APPLICANT: Ulrich Bogdan
; APPLICANT: Reinhard Buttner
; APPLICANT: Brigitte Kaluza
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/578,649
; FILING DATE: 29-July-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 24 247.2
; FILING DATE: 20-July-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Andrew L. Tiajolloff
; REGISTRATION NUMBER: 31,575
; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 581 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:

; NAME/KEY: CDS
; LOCATION: 110...499
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 110...178
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 179...499
US-08-578-649-4

Query Match      19.2%; Score 63.2; DB 1; Length 581;
Best Local Similarity 54.3%; Pred. No. 6.5e-11;
Matches 175; Conservative 0; Mismatches 138; Indels 9; Gaps 2;

QY 12 TATGACCGTCTAGCTTCCAAAGAGCTCTGTCAGATGATGCTGTCTATATCTTTC 71
DB 184 TATGCCCAAGCTGGCTGACTGGAAGCTGTGTGCGAAGAGAAATGACGCCATCCTATCTC 243
QY 72 TCTGCTAGTCTCAAGAGATTAAATGCCCCGAGCTGTAGATTCATTAACGTTAAAAA 131
DB 244 CATGCTGTGGCCCTTCAGGACTACGTCGCCCTGATTCGCCCTTCTTGACTATATATAG 303
QY 132 AGGCAGCAGATCTATGTCTACTCAAGCTGTTAAAGAAATGAGCTGGAGATTTTG 191
DB 304 GGGCCCAAGTGGTGTATGCTCTTCTCAAGTTG-----AAGGCCGTGGCGGCTCTTCTG 357
QY 192 GGCTGGCAGTGTATTATGGTGTATGGCCAGGACGAGATGGGAG---TCGTGGGTTATTTCC 248
DB 358 GGGAGGCGAGTGTTCAGGAGGTTACTATGAGACTGCGAGCCGCCCTGGGCTATTTCCC 417
QY 249 CAGGAACCTGGTCAAGGAAACAGCGTGTGTACCCAGGAAGCTACCAAGGAAGTTCCACCCAC 308
DB 418 CAGTAGCATTGTCGGGAGGACCTGAACTCGAAACCTGCAAAATTTGATATGAAGACCGA 477
QY 309 GGATATTGACTTCTTCTGCGAG 330
DB 478 TCAATGGGATTTCTACTGCCAG 499

RESULT 3
US-08-578-649-18
; Sequence 18, Application US/08578649
; Patent No. 5770366
; GENERAL INFORMATION:
; APPLICANT: Ulrich Bogdan
; APPLICANT: Reinhard Buttner
; APPLICANT: Brigitte Kaluza
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/578,649
; FILING DATE: 29-July-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 24 247.2
; FILING DATE: 20-July-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Andrew L. Tiajolloff
; REGISTRATION NUMBER: 31,575
; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 581 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:

```

NAME: Andrew L. Tiajolofoff  
REGISTRATION NUMBER: 31,575  
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 305 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
FEATURE:  
NAME/KEY: misc RNA  
LOCATION: join(1..29, 277..305)  
OTHER INFORMATION: /function= "Primer"  
US-08-578-649-8

Query Match 16.4%; Score 54.2; DB 1; Length 305;  
Best Local Similarity 57.7%; Pred. No. 4e-08;  
Matches 139; Conservative 0; Mismatches 93; Indels 9; Gaps 2

QY 34 AAGCTCTGTCAGATGATGATGTCTATACTATTTCTCTGGCTAGTGCTCAAGAAAGAT 93  
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DB 67 TACATGCCCCCGACTGCTCCGATTCTGACCAATTCACGGGGCCCAAGTGGTGATGCTTC 126  
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QY 271 C 271  
DB 241 C 241

RESULT 5  
US-08-578-649-24  
Sequence 24, Application US/08578649  
Patent No. 5770366  
GENERAL INFORMATION:  
APPLICANT: Ulrich Bogdan  
APPLICANT: Reinhard Buttner  
APPLICANT: Brigitte Kaluza  
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/578,649  
FILING DATE: 29-July-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P 43 24 247.2  
FILING DATE: 20-July-1993

ATTORNEY/AGENT INFORMATION:  
NAME: Andrew L. Tiajolloff  
REGISTRATION NUMBER: 31,575  
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 596 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: join(40...111, 40...166, 214...347, 393...503, 549  
LOCATION: ..569)  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 40...111  
FEATURE:  
NAME/KEY: exon  
LOCATION: 40...166  
FEATURE:  
NAME/KEY: exon  
LOCATION: 214...347  
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NAME/KEY: exon  
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LOCATION: 549...569  
FEATURE:  
NAME/KEY: -  
LOCATION: one-of(194, 369, 527)  
OTHER INFORMATION: /note= "N in positions 194, 369  
OTHER INFORMATION: and 527 denotes an indefinite number and sequence  
OTHER INFORMATION: of nucleotides "  
US-08-578-649-24  
Query Match 12.2%; Score 40.4; DB 1; Length 596;  
Best Local Similarity 63.3%; Pred. No. 0.0016;  
Matches 62; Conservative 0; Mismatches 36; Indels 0; Gaps 0;  
QY 65 CTATTTCTCGGTAGTGTCTCAAGAGATTATATGCCCCGAGCTGTAGATTCAATTAACG 124  
Db 217 CTATCTCCATGGTGTGGCCCTTCAGGACTACATGCCCCCGAGCTGCCGATTCTTGACCA 276  
QY 125 TTAATAAAGGCGACAGATCTATGTGTACTCAAGCTG 162  
Db 277 TTCACCGGGCCCAAGTGTGTATGTCTTCTCCAAGCTG 314  
RESULT 6  
US-08-578-649-3  
Sequence 3, Application US/08578649  
Patent No. 5770366  
GENERAL INFORMATION:  
APPLICANT: Ulrich Bogdan  
APPLICANT: Reinhard Buttner  
APPLICANT: Brigitte Kaluza  
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette

COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/578,649  
FILING DATE: 29-July-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P 43 24 247.2  
FILING DATE: 20-July-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Andrew L. Tiajolloff  
REGISTRATION NUMBER: 31,575  
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3565 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 1378..1449  
FEATURE:  
NAME/KEY: exon  
LOCATION: 1378..1504  
FEATURE:  
NAME/KEY: exon  
LOCATION: 1586..1719  
FEATURE:  
NAME/KEY: exon  
LOCATION: 2804..2914  
FEATURE:  
NAME/KEY: exon  
LOCATION: 3232..3252  
FEATURE:  
NAME/KEY: -  
LOCATION: one-of(2216)  
OTHER INFORMATION: /note= "N in position 2216  
OTHER INFORMATION: denotes an indefinite number and sequence of  
OTHER INFORMATION: nucleotides"  
US-08-578-649-3  
Query Match 12.2%; Score 40.4; DB 1; Length 3565;  
Best Local Similarity 63.3%; Pred. No. 0.0037;  
Matches 62; Conservative 0; Mismatches 36; Indels 0; Gaps 0;  
QY 65 CTATTTCTCGGTAGTGTCTCAAGAGATTATATGCCCCGAGCTGTAGATTCAATTAACG 124  
Db 1589 CTATCTCCATGGTGTGGCCCTTCAGGACTACATGCCCCCGAGCTGCCGATTCTTGACCA 1648  
QY 125 TTAATAAAGGCGACAGATCTATGTGTACTCAAGCTG 162  
Db 1649 TTCACCGGGCCCAAGTGTGTATGTCTTCTCCAAGCTG 1686  
RESULT 7  
US-08-232-463-14/c  
Sequence 14, Application US/08232463  
Patent No. 5670367  
GENERAL INFORMATION:  
APPLICANT: DORNER, F.  
APPLICANT: SCHEIFLINGER, F.  
APPLICANT: FALKNER, F. G.  
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500

CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232.463  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/935.313  
FILING DATE:  
APPLICATION NUMBER: EP 91 114 300.6  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)836-9300  
TELEFAX: (703)683-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7218 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: ptzgt-F1s  
US-08-232-463-14

Query Match 10.3%; Score 34; DB 1; Length 7218;  
Best Local Similarity 8.1%; Pred. No. 0.6;  
Matches 19; Conservative 120; Mismatches 95; Indels 0; Gaps 0;

Qy 65 CTATTTCTGGTGTGCTCAAGAGATTATAATGCCCGAGCTGTAGATTCTTAACG 124  
Db 1471 CTTATCAAGTAGTTAAAGAGATAGAAGATTGGTACRRRRRRRRRRRRRRRRRR 1412

Qy 125 TTAAGAAAGGCACACAGATCTATGTGTACTCAAGCTGGTAAAGAAATCGAGCTGAG 184  
Db 1411 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1352

Qy 185 AATTTTGGGCTGGCAGTGTATTATGCTGATGCCAGGACGAGATGGAGTCTGGGTATT 244  
Db 1351 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1292

Qy 245 TCCCAGGAAGCTTGGTCAAGAAACAGCGTGTGTACCAAGAACTACCAAGAAAG 298  
Db 1291 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1238

RESULT 8  
US-08-860-820-1  
Sequence 1, Application US/08960820  
Patent No. 6245967  
GENERAL INFORMATION:  
APPLICANT: Sonnewald, Uwe  
APPLICANT: Kossmann, Jens  
APPLICANT: Bowien, Bocho  
TITLE OF INVENTION: PROCESS AND DNA MOLECULES FOR INCREASING  
TITLE OF INVENTION: THE PHOTOSYNTHESIS RATE IN PLANTS  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York

COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/860.820  
FILING DATE: 04-SEP-1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 19502053.7  
FILING DATE: 13-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley, James P.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: AGREVO-7  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-596-9000  
TELEFAX: 212-596-9090  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1136 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 30..1121  
US-08-860-820-1

Query Match 10.2%; Score 33.6; DB 3; Length 1136;  
Best Local Similarity 56.2%; Pred. No. 0.34;  
Matches 63; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

Qy 172 AATGAGCTGAGAAATTTGGCTGGCAGTGTATGTGATGCCAGGACGAGATGGA 231  
Db 204 AATCAAGCCGGAAGCAGGGCGCTCAAGCTGCGGGCGAAATCCAGCAAGCTGAC 263

Qy 232 GTCTGTGGTATTATTTCCCGAGAACTTGTCTCAAGCAACAGCGTGTGTACCAGG 283  
Db 264 GTCTGAGCAATACCACTTCTCGCGCTCAACAGATGGGGGGGTACTCTGG 315

RESULT 9  
US-09-359-161-4/c  
Sequence 4, Application US/09359161A  
Patent No. 6342656  
GENERAL INFORMATION:  
APPLICANT: Bradford, Kent J.  
APPLICANT: Dahal, Peetambar  
APPLICANT: Yang, Hong  
APPLICANT: Cooley, Michael  
APPLICANT: Downie, Bruce  
APPLICANT: Gee, Oliver  
APPLICANT: The Regents of the University of California  
TITLE OF INVENTION: Regulation of Source-Sink Relationships and Responses  
TITLE OF INVENTION: to Stress Conditions in Plants  
FILE REFERENCE: 023070-095900US  
CURRENT APPLICATION NUMBER: US/09/359.161A  
CURRENT FILING DATE: 1999-07-21  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 4  
LENGTH: 1929  
TYPE: DNA  
ORGANISM: Lycopersicon esculentum  
FEATURE:  
OTHER INFORMATION: Lycopersicon esculentum plant homolog of yeast



```
/ OTHER INFORMATION: SNF1 kinase subunit of protein kinase (LeSNF1)
US-09-359-161-4

Query Match      10.2%; Score 33.6; DB 4; Length 1929;
Best Local Similarity 52.9%; Pred. No. 0.44;
Matches 72; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 84 TCAGAAGATTATTAATCCCGGACTGTAGATTCAATTAAGTTAAAAAGGCGACGAT 143
Db 1793 TCTGTAAGTAGACTGTAGTAACTGAAATTCATAAAGCTTAAAAAAGAGAGTGAGCT 1734

QY 144 CTATGTTACTCAAGCTGTTAAAGAAATGGAGCTGGAGAAATTTTGGGCTGSCAGTGT 203
Db 1733 AGATCTCTAGCGAATCAAAAGAAAAAAGAGTTGCTAGGCACCTCTGACCAACAGCGGT 1674

QY 204 TTATGGTGATGGCCAG 219
Db 1673 GGAATTGTTAACAAG 1658

RESULT 10
US-08-286-870A-7/c
; Sequence 7, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; ADDRESSEE: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENK, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,870A
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/520228
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8910624.9
; FILING DATE: 09-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/220720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2159 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2159
US-08-286-870A-7

Query Match      10.2%; Score 33.6; DB 3; Length 2159;
Best Local Similarity 52.1%; Pred. No. 0.46;
Matches 75; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 174 TCGAGCTGGAGAAATTTTGGGCTGGCAGTGTATTATGTTATGTTGATGGCCAGACGAGATGGGAGT 233
Db 2002 TGTGCTGGTGAACAGCGCGGTGACCTTCTCCTGGGCTTCTCGAAGTCGTACTCGGCCT 1943

QY 234 CGTGGGTTATTTCCCAAGGAACCTTGTCAAGGAACACGCGTGTGTACAGGAGCTACCAA 293
Db 1942 CGTAGGTCACTCCACGGGCGACGAACCTCGATGCGGTGTACACCTCGTTGCCGCTGC 1883

QY 294 GGAAGTTCCCAACCGGATATTGA 317
Db 1882 TGAAGTTCAGGCGCCGATGTGA 1859

RESULT 11
US-09-767-515-1
; Sequence 1, Application US/09767515
; Patent No. 6586207
; GENERAL INFORMATION:
; APPLICANT: Tirrell, David A
; APPLICANT: Kiick, Kristi L
; TITLE OF INVENTION: Overexpression of Aminoacyl-tRNA Synthetases for
; TITLE OF INVENTION: Efficient Production of Engineered Proteins Containing
; TITLE OF INVENTION: Amino Acid Analogues
; FILE REFERENCE: 30431.6US01
; CURRENT APPLICATION NUMBER: US/09/767,515
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/207,627
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1
; LENGTH: 6501
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pOE15-MRS
US-09-767-515-1

Query Match      9.9%; Score 32.8; DB 4; Length 6501;
Best Local Similarity 54.0%; Pred. No. 1.4;
Matches 67; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 180 TGGAGAATTTTGGGCTGGCAGTGTATTATGTTATGTCGATGGCCAGACGAGATGGGAGTGGTGG 239
Db 2259 TGGTGAAGCTGGGAAAGCCGTGAATTTGGTAAAGCCGTGGCGGAAATCATGGCGCTGC 2318

QY 240 TTATTTCCCAAGAACTTGGTCAAGGAACGCGTGTGTACCAAGGAAGCTTACCAAGGAAGT 299
Db 2319 TGATCTGGCTAACCGCTATGTCGATGAACAGGCTCGTGGGTGGTGGCGAAACAGGAGG 2378

QY 300 TCCC 303
Db 2379 CCGC 2382

RESULT 12
US-09-767-515-2
; Sequence 2, Application US/09767515
; Patent No. 6586207
; GENERAL INFORMATION:
; APPLICANT: Tirrell, David A
; APPLICANT: Kiick, Kristi L
; TITLE OF INVENTION: Overexpression of Aminoacyl-tRNA Synthetases for
; TITLE OF INVENTION: Efficient Production of Engineered Proteins Containing
; TITLE OF INVENTION: Amino Acid Analogues
; FILE REFERENCE: 30431.6US01
; CURRENT APPLICATION NUMBER: US/09/767,515
; CURRENT FILING DATE: 2001-01-23
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Tue Dec 30 10:20:39 2003

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; PRIOR APPLICATION NUMBER: 60/207,627
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 6501
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pOE15-W305F
US-09-767-515-2

Query Match          9.8%; Score 32.8; DB 4; Length 6501;
Best Local Similarity 54.0%; Pred. No. 1.4;
Matches 67; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

Qy 180 TGGAGATTTTGGCTGCGACGTGTTATGTTGATGGCCAGCAGCAGATGGAGTCGTGGG 239
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 240 TTATTTCCCGAGGAACCTTGGTCAAGGAACAGCGTGTGTACCGAAGCTACCAAGGAAGT 299
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 300 TCCC 303
Db |||||
Qy 2379 CCGC 2382
Db |||||

RESULT 13
US-09-734-674-3
; Sequence 3, Application US/09734674
; Patent No. 6498022
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001018
; CURRENT APPLICATION NUMBER: US/09/734,674
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 202001
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(202001)
; OTHER INFORMATION: n = A,T,C or G
US-09-734-674-3

Query Match          9.8%; Score 32.2; DB 4; Length 202001;
Best Local Similarity 49.7%; Pred. No. 11;
Matches 82; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

Qy 65 CTATTTCTGCTAGTCTCAGAGATTATATGCCCCGACCTGTAGATTCATTAACG 124
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 183409 CTAGAACTCAGGAGAGCTAAGGCAGACGCTAGGTCGCGTGAATCATTTAGCAAGTCTGT 183468

Qy 125 TTAATAAGGGCAGCAGATCTATGTACTCAAAGCTGTAAGAAATGGAGCTGGAG 184
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 183469 GAAAGTCAAGCATGGGTATGATGAATCTATTCAGGAGAAAGAAACAGAGATGAG 183528

Qy 185 AATTTTGGGCTGGCAGTGTATGTTATGTTGATGGCCAGCAGAGATGG 229
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 183529 AGTCCAGGAATCCCAATGTTGAGGGGCAATAAAGAGAGATTG 183573

RESULT 14
US-09-252-991A-889/c
; Sequence 889, Application US/09252991A

; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 889
; LENGTH: 1944
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-889

Query Match          9.5%; Score 31.4; DB 4; Length 1944;
Best Local Similarity 51.8%; Pred. No. 2.3;
Matches 71; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Qy 181 GGAGAAATTTTGGCTGCGACGTGTTTATGTTGATGGCCAGCAGCAGATGGAGTCGTGGGT 240
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 241 TATTTCCCGAGGAACCTTGGTCAAGGAACAGCGTGTGTACCGAAGCTACCAAGGAAGTT 300
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 301 CCCACCAAGGATATTGA 317
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 300 CCGACCCCTGGCGGTGA 284
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match          9.5%; Score 31.2; DB 3; Length 4403765;
Best Local Similarity 47.9%; Pred. No. 62;
Matches 90; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

Qy 99 TGCCCCGACCTGTAGATTCATTAACGTTTAAAGGCGCAGCAGATCTATGTGTACTCAA 158
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 426225 TGTCCAGCGGGGCCGCGCGTCCCGCATGCGAGGTGATCGACCGCGGCGCAAGA 426284

Qy 159 GCTGTAAAGAAATGGAGCTGGAGAAATTTTGGGCTGGCAGTGTATGTGTATGGTGA 218
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 426285 CGGTGCCACTGAGGATGCTATGTCGAGCTTCCGCTGGCGTTCGAGGAAACGTA 426344
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Tue Dec 30 10:20:39 2003

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QY      219  GGACGAGATGGGAGTCGTGGGTTATTTCCGAGGAACTTGGTCAAGGAACACCGTGTGTA 278
Db      426345  TGGCGGGGATGGAGACATTGGGTGATGTCGCCGGTGATGGGGATGTTGACCGGGATGTCCA 426404

QY      279  CCAGGAAG 286
Db      426405  CATTGAGG 426412
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Search completed: December 30, 2003, 06:10:50  
Job time : 36.6527 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: December 29, 2003, 16:03:18 ; Search time 11.4006 Seconds  
(without alignments)  
927.898 Million cell updates/sec

Title: US-10-019-455A-24  
Perfect score: 590  
Sequence: 1 HGIFMDRLASKKLCADDECVC.....RVYQEAKEVPTTIDIFFCE 110

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 76:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	253.5	43.0	131	2 I38019	melanoma-derived g
2	86.5	14.7	839	1 TVHUVV	transforming prote
3	85.5	14.5	844	1 TVMSVV	transforming prote
4	81.5	13.8	878	2 I51940	gene VAV2 protein
5	78.5	13.3	1589	1 RBYC5	cell division cont
6	74.5	12.6	1215	2 T32734	myosin-IA - Acanth
7	74	12.5	308	2 T48525	hypothetical prote
8	71.5	12.1	541	2 C64439	asparagine synthas
9	71.5	12.1	671	1 C69621	fructose-bisphosph
10	71	12.0	383	2 A23516	Balbani ring 1 ch
11	71	12.0	585	2 G96995	ATP-dependent RNA
12	71	12.0	769	2 C90186	AAA family ATPase
13	70.5	11.9	669	2 D72278	endo-1,4-beta-mann
14	70	11.9	209	2 D86758	orotate phosphorib
15	69.5	11.8	295	2 F90113	cell division cycl
16	69.5	11.8	1199	2 T47442	disease resistance
17	69	11.7	328	2 E86714	quinone oxidoreduc
18	69	11.7	392	2 I39521	redoxin-NAD+ re
19	69	11.7	444	1 A64417	phosphoribosylamin
20	69	11.7	670	2 S67383	probable signal tr
21	69	11.7	2541	2 T29340	hypothetical prote
22	68.5	11.6	461	2 AF2340	sugar ABC transpor
23	68.5	11.6	505	1 S24550	protein-tyrosine k
24	68.5	11.6	506	1 S24553	protein-tyrosine k
25	68	11.5	162	2 B29662	Balbani ring 2 ch
26	68	11.5	259	2 C64427	hypothetical prote
27	68	11.5	359	2 B29960	Balbani ring 2 ch
28	68	11.5	782	2 B83966	formate dehydrogen
29	67.5	11.4	374	2 B97258	glycosyltransferas

30 67.5 11.4 839 2 G96719 probable chromomet  
31 67 11.4 142 2 C75325 methylmalonyl-CoA  
32 67 11.4 373 2 T39655 VHS domain contain  
33 67 11.4 383 2 S24156 polygalacturonase  
34 67 11.4 509 2 G82104 glutamyl-tRNA synt  
35 67 11.4 518 1 P2WL8 L2 protein - human  
36 67 11.4 524 2 S36483 L2 protein - human  
37 67 11.4 542 2 D70873 probable ABC trans  
38 67 11.4 1187 2 T19413 hypothetical prote  
39 66.5 11.3 209 2 AG1303 orotate phosphorib  
40 66.5 11.3 258 2 E81308 hypothetical prote  
41 66.5 11.3 493 2 S11148 amfA protein - Str  
42 66.5 11.3 847 1 A53800 mixed-lineage prot  
43 66 11.2 162 2 A29662 Balbani ring 1 ch  
44 66 11.2 229 2 AG2737 acetyltransferase  
45 66 11.2 229 2 E97518 probable acetyltra

## ALIGNMENTS

## RESULT 1

I38019  
melanoma-derived growth regulatory protein MIA - human  
C:Species: Homo sapiens (man)  
C:Date: 17-May-1996 #sequence\_revision 17-May-1996 #text\_change 04-Mar-2000  
C:Accession: I38019; S40238  
R:Blesch, A.; Bosserhoff, A.K.; Apfel, R.; Behl, C.; Hoesdoerfer, B.; Schmitt, A.; Ja  
Cancer Res. 54, 5695-5701, 1994  
A:Title: Cloning of a novel malignant melanoma-derived growth-regulatory protein, MIA  
A:Reference number: I38019; MUID:95007612; PMID:7923218  
A:Accession: I38019  
A>Status: Preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-131 <RES>  
A:Cross-references: EMBL:X75450; NID:g438057; PIDN:CAAS3203.1; PID:g438058  
C:Genetics:  
A:Gene: mia  
C:Superfamily: human melanoma-derived growth regulatory protein MIA

Query Match 43.0%; Score 253.5; DB 2; Length 131;  
Best Local Similarity 45.4%; Pred. No. 4.2e-19;  
Matches 49; Conservative 21; Mismatches 33; Indels 5; Gaps 3;

QY 5 MDRLASKKLCADDECVCYTISLASAQEDYNAPCRFINVKQQIYVYKLVKENGAGE-F 63  
DB 27 MPKLAADRLKLCADQECSHPIISMAVALQDYNAPCRFLTHRGQVYVYFSKL---KGRGRUP 83

QY 64 WAGSVYVGDQDWMGV-VGYFPRNLVKEQRVYQBATKEVPTTIDIFFCE 110  
DB 84 WGSVQGDYVYGDLAARLGYPFSSIVREDQTLKPKGVVDVTKDKWDFYCO 131

## RESULT 2

TVHUVV  
Transforming protein vav - human (fragments)  
N:Alternate names: finger protein vav  
C:Species: Homo sapiens (man)  
C:Date: 31-Mar-1991 #sequence\_revision 03-May-1996 #text\_change 18-Jun-1999  
C:Accession: B39576; S05382  
R:Katzav, S.; Cleveland, J.L.; Heslop, H.E.; Pulido, D.  
Mol. Cell. Biol. 11, 1912-1920, 1991  
A:Title: Loss of the amino-terminal helix-loop-helix domain of the vav proto-oncogene  
A:Reference number: A39576; MUID:91172176; PMID:2005987  
A:Accession: B39576  
A:Molecule type: mRNA  
A:Residues: 1-61 <KAT>  
A:Cross-references: GB:M59834; NID:g340189; PIDN:AAA63267.1; PID:g340190  
A:Note: the authors translated the codon CAG for residue 6 as Glu, CAG for residue 13  
R:Katzav, S.; Martin-Lanca, D.; Barbacid, M.  
EMBO J. 8, 2283-2290, 1989  
A:Title: vav, a novel human oncogene derived from a locus ubiquitously expressed in h  
A:Reference number: S05382; MUID:90005432; PMID:2477241

F:522-542/Region: zinc finger CCCC motif  
F:547-560/Region: zinc finger HCCH motif  
F:598-648/Domain: SH3 homology <SH3A>  
F:664-756/Domain: SH2 homology <SH2>  
F:783-831/Domain: SH3 homology <SH3B>  
F:433/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status pro

Query Match	14.5%	Score 85.5	DB 1	Length 844
Best Local Similarity	34.4%	Pred. No. 0.87		
Matches	22	Conservative 14	Mismatches 21	Indels 13
			Gaps	3
Qy	26	ASAQEDYNAPCRFINVKKGQIIYYYSKLKVENGAGEFWAGSVYGGDQEMGVGVYFPPN	85	
Db	786	AKARYDFCARDSELSLEKEDI-----KILNKGQGGWVRGEIYGR-----IGWFPSN	834	
Qy	86	LVKEQRVYQE	95	
Db	835	YVEED--YSE	842	

```

RESULT 4
Gene VAV2 protein - human
151940
C:Species: Homo sapiens (man)
C:Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 16-Jul-1999
C:Accession: I51940
R:Henske, E.P.; Short, M.P.; Jozwiak, S.; Bovey, C.M.; Ramlakhan, S.; Haines, J.L.; K
Ann. Hum. Genet. 59, 25-37, 1995
A:Title: Identification of VAV2 on 9q34 and its exclusion as the tuberous sclerosis 9
A:Reference number: I51940; MUID:95283235; PMID:7762982
A:Accession: I51940
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-878 <RES>
A:Cross-references: GB:S76992; NID:G913345; PIDN:AA834377.1; PID:G913346
C:Genetics;
A:Gene: GDB.VAV2
A:Cross-references: GDB:370880; OMIM:600428
A:Map position: 9q34-9q34
C:Superfamily: vav transforming protein; CDC24 homology; protein kinase C zinc-binding
F:198-462/Domain: CDC24 homology <CD24>
F:524-572/Domain: protein kinase C zinc-binding repeat homology <K22>
F:673-764/Domain: SH2 homology <SH2>
F:823-872/Domain: SH3 homology <SH3>

Query Match 13.8%; Score 81.5; DB 2; Length 878;
Best Local Similarity 26.3%; Pred. No. 2.4; Indels 13; Gaps 3;
Matches 20; Conservative 21; Mismatches 22;

Qy 20 VYT---ISLASAQEDYNAPDCRFINVKGQOIYVYSKLVKENGAGFEWAGSVYGDGDEM 76
ph r12 VETPVTICAVARYNFAARDMRELISLREGDVRVYISPGIDOG---WWKG-----ETN 861

```

A:Accession: T32734  
A:Status: preliminary; translated from GB/EMBL/DBD  
A:Molecule type: DNA  
A:Residues: 1-1215 <LEE>  
A:Cross-references: EMBL:AF085185; NID:g3599477; PID:g3599478; PIDN:AAC35357.1  
A:Experimental source: strain Neff  
C:Genetics:  
A:Gene: MIA  
A:Introns: 1/3; 41/3; 72/2; 103/2; 162/3; 184/1; 217/1; 296/1; 340/3; 390/3; 447/3; 50/3  
C:Superfamily: protozoan myosin heavy chain IB; myosin motor domain homology; SH3 homo  
F:14-674/Domain: myosin motor domain homology <MMO>

Query Match 12.6%; Score 74.5; DB 2; Length 1215;  
Best Local Similarity 28.6%; Pred. No. 18;  
Matches 20; Conservative 12; Mismatches 25; Indels 13; Gaps 2;

Qy 20 VYITLSAQQDYVADPCRFNVKKGQIYVYKLVKENGAFWAGSVYGGQDEMGVV 79  
Db 1158 VPTVGRALYDYGAQEADELTLREGDVIDVIQK-----SGEWEGTLNGK-----T 1204  
Qy 80 GYFPRNLVKE 89  
Db 1205 GYFFANYVED 1214

RESULT 7  
T48525  
hypothetical protein T22P22.50 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
C:Accession: T48525  
R:Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft  
submitted to the Protein Sequence Database, April 2000  
A:Reference number: 224490  
A:Accession: T48525  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-308 <BEV>  
A:Cross-references: EMBL:AL163814  
A:Experimental source: cultivar Columbia; BAC clone T22P22  
C:Genetics:  
A:Map position: 5  
A:Introns: 63/3; 117/3; 135/3; 180/3  
A:Note: T22P22.50

Query Match 12.5%; Score 74; DB 2; Length 308;  
Best Local Similarity 37.2%; Pred. No. 4.5;  
Matches 16; Conservative 8; Mismatches 17; Indels 2; Gaps 1;

Qy 44 KGQIYVYKLVKENGAFWAGSVYGGQDEMGVVGYFPRNL 86  
Db 168 KGQERAVYASIVQEKIGNVWVTVRYDRPDVH--IGYWPKEI 208

RESULT 8  
C64439  
asparagine synthase (glutamine-hydrolysing) (EC 6.3.5.4) [similarity] - Methanococcus  
C:Species: Methanococcus jannaschii  
C:Date: 13-Sep-1996 #sequence\_revision 09-Jun-2000 #text\_change 19-Jul-2002  
C:Accession: C64439  
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake  
rsen, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.  
Science 273, 1058-1073, 1996  
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese,  
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasch  
A:Reference number: A64300; MUID:96337999; PMID:8688087  
A:Accession: C64439  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 'WRD', 1-541 <BUH>  
A:Cross-references: GS:U67554; GB:L77117; NID:g2826365; PIDN:AAB99117.1; PID:g1591755;  
A:Note: an incorrect initiation codon was used

C;Genetics:  
A;Map position: REV1058315-1056681  
C;Superfamily: asparagine synthetase (glutamine-hydrolyzing)  
C;Keywords: asparagine biosynthesis; ligase  
F;2-541/Product: asparagine synthase (glutamine-hydrolyzing) #status predicted <MAT>  
F;2/Active site: Cys #status predicted

Query Match 12.1%; Score 71.5; DB 2; Length 541;  
Best Local Similarity 25.7%; Pred. No. 15;  
Matches 27; Conservative 22; Mismatches 33; Indels 23; Gaps 6;

QY 3 IFMDRLAS-----KKLCADDEC-VYTTISLASAQEDYNAPDCRFINVKKGQOIYVYVKL 54  
DB 298 IYAEKALDLNKLKRIISBEYEVFKAKAIDEVD-----LMKIGVGPIYVASEM 352

QY 55 VKENGAGFFWAGSVYGDQDMGVGVYFPRNLVKEQRYVQATKE 99  
DB 353 ANEDGLKVV-----LSGQGADEL-FGY-----ARHERIYRERGE 387

RESULT 9  
C9621  
fructose-bisphosphatase (EC 3.1.3.11) [validated] - Bacillus subtilis  
C;Species: Bacillus subtilis  
C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 03-Jun-2002  
C;Accession: C69621  
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter  
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho  
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
Nature 390, 249-256, 1997  
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallen  
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.  
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,  
A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mausel  
Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,  
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron  
akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K  
A;Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.  
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A;Reference number: A69580; MUID:98044033; PMID:9384377  
A;Accession: C69621  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-671 <XUN>  
A;Cross-references: GB:Z99124; GB:AL009126; NID:G2636442; FIDN:CAB16056.1; PID:G2636566  
A;Experimental source: strain 168  
C;Genetics:  
A;Gene: fbp; yydE  
C;Function:  
A;Description: catalyzes the hydrolysis of fructose-1,6-bisphosphate to fructose-6-phosph  
A;Pathway: gluconeogenesis  
A;Note: requires manganese ion for stability and phosphoenolpyruvate for activation  
C;Superfamily: Bacillus subtilis fructose-bisphosphatase; phosphoenolpyruvate core homology  
C;Keywords: carbohydrate metabolism; gluconeogenesis; metalloprotein; phosphoric monoest

Query Match 12.4%; Score 71.5; DB 1; Length 671;  
Best Local Similarity 22.8%; Pred. No. 19;  
Matches 26; Conservative 21; Mismatches 38; Indels 29; Gaps 4;

QY 4 FMRLASKKLCADDEC-VYTTISLASAQEDYNAPDCRFINVKKGQOIYVYV 55  
DB 35 YLDLAAQYDCEEKVWVTEINLKA-----IINLPRGTBFHVSDDLHGEYQAFQHV 83

QY 56 KENGAG-----EFWAGSVYGDQDMGVGVYFPRNLVKEQRYVQATKE 99  
DB 84 LRNGSGRVKKEKIRDFISGVYDREIDELALVYVPEKLIKLIKHDPAKEALNE 137

RESULT 10  
A23516  
Balbiani ring 1 chain - midge (Chironomus tentans) (fragment)

C;Species: Chironomus tentans  
C;Date: 23-Aug-1987 #sequence\_revision 23-Aug-1987 #text\_change 21-Jul-2000  
C;Accession: A23516  
R;Hoog, C.; Engberg, C.; Wieslander, L.  
Nucleic Acids Res. 14, 703-719, 1986  
A;Title: A BR 1 gene in Chironomus tentans has a composite structure: a large repetiti  
A;Reference number: A23516; MUID:86120366; PMID:3003693  
A;Accession: A23516  
A;Molecule type: DNA  
A;Residues: 1-383 <HOO>  
A;Cross-references: GB:X03490; NID:G7043; PIDN:CAA27206.1; PID:G769785  
A;Note: the authors translated the codon GAA for residue 118 as Gly and TTC for residu  
C;Genetics:  
A;Introns: 273/1  
C;Superfamily: unassigned Balbiani ring proteins

Query Match 12.0%; Score 71; DB 2; Length 383;  
Best Local Similarity 28.0%; Pred. No. 12;  
Matches 26; Conservative 10; Mismatches 37; Indels 20; Gaps 3;

QY 6 DRLASKKLCADDEC-VYTTISLASAQEDYNAPDCRFINVKKGQOIYVYVKLVKENGAGETWA 65  
DB 303 DKCCCKKNCNCDGAKF-----PECESNSKQSGMFDILAKLFRPQG-GDPEA 348

QY 66 GSVYGDQDMGVGVYFPRNLVKEQRYVQATK 98  
DB 349 GSVEVDGKK-----LSPEKKEKFGKALQDAVK 375

RESULT 11  
G96995  
ATP-dependent RNA helicase, superfamily II [imported] - Clostridium acetobutylicum  
C;Species: Clostridium acetobutylicum  
C;Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 14-Sep-2001  
C;Accession: G96995  
R;Nolling, J.; Bretton, G.; Onelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Le  
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C  
A;Reference number: A96900; MUID:21359325; PMID:21359325  
A;Accession: G96995  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-585 <KUR>  
A;Cross-references: GB:AB001437; PIDN:BAK78754.1; PID:G15023664; GSPDB:GN00168  
A;Experimental source: Clostridium acetobutylicum ATCC824  
C;Genetics:  
A;Gene: CAC0778

Query Match 12.0%; Score 71; DB 2; Length 585;  
Best Local Similarity 29.4%; Pred. No. 19;  
Matches 30; Conservative 13; Mismatches 37; Indels 22; Gaps 5;

QY 12 KLCADD-----ECVYTTISLASAQEDYNAPDCRFINVKKGQOIYVYVK-----LVKENGAGE 62  
DB 272 KCDEDEYKEIKYKRAIPLEVEDSEFNKYD-----IXEGDAVVVFSKRVLEIAQSYSARG 326

QY 63 FWAGSVYGDQDMGVGVYFPRNLVKEQRYVQATKEVPTTD 104  
DB 327 IKASIIYGLPPEV-----RKLQYEQFIKKE-TKVLVTTD 360

RESULT 12  
C90186  
AAA family ATPase [imported] - Sulfolobus solfataricus  
C;Species: Sulfolobus solfataricus  
C;Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 15-Jun-2001  
C;Accession: C90186  
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Cha  
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder,  
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.  
submitted to GenBank, April 2001  
A;Description: Sulfolobus solfataricus complete genome.



A;Reference number: A99139  
A;Accession: C90186  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-769 <KUR>  
A;Cross-references: GB:AE006641; NID:gl13813572; PIDN:AAK0746.1; GSPDB:GN00155  
C;Genetics:  
C;Superfamily: transitional endoplasmic reticulum ATPase; FtsH/SEC18/CDC48-type ATP-bind

Query Match 12.0%; Score 71; DB 2; Length 769;  
Best Local Similarity 35.0%; Pred. No. 25;  
Matches 28; Conservative 10; Mismatches 20; Indels 22; Gaps 5;  
QY 49 YVYSKLVKENG-----AGFEWAGSVVYDG--QDEMGVGVYFPRNL-----VKE 89  
DB 51 YTISRGIENGVDYVEIIIGSGSALQAALIGDGIADNEIRVDGYIRRSIGVGIGDEVTVKR 110  
QY 90 QRVYQATKEV--PTDIDF 107  
DB 111 AQV-QDATKVLAPTQPISF 129

RESULT 13  
D72278  
endo-1,4-beta-mannosidase - Thermotoga maritima (strain MSB8)  
C;Species: Thermotoga maritima  
C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 21-Jul-2000  
C;Accession: D72278  
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey  
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;  
C.M.  
Nature 399, 323-329, 1999  
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq  
A;Reference number: A72200; MUID:99287316; PMID:10360571  
A;Accession: D72278  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-669 <ARN>  
A;Cross-references: GB:AE001779; GB:AE000512; NID:g4981777; PIDN:AAD36302.1; PID:g498178  
A;Experimental source: strain MSB8  
C;Genetics:  
A;Gene: TM1227

Query Match 11.9%; Score 70.5; DB 2; Length 669;  
Best Local Similarity 27.6%; Pred. No. 24;  
Matches 32; Conservative 12; Mismatches 37; Indels 35; Gaps 6;  
QY 25 LASAQEDYNAPDCRFNVKKGQOI-----YVYSK-----LVKENGAGEF 63  
DB 393 LFWTGDIEDTCFSLPKDGMIEIKTVVEVRAGVFDYSNTFEKLSVKVEDLVFENEIHL 452  
QY 64 WAGSVYVG-----DGQDEMGVGVYFPRNLVKEQ---RVYQATKEVPTTIDF 107  
DB 453 GYG-IYGFDLDTTRIPDGEHEMFEGHFGQKTVKDSIKAKVNEA-RYVLAEEVDF 506

RESULT 14  
D86758  
orotate phosphoribosyltransferase (EC 2.4.2.10) [imported] - Lactococcus lactis subsp. l  
C;Species: Lactococcus lactis subsp. lactis  
C;Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 17-May-2002  
C;Accession: D86758  
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jalllon, O.; Malarne, K.; Weissenbach, J.; Ehrli  
Genome Res. 11, 731-753, 2001  
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s  
A;Reference number: A86625; MUID:21235186; PMID:11337471  
A;Accession: D86758  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-209 <STO>  
A;Cross-references: GB:AE005176; PID:gl12724022; PIDN:AAK05166.1; GSPDB:GN00146  
A;Experimental source: strain IL1403

C;Genetics:  
A;Gene: pyrE  
C;Superfamily: orotate phosphoribosyltransferase; orotate phosphoribosyltransferase hom  
C;Keywords: glycosyltransferase; pentosyltransferase

Query Match 11.9%; Score 70; DB 2; Length 209;  
Best Local Similarity 26.9%; Pred. No. 7.7;  
Matches 21; Conservative 15; Mismatches 42; Indels 0; Gaps 0;  
QY 25 LASAQEDYNAPDCRFNVKKGQOIYVYSKLVKENGAGFEWAGSVVYDGQDEMGVGVYFPR 84  
DB 95 IRSKPKDHGAGNQVGRVTKGQRMVVVEDLSTGGSVLEAVAAAREGADVILGVVAIFTY 154  
QY 85 NLVKEQRVYQATKEVPT 102  
DB 155 ELEKANRRFADAGVKLAT 172

RESULT 15  
F90113  
cell division cycle 2 homolog [imported] - Guillardia theta nucleomorph  
C;Species: nucleomorph Guillardia theta  
A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont  
C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 15-Jun-2001  
C;Accession: F90113  
R;Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Re  
Nature 410, 1091-1096, 2001  
A;Title: The highly reduced genome of an enslaved algal nucleus.  
A;Reference number: A99082; MUID:11323671; PMID:11323671  
A;Accession: F90113  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-235 <DOU>  
A;Cross-references: GB:AJ010592; NID:gl2580757; PIDN:CAC27075.1; GSPDB:GN00151  
C;Genetics:  
A;Map position: 2  
A;Genome: nucleomorph  
C;Superfamily: kinase-related transforming protein; protein kinase homology  
C;Keywords: nucleomorph

Query Match 11.8%; Score 69.5; DB 2; Length 295;  
Best Local Similarity 28.0%; Pred. No. 13;  
Matches 28; Conservative 14; Mismatches 31; Indels 27; Gaps 6;  
QY 8 LASKKLADDECYVTISLASAQEDYNAPDCRFNVKKGQOIYVYSKLVKENGAG--GEFWA 65  
DB 157 LCSKKICLSKIV-TLW-----YEAPE-----ILLQHFYDYSVDMWSFGCVIGELIT 203  
QY 66 GSVYGDQDEMGVGVYFPRNLVKEQRYVYQATKEVPTTDI 105  
DB 204 GEILFGKSELDOJ-----NKIFQ--TIGTPTTEI 231

Search completed: December 29, 2003, 16:10:40  
Job time : 12.4006 secs



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OM protein - protein search, using sw model

Run on: December 29, 2003, 16:03:18 ; Search time 4.31373 Seconds  
(without alignments)  
1199.181 Million cell updates/sec

Title: US-10-019-455A-24

Perfect score: 590

Sequence: 1 HGFMRLASKKLCADCEV.....RVQEQATKEVPTDIDFCE 110

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query %	Length	DB ID	Description
1	590	100.0	128	1	Q9NRC9 homo sapien
2	547	92.7	128	1	Q9JIE3 mus musculus
3	477.5	80.9	132	1	Q9I8P6 gallus gall
4	390	66.1	133	1	Q9I8P5 rana catesb
5	253.5	43.0	131	1	Q16674 homo sapien
6	252.5	42.8	130	1	Q28038 bos taurus
7	250.5	42.5	130	1	Q62946 rattus norv
8	235.5	39.9	130	1	Q61865 mus musculus
9	88.5	15.0	847	1	Q9R0C8 mus musculus
10	86.5	14.7	845	1	P15498 homo sapien
11	86.5	14.7	847	1	Q9UKW4 homo sapien
12	85.5	14.5	843	1	P34100 rattus norv
13	85.5	14.5	845	1	P27870 mus musculus
14	82.5	14.0	868	1	Q60992 mus musculus
15	81.5	13.8	878	1	P52735 homo sapien
16	78.5	13.3	1589	1	P04821 saccharomyc
17	74	12.5	2161	1	Q9Y566 homo sapien
18	71.5	12.1	541	1	Q36516 methanococc
19	71	12.0	2167	1	Q9WV48 rattus norv
20	70.5	11.9	905	1	Q9GXY1 mus musculus
21	70	11.9	209	1	Q9CGM8 lactococcus
22	70	11.9	209	1	P58857 streptococc
23	70	11.9	209	1	Q9A076 streptococc
24	70	11.9	1217	1	Q9WVE9 rattus norv
25	70	11.9	1815	1	Q9JLU4 rattus norv
26	69	11.7	392	1	P42454 acinetobact
27	69	11.7	444	1	Q58347 methanococc
28	69	11.7	670	1	Q10199 schizosacch
29	68.5	11.6	505	1	P42686 spongilla l
30	68.5	11.6	506	1	SRK1 SPOLA
31	68	11.5	162	1	SRK4 SPOLA
32	68	11.5	259	1	BAR2 CHIPA
33	68	11.5	534	1	YA20 METJA
					Q80905 human papil
					VL2_Hpv37

#### ALIGNMENTS

##### RESULT 1

ID	OTOR_HUMAN	STANDARD;	PRT;	128 AA.
AC	Q9NRC9;	2001 (Rel. 40, Created)		
DT	16-OCT-2001	(Rel. 40, Last sequence update)		
DT	28-FEB-2003	(Rel. 41, Last annotation update)		
DE	Otoraplin precursor (Fibrocyte-derived protein)	(Melanoma inhibitory activity like protein).		
DE	OTOR OR FDP OR MIAL.			
GN	Homo sapiens (Human).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Cochlea;			
RX	MEDLINE=20334619; PubMed=10873378;			
RA	Robertson N.G., Heller S., Lin J.S., Resendes B.L., Weremowicz S., Denis C.S., Bell A.M., Hudspeth A.J., Morton C.C.;			
RA	"A novel conserved cochlear gene, OTOR: identification, expression analysis, and chromosomal mapping."			
RL	Genomics 66:242-248 (2000).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20568254; PubMed=10998416;			
RA	Cohen-Salmon M., Frenz D., Liu W., Verpy E., Voegelings S., Petit C.;			
RA	"Fdp, a new fibrocyte-derived protein related to MIA/CD-RAP, has an in vitro effect on the early differentiation of the inner ear mesenchyme."			
RL	J. Biol. Chem. 275:40036-40041 (2000).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain, and Cochlea;			
RX	MEDLINE=21100875; PubMed=1161796;			
RA	Rendtorff N.D., Frodin M., Attie-Bitach T., Vekemans M., Tommerup N.;			
RA	"Identification and characterization of an inner ear-expressed human melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent polymorphism that abolishes translation."			
RL	Genomics 71:40-52 (2001).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21638749; PubMed=11780052;			
RA	Deloukas P., Matthews L.H., Ashurst J., Babbage A.K., Bagguley C.L., Jones M., Stavridis G., Almeida J.P., Beare D.M., Beare D.M., Bailey J., Barlow K.P., Bates K.N., Bridgeman A.M., Brown A.J., Beasley O.P., Bird C.P., Blakey S.E., Carder C., Carter N.P., Buck D., Burrill W.D., Butler A.P., Clark L.N., Clark S.Y., Clee C.M., Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R., Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M., Ellington A.G., Frankland J.A., Fraser A., French L., Garner P., Graffham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E., Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,			

34	68	11.5	1714	1	ITN1_MOUSE
35	68	11.5	1721	1	ITN1_HUMAN
36	67	11.4	383	1	PGL3_ASPNG
37	67	11.4	474	1	SYE_VIBCH
38	67	11.4	518	1	VL2_HPV08
39	67	11.4	524	1	VL2_HPV17
40	66.5	11.3	209	1	PYRE_LISMO
41	66.5	11.3	793	1	VAV_DROME
42	66	11.2	209	1	PYRE_STRMU
43	66	11.2	326	1	BAR1_CHIPA
44	66	11.2	518	1	VL2_HPV36
45	66	11.2	898	1	ZO3_CANFA

Q9Z0Z4	mus musculus
Q15811	homo sapien
Q12554	aspergillus
Q31153	vibrio chol
P06419	human papil
P36751	human papil
Q8Y668	listeria mo
Q9NHV9	drosofila
Q8dtv2	streptococc
P08724	chironomus
P50827	human papil
O62683	canis famil

RA Levaeslaih M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
RA Marsh V.L., Martin S.L., McConnachie L.J., McIlroy K., McMurray A.A.,  
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,  
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,  
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,  
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,  
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,  
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
RA Rogers J.;  
RT "The DNA sequence and comparative analysis of human chromosome 20.";  
RL Nature 414:865-871(2001).  
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).  
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN COCHLEA.  
CC -!- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.  
CC -!- SIMILARITY: Contains 1 SH3 domain.  
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CC  
CC EMBL; AF233261; AAF82078.1; -;  
CC EMBL; AF243505; AAG42356.1; -;  
CC EMBL; AJ242582; CAC27443.1; -;  
CC EMBL; AJ252324; CAC28085.1; -;  
CC EMBL; AJ252325; CAC28085.1; JOINED.  
CC EMBL; AJ252326; CAC28085.1; JOINED.  
CC EMBL; AJ252327; CAC28085.1; JOINED.  
CC EMBL; AL034428; CAC16848.1; -;  
CC HSP; Q16674; 111J.  
CC Gene; HGNC:8517; OTOR.  
CC MIM; 606067; -;  
CC GO; GO:0007605; P:hearing; TAS.  
CC InterPro; IPR001452; SH3.  
CC Pfam; PF00018; SH3; 1.  
CC SMART; SM00326; SH3; 1.  
CC PROSITE; PS50002; SH3; 1.  
CC Signal; SH3 domain; 18  
CC SIGNAL 1 18  
CC CHAIN 19 128  
CC OTORAPLIN.  
CC DOMAIN 39 110  
CC SH3.  
CC DISULFID 32 37  
CC BY SIMILARITY.  
CC DISULFID 55 127  
CC BY SIMILARITY.  
CC SEQUENCE 128 AA; 14332 MW; 9B852C7F5D4FB700 CRC64;  
Query Match 100.0%; Score 590; DB 1; Length 128;  
Best Local Similarity 100.0%; Pred. No. 6.5e-54;  
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HGIFNDRASKKLCADDECVYTIISASQEDYNAPDCRFINVKGGQIYVYVKLVKNGA 60  
DB 19 HGIFNDRASKKLCADDECVYTIISASQEDYNAPDCRFINVKGGQIYVYVKLVKNGA 78  
QY 61 GEFWAGSVYGDQDEMGVYFPNRLVKEQRYQVQATKEVPTTIDIDFCE 110  
DB 79 GEFWAGSVYGDQDEMGVYFPNRLVKEQRYQVQATKEVPTTIDIDFCE 128  
RESULT 2  
OTOR MOUSE  
ID OTOR MOUSE STANDARD; PRT; 128 AA.  
AC Q9JTE3;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Otoraplin precursor (Melanoma inhibitory activity-like protein).  
GN OTOR OR MIAL.

OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
CX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20334619; PubMed=10873378;  
RX Robertson N.G.; Heller S.; Lin J.S.; Resendes B.L.; Weremowicz S.,  
RA Denis C.S.; Bell A.M.; Hudspeth A.J.; Morton C.C.;  
RA "A novel conserved cochlear gene, OTOR: identification, expression  
RT analysis, and chromosomal mapping.";  
RL Genomics 66:242-248(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Petal;  
RX MEDLINE=21100875; PubMed=1161796;  
RX Rendtorff N.D.; Frodin M.; Attie-Bitach T.; Vekemans M.; Tommerup N.;  
RA "Identification and characterization of an inner ear-expressed human  
RT melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent  
RT polymorphism that abolishes translation.";  
RL Genomics 71:40-52(2001).  
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).  
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN COCHLEA.  
CC -!- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.  
CC -!- SIMILARITY: Contains 1 SH3 domain.  
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CC  
CC EMBL; AF233333; AAF82079.1; -;  
CC EMBL; AJ243939; CAC27444.1; -;  
CC HSP; Q16674; 111J.  
CC MGD; MGI:188678; Otor.  
CC GO; GO:0001502; P:cartilage condensation; IMP.  
CC InterPro; IPR001452; SH3.  
CC Pfam; PF00018; SH3; 1.  
CC SMART; SM00326; SH3; 1.  
CC PROSITE; PS50002; SH3; 1.  
CC Signal; SH3 domain; 18  
CC SIGNAL 1 18  
CC CHAIN 19 128  
CC OTORAPLIN.  
CC DOMAIN 39 110  
CC SH3.  
CC DISULFID 32 37  
CC BY SIMILARITY.  
CC DISULFID 55 127  
CC BY SIMILARITY.  
CC SEQUENCE 128 AA; 14328 MW; 3DD47D4C77C4A7FD CRC64;  
Query Match 92.7%; Score 547; DB 1; Length 128;  
Best Local Similarity 90.0%; Pred. No. 1.7e-49;  
Matches 99; Conservative 7; Mismatches 4; Indels 0; Gaps 0;  
QY 1 HGIFNDRASKKLCADDECVYTIISASQEDYNAPDCRFINVKGGQIYVYVKLVKNGA 60  
DB 19 HGIFNDRASKKLCADDECVYTIISASQEDYNAPDCRFINVKGGQIYVYVKLVKNGA 78  
QY 61 GEFWAGSVYGDQDEMGVYFPNRLVKEQRYQVQATKEVPTTIDIDFCE 110  
DB 79 GEFWAGSVYGDQDEMGVYFPNRLVKEQRYQVQATKEVPTTIDIDFCE 128  
RESULT 3  
OTOR CHICK  
ID OTOR CHICK STANDARD; PRT; 132 AA.  
AC Q918P6;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Otoraplin precursor.  
GN OTOR.

```

OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=20334619; PubMed=10873378;
RA Robertson N.G., Heller S., Lin J.S., Resendes B.L., Weremowicz S.,
RA Denis C.S., Bell A.M., Hudspeth A.J., Morton C.C.;
RT "A novel conserved cochlear gene, OTOR: identification, expression
RT analysis, and chromosomal mapping.";
RL Genomics 66:242-248(2000).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN COCHLEA.
CC -1- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
CC -1- SIMILARITY: Contains 1 SH3 domain.
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CC -----
DR EMBL; AF233518; AAF82727.1; -
DR HSSP; Q16674; 111J.
DR InterPro; IPR001452; SH3.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS50002; SH3; 1.
DR SIGNAL; SH3 domain. 23
FT CHAIN 1 123 POTENTIAL.
FT CHAIN 24 132 OTORAPLIN.
FT DOMAIN 42 114 SH3.
FT DISULFID 35 40 BY SIMILARITY.
FT DISULFID 58 131 BY SIMILARITY.
FT SEQUENCE 132 AA; 15177 MW; 9D1CB07FD353CE1C CRC64;
Query Match 80.9%; Score 477.5; DB 1; Length 132;
Best Local Similarity 80.0%; Pred. No. 2.6e-42;
Matches 88; Conservative 9; Mismatches 12; Indels 1; Gaps 1;
QY 2 GIPMDRLASKKLCADDECYVITISLASAQEDYNAPDCRFNVKKGQIYVYKLVKENGAG 61
Db GIPMDRLASKKLCADDECYVITISLVRABEDYNAPDCRFNVKKGQIYVYKLVKESG 82
QY 62 EFWAGSVYGDG-QDEMGVGVYFPRNLVKEQRYQATKVEPTTIDIDFFCE 110
Db EFWAGSVYGEYEDHMGTVGVYFPRSLVSEQHVYQEAANKTPTTIDIDFFCE 132
RESULT 4
OTOR_RANCA
ID OTOR_RANCA STANDARD; PRT; 133 AA.
AC Q918P5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Otoraplin precursor.
DE OTOR.
GN OTOR.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
OX NCBI_TaxID=8400;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=20334619; PubMed=10873378;
RA Robertson N.G., Heller S., Lin J.S., Resendes B.L., Weremowicz S.,
RA Denis C.S., Bell A.M., Hudspeth A.J., Morton C.C.;
RT "A novel conserved cochlear gene, OTOR: identification, expression
RT analysis, and chromosomal mapping.";
RL Genomics 66:242-248(2000).

```

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CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
CC -1- SIMILARITY: Contains 1 SH3 domain.
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CC -----
DR EMBL; AF233519; AAF82728.1; -
DR HSSP; Q16674; 111J.
DR InterPro; IPR001452; SH3.
DR PFAM; PF00018; SH3; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS50002; SH3; 1.
DR SIGNAL; SH3 domain. 23
FT CHAIN 1 133 POTENTIAL.
FT CHAIN 24 115 OTORAPLIN.
FT DOMAIN 48 115 SH3.
FT DISULFID 35 40 BY SIMILARITY.
FT DISULFID 58 132 BY SIMILARITY.
FT SEQUENCE 133 AA; 15243 MW; 25440C1A3CF911AE CRC64;
Query Match 66.1%; Score 390; DB 1; Length 133;
Best Local Similarity 58.9%; Pred. No. 2.6e-33;
Matches 66; Conservative 26; Mismatches 18; Indels 2; Gaps 2;
QY 1 HGIFMDRLASKKLCADDECYVITISLASAQEDYNAPDCRFNVKKGQIYVYKLVKEN-G 59
Db YGVIMQKLSKDKLCADDECYVITISFGRAEDYNAPDCRFVNLKKGELVYITKLVKENDD 81
QY 60 AGEFWAGSVYGDG-QDEMGVGVYFPRNLVKEQRYQATKVEPTTIDIDFFCE 110
Db AGEFWAGSVYSDQYRQDQGLVGFPSLSVLTLYKDELQELPTTAVDFFCD 133
RESULT 5
MIA_HUMAN
ID MIA_HUMAN STANDARD; PRT; 131 AA.
AC Q16674;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Melanoma derived growth regulatory protein precursor (Melanoma
DE inhibitory activity).
DE MIA.
GN MIA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=95007612; PubMed=7923218;
RA Blesch A., Bosserhoff A.-K., Apfel R., Behl C., Hessdoerfer B.,
RA Schmitt A., Jachimczak P., Lottspeich F., Buettner R., Bogdahn U.;
RT "Cloning of a novel malignant melanoma-derived growth-regulatory
RT protein, MIA.";
RL Cancer Res. 54:5695-5701(1994).
RN [2]_
RP SEQUENCE FROM N.A.
RX TISSUE=Placenta;
RC MEDLINE=96132947; PubMed=8550608;
RA Bosserhoff A.-K., Hein R., Bogdahn U., Buettner R.;
RT "Structure and promoter analysis of the gene encoding the human
RT melanoma-inhibiting protein MIA.";
RL J. Biol. Chem. 271:490-495(1996).
RN [3]_
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932;

```



KW Growth factor; Signal; SH3 domain.  
FT SIGNAL 1 22 BY SIMILARITY  
FT CHAIN 23 130 MELANOMA DERIVED GROWTH REGULATORY PROTEIN.  
FT DOMAIN 42 112 SH3.  
FT DISULFID 35 40 BY SIMILARITY.  
FT DISULFID 58 129 BY SIMILARITY.  
SQ SEQUENCE 130 AA; 14353 MW; 95D153161C78E02A CRC64;  
Query Match 42.8%; Score 252.5; DB 1; Length 130;  
Best Local Similarity 45.0%; Pred. No. 3.7e-19;  
Matches 50; Conservative 22; Mismatches 28; Indels 11; Gaps 4;  
QY 5 MDRASKKLCADCECVYITSLASQAQEDYNAPDCRFNVKKGQIYVYVKLVKENGAGE-F 63  
Db 26 MPKLAQRKCADECSHPISMAVALQDYVAPDCRFLLIHOGVYVIFSKL---KGRGLRF 82  
QY 64 WAGSV---YGDQDQDGVGVYPPRNVLKQRYVQATKEVPTTDIDFFCE 110  
Db 83 WGSVQGDYGYDGAARL---GYFPSSIVREDQTLKPAKTDVKTIDWDFYQC 130  
RESULT 7  
MIA RAT  
ID MIA RAT STANDARD; PRT; 130 AA.  
AC Q62946; P97591;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Melanoma derived growth regulatory protein precursor (Melanoma inhibitory activity) (Cartilage-derived retinoic acid-sensitive protein) (CD-RAP).  
DE protein (CD-RAP).  
GN MIA OR CDAP.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley; TISSUE=Mammary gland;  
RA Lu J.X.;  
RT "Gene expression changes associated with chemically-induced rat mammary carcinogenesis.";  
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE OF 34-124 FROM N.A.  
RC TISSUE=Cartilage;  
RX MEDLINE=96216414; PubMed=8621736;  
RA Dietz U.H., Sandell L.J.;  
RT "Cloning of a retinoic acid-sensitive mRNA expressed in cartilage and during chondrogenesis.";  
RL J. Biol. Chem. 271:3311-3316 (1996).  
CC -!- FUNCTION: MAY FUNCTION DURING CARTILAGE DEVELOPMENT AND MAINTENANCE.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: CARTILAGE PRIMORDIA AND CARTILAGE.  
CC -!- INDUCTION: Repressed by retinoic acid.  
CC -!- PTM: MAY POSSESS TWO INTRAMOLECULAR DISULFIDE BONDS.  
CC -!- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.  
CC -!- SIMILARITY: Contains 1 SH3 domain.  
CC -----  
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CC -----  
DR EMBL; U51438; AAC52481.1; -;  
DR EMBL; U67884; BAB40659.1; -;  
DR HSSP; Q16674; 111J.  
DR InterPro; IPR001452; SH3.

DR Pfam; PF00018; SH3; 1.  
DR SMART; SM00326; SH3; 1.  
DR PROSITE; PS00002; SH3; FALSE NEG.  
KW Growth factor; Signal; SH3 domain.  
FT SIGNAL 1 22 POTENTIAL.  
FT CHAIN 23 130 MELANOMA DERIVED GROWTH REGULATORY PROTEIN.  
FT DOMAIN 42 112 SH3.  
FT DISULFID 35 40 BY SIMILARITY.  
FT DISULFID 58 129 BY SIMILARITY.  
FT CONFLICT 46 47 MA -> VT (IN REF. 2).  
SQ SEQUENCE 130 AA; 14536 MW; 5F99149AECF74501 CRC64;  
Query Match 42.5%; Score 250.5; DB 1; Length 130;  
Best Local Similarity 44.4%; Pred. No. 5.9e-19;  
Matches 48; Conservative 23; Mismatches 32; Indels 5; Gaps 3;  
QY 5 MDRASKKLCADCECVYITSLASQAQEDYNAPDCRFNVKKGQIYVYVKLVKENGAGE-F 63  
Db 26 MPKLAQRKCADECSHPISMAVALQDYVAPDCRFLLIHOGVYVIFSKL---KGRGLRF 82  
QY 64 WAGSVGDQDQDGVGVYPPRNVLKQRYVQATKEVPTTDIDFFCE 110  
Db 83 WGSVQGDYGYDGAARL---GYFPSSIVREDQTLKPAKTDVKTIDWDFYQC 130  
RESULT 8  
MIA MOUSE  
ID MIA MOUSE STANDARD; PRT; 130 AA.  
AC Q61865; O09086; P97495;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Melanoma derived growth regulatory protein precursor (Melanoma inhibitory activity) (Cartilage-derived retinoic acid-sensitive protein) (CD-RAP).  
DE protein (CD-RAP).  
GN MIA OR CDAP.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RX MEDLINE=95007612; PubMed=793218;  
RA Blesch A., Bosserhoff A.-K., Apfel R., Behl C., Hessdoerfer B., Schmitt A., Jachimczak P., Lottspeich F., Buettner R., Bogdahn U.;  
RT "Cloning of a novel malignant melanoma-derived growth-regulatory protein, MIA.";  
RL Cancer Res. 54:5695-5701 (1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SV;  
RX MEDLINE=97251341; PubMed=9097023;  
RA Bosserhoff A.K., Kondo S., Moser M., Dietz U., Copeland N.G., Gilbert D.J., Jenkins N.A., Buettner R., Sandell L.J.;  
RT "Mouse CD-RAP/MIA gene: Structure, chromosomal localization, and expression in cartilage and chondrosarcoma.";  
RL Dev. Dyn. 208:516-525 (1997).  
CC -!- FUNCTION: ELICITS GROWTH INHIBITION ON MELANOMA CELLS IN VITRO AS WELL AS SOME OTHER NEUROECTODERMAL TUMORS, INCLUDING GLIOMAS (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: ALL MALIGNANT MELANOMA CELL LINES TESTED AND INFREQUENTLY IN GLIOMA CELL LINES.  
CC -!- PTM: MAY POSSESS TWO INTRAMOLECULAR DISULFIDE BONDS.  
CC -!- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.  
CC -!- SIMILARITY: Contains 1 SH3 domain.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL; X94322; CAA63983.1; --  
DR EMBL; U85612; AAB42082.1; --  
DR EMBL; X97965; CAA66608.1; --  
DR HSSP; Q16674; I11J.  
DR MGD; MGI:109615; Mia.  
DR GO; GO:0007160; P:cell-matrix adhesion; IMP.  
DR GO; GO:0030198; P:extracellular matrix organization and bioge. . .; IMP.  
DR InterPro; IPR001452; SH3.  
DR Pfam; PF00018; SH3; 1.  
DR SMART; SM00326; SH3; 1.  
DR PROSITE; PS50002; SH3; FALSE NEG.  
KW Growth factor; Signal; SH3 domain.  
FT SIGNAL 1 22 POTENTIAL.  
FT CHAIN 23 130 MELANOMA DERIVED GROWTH REGULATORY  
FT PROTEIN.

FT DOMAIN 42 112  
FT DISULFID 35 40 BY SIMILARITY.  
FT DISULFID 58 129 BY SIMILARITY.  
FT CONFLICT 112 113 TL -> NS (IN REF. 1).  
SQ SEQUENCE 130 AA; 14593 MW; 16C957453C5BB5F9 CRC64;  
Query Match 39.9%; Score 235.5; DB 1; Length 130;  
Best Local Similarity 43.5%; Pred. No. 2.1e-17;  
Matches 47; Conservative 21; Mismatches 35; Indels 5; Gaps 3;  
QY 5 MDRLASKKLCADDCCVYVTSIASAOEDYNAPCRFINVKKGQIIVVSKLVKENGAGB-F 63  
DB 26 MKPLADWKLCADEECSPHSVAVALQDYVADPCFLTYRGQVTVFSLK---KGRGLP 82  
QY 64 WAGSVYGGQDEMVG-VGYFFRNVLKEQRVQEATKEVPTTIDPFCE 110  
DB 83 WGGSVQGGYVGDLAARLGYFFSSIVREDTLKPGKIDMKTKQWDFYCQ 130

RESULT 9  
ID VAV3 MOUSE STANDARD; PRT; 847 AA.  
AC Q9R0C8;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Vav-3 protein.  
GN VAV3.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20179693; PubMed=10713454;  
RA Trenkle T., McClelland M., Adlkofer K., Welsh J.;  
RT "Major transcript variants of VAV3, a new member of the VAV family of  
RT guanine nucleotide exchange factors.";  
RL Gene 245:139-149(2000).  
CC -!- FUNCTION: EXCHANGE FACTOR FOR GTP-BINDING PROTEINS RHOA, RHOG AND,  
CC TO A LESSER EXTENT, RAC-1. BINDS PHYSICALLY TO THE NUCLEOTIDE-FREE  
CC STATES OF THOSE GTPASES (BY SIMILARITY).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=Alpha;  
CC IsoId=Q9R0C8-1; Sequence=Displayed;  
CC Name=Beta;  
CC IsoId=Q9R0C8-2; Sequence=Not described;  
CC -!- SIMILARITY: Contains 1 calponin-homology (CH) domain.  
CC -!- SIMILARITY: Contains 1 DBU-nomology (DH) domain.  
CC -!- SIMILARITY: Contains 1 PH domain.  
CC -!- SIMILARITY: Contains 1 zinc-dependent phorbol-ester and DAG  
CC binding domain.  
CC -!- SIMILARITY: Contains 1 SH2 domain.

CC -!- SIMILARITY: Contains 2 SH3 domains.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL; AF067816; AAF09171.1; --  
DR HSSP; P29355; 1SEM.  
DR MGD; MGI:1888518; Vav3.  
DR InterPro; IPR001715; Calponin-like.  
DR InterPro; IPR003247; CH type.  
DR InterPro; IPR002219; DAG\_PE-Bind.  
DR InterPro; IPR001331; GDS\_CDC24.  
DR InterPro; IPR001849; PH\_1.  
DR InterPro; IPR000219; RhoGEF.  
DR InterPro; IPR000980; SH2.  
DR InterPro; IPR001452; SH3.  
DR InterPro; IPR003096; SM22\_calponin.  
DR Pfam; PF00307; CH; 1.  
DR Pfam; PF00130; DAG\_PE-bind; 1.  
DR Pfam; PF00169; PH; 1.  
DR Pfam; PF00621; RhoGEF; 1.  
DR Pfam; PF00017; SH2; 1.  
DR Pfam; PF00018; SH3; 1.  
DR PRINTS; PR00401; SH2DOMAIN.  
DR PRINTS; PR00452; SH3DOMAIN.  
DR PRINTS; PR00888; SM22CALPONIN.  
DR ProDom; PD001527; CH\_type; 1.  
DR ProDom; PD000093; SH2; 1.  
DR ProDom; PD000066; SH3; 1.  
DR SMART; SM00109; C1; 1.  
DR SMART; SM00033; CH; 1.  
DR SMART; SM00233; PH; 1.  
DR SMART; SM00325; RhoGEF; 1.  
DR SMART; SM00252; SH2; 1.  
DR SMART; SM00326; SH3; 2.  
DR PROSITE; PS50021; CH; 1.  
DR PROSITE; PS00479; DAG\_PE\_BIND\_DOM\_1; 1.  
DR PROSITE; PS50081; DAG\_PE\_BIND\_DOM\_2; 1.  
DR PROSITE; PS50010; DH\_2; 1.  
DR PROSITE; PS00741; DH\_1; 1.  
DR PROSITE; PS50003; PH DOMAIN; 1.  
DR PROSITE; PS50001; SH2; 1.  
DR PROSITE; PS50002; SH3; 2.  
KW Phorbol-ester binding; Zinc; SH2 domain; SH3 domain; Repeat;  
KW Guanine-nucleotide releasing factor; Alternative splicing.  
FT DOMAIN 1 119 CH.  
FT DOMAIN 192 371 DH.  
FT DOMAIN 400 502 PH.  
FT DOMAIN 514 562 PHORBOL-ESTER AND DAG BINDING.  
FT DOMAIN 592 660 SH3 1.  
FT DOMAIN 672 766 SH2.  
FT DOMAIN 788 847 SH3 2.  
SQ SEQUENCE 847 AA; 97946 MW; 9A6B63F0D9E60F8F CRC64;

Query Match 15.0%; Score 88.5; DB 1; Length 847;  
Best Local Similarity 31.3%; Pred. No. 0.21;  
Matches 21; Conservative 14; Mismatches 21; Indels 11; Gaps 2;  
QY 23 ISLASAQEDYNAPCRFINVKKGQIIVVSKLVKENGAGBFWAGSVYGGQDEMVGTVGYF 82  
DB 790 LGIAIARYDFPCARDRELSLKGDWVKYTKN----SANGWWRGEVNGR-----VGWF 838  
QY 83 PRLVKE 89  
DB 839 PSTYVEE 845  
RESULT 10

VAV\_HUMAN  
ID VAV\_HUMAN STANDARD; PRT; 845 AA.  
AC P15498; Q15860;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Vav proto-oncogene.  
GN VAV1 OR VAV.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Denninger D.J., Borges C.R., Shaw C.L., Cushman A.M., Kawahara R.S.;  
RT "Transcriptional regulation of the vav proto-oncogene.";  
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE OF 62-845 FROM N.A.  
RX MEDLINE=90005432; PubMed=2477241;  
RA Katrav S., Martin-Zanca D., Barbacid M.;  
RT "vav, a novel human oncogene derived from a locus ubiquitously  
expressed in hematopoietic cells.";  
RL EMBO J. 8:2283-2290(1989).  
RN [3]  
RP SEQUENCE OF 1-61 FROM N.A.  
RX MEDLINE=91172176; PubMed=2005887;  
RA Katrav S., Cleveland J.L., Heslop H.E., Pulido D.;  
RT "Loss of the amino-terminal helix-loop-helix domain of the vav proto-  
oncogene activates its transforming potential.";  
RL Mol. Cell. Biol. 11:1912-1920(1991).  
RN [4]  
RP SEQUENCE OF 299-837 FROM N.A.  
RA Romero F.;  
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE OF 299-334 FROM N.A.  
RX MEDLINE=96038895; PubMed=7478592;  
RA Ramos-Morales F., Romero F., Schweighoffer F., Bismuth G., Camonis J.,  
RA Tortolero M., Fischer S.;  
RT "The proline-rich region of Vav binds to Grb2 and Grb3-3.";  
RL Oncogene 11:1665-1669(1995).  
RN [6]  
RP SIMILARITY TO CDC24 FAMILY.  
RX MEDLINE=92282488; PubMed=1565462;  
RA Adams J.M., Houston H., Allen J., Lints T., Harvey R.;  
RT "The hematopoietically expressed vav proto-oncogene shares homology  
with the db1 Gbp-GTP exchange factor, the bcr gene and a yeast gene  
(CDC24) involved in cytoskeletal organization.";  
RL Oncogene 7:611-618(1992).  
CC -1- FUNCTION: Couples tyrosine kinase signals with the activation of  
the Rho/Rac GTPases, thus leading to cell differentiation and/or  
proliferation.  
CC -1- SUBUNIT: Interacts with SLA (By similarity). Interacts with Grb2  
and Grb3.  
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN HEMATOPOIETIC CELLS BUT  
NOT IN OTHER CELL TYPES.  
CC -1- PTM: Phosphorylated on tyrosine residues.  
CC -1- MISCELLANEOUS: 'Vav' stands for the sixth letter of the Hebrew  
alphabet.  
CC -1- SIMILARITY: Contains 1 calponin-homology (CH) domain.  
CC -1- SIMILARITY: Contains 1 DBL-homology (DH) domain.  
CC -1- SIMILARITY: Contains 1 PH domain.  
CC -1- SIMILARITY: Contains 1 zinc-dependent phorbol-ester and DAG  
binding domain.  
CC -1- SIMILARITY: Contains 1 SH2 domain.  
CC -1- SIMILARITY: Contains 2 SH3 domains.  
CC -1- CAUTION: Ref.2 sequence differs from that shown due to frameshifts  
in position 322 and 355.  
CC  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).  
-----  
CC EMBL; AF030227; AAC25011.1; JOINED.  
CC EMBL; AF030201; AAC25011.1; JOINED.  
CC EMBL; AF030202; AAC25011.1; JOINED.  
CC EMBL; AF030203; AAC25011.1; JOINED.  
CC EMBL; AF030204; AAC25011.1; JOINED.  
CC EMBL; AF030205; AAC25011.1; JOINED.  
CC EMBL; AF030206; AAC25011.1; JOINED.  
CC EMBL; AF030207; AAC25011.1; JOINED.  
CC EMBL; AF030208; AAC25011.1; JOINED.  
CC EMBL; AF030209; AAC25011.1; JOINED.  
CC EMBL; AF030210; AAC25011.1; JOINED.  
CC EMBL; AF030211; AAC25011.1; JOINED.  
CC EMBL; AF030212; AAC25011.1; JOINED.  
CC EMBL; AF030213; AAC25011.1; JOINED.  
CC EMBL; AF030214; AAC25011.1; JOINED.  
CC EMBL; AF030215; AAC25011.1; JOINED.  
CC EMBL; AF030216; AAC25011.1; JOINED.  
CC EMBL; AF030217; AAC25011.1; JOINED.  
CC EMBL; AF030218; AAC25011.1; JOINED.  
CC EMBL; AF030219; AAC25011.1; JOINED.  
CC EMBL; AF030220; AAC25011.1; JOINED.  
CC EMBL; AF030221; AAC25011.1; JOINED.  
CC EMBL; AF030222; AAC25011.1; JOINED.  
CC EMBL; AF030223; AAC25011.1; JOINED.  
CC EMBL; AF030224; AAC25011.1; JOINED.  
CC EMBL; AF030225; AAC25011.1; JOINED.  
CC EMBL; AF030226; AAC25011.1; JOINED.  
CC EMBL; X16316; CAA34383.1; ALT\_FRAME.  
CC EMBL; M59834; AAA63267.1; -.  
CC EMBL; X83931; CAA58783.1; -.  
CC PIR; B39576; TVHUVV.  
CC HGSP; P29354; IGRI.  
CC TRANSFAC; T00880; -.  
CC Genew; HGNC:12657; VAV1.  
CC MIM; 164875; -.  
CC GO; GO:0003700; F:transcription factor activity; TAS.  
CC GO; GO:0007048; P:oncogenesis; TAS.  
CC InterPro; IPR001715; Calponin-like.  
CC InterPro; IPR003247; CH type.  
CC InterPro; IPR002219; DAG\_PE-bind.  
CC InterPro; IPR001331; GDS\_CDC24.  
CC InterPro; IPR001849; PH.  
CC InterPro; IPR000219; RhoGEF.  
CC InterPro; IPR000980; SH2.  
CC InterPro; IPR001452; SH3.  
CC InterPro; IPR003096; SM22\_calponin.  
CC Pfam; PF00307; CH; 1.  
CC Pfam; PF00130; DAG\_PE-bind; 1.  
CC Pfam; PF00169; PH; 1.  
CC Pfam; PF00621; RhoGEF; 1.  
CC Pfam; PF00017; SH2; 1.  
CC Pfam; PF00018; SH3; 2.  
CC PRINTS; PR00401; SH2DOMAIN.  
CC PRINTS; PR00452; SH3DOMAIN.  
CC PRINTS; PR00888; SM22CALPONIN.  
CC ProDom; PD001527; CH type; 1.  
CC ProDom; PD000033; SH2; 1.  
CC ProDom; PD000066; SH3; 1.  
CC SMART; SM00109; C1; 1.  
CC SMART; SM00033; CH; 1.  
CC SMART; SM00233; PH; 1.  
CC SMART; SM00325; RhoGEF; 1.  
CC SMART; SM00252; SH2; 1.  
CC SMART; SM00326; SH3; 2.  
CC PROSITE; PS50021; CH; 1.  
CC PROSITE; PS00479; DAG\_PE\_BIND\_DOM\_1; 1.  
CC PROSITE; PS50081; DAG\_PE\_BIND\_DOM\_2; 1.  
CC PROSITE; PS50010; DH\_2; 1.



```

Query Match          14.7%; Score 86.5; DB 1; Length 847;
Best Local Similarity 31.3%; Pred. No. 0.33;
Matches 2; Conservative 14; Mismatches 21; Indels 11; Gaps 2;

QY 23 ISLASAQEDYNAPCRFINVKKGQOIYVYSLVKENGAGFEWAGSVYGDQDENVGVYGF 82
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 790 LGIAIARYDFCARDMRELSLLKGDVWKYITQM-----SANGWVRGEVNGR-----VGWF 838

QY 83 PRNLVKE 89
    | : : |
Db 839 PSTYVEE 845

RESULT 12
VAV_RAT
ID -VAV_RAT STANDARD; PRT; 843 AA.
AC PS4100;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Vav proto-oncogene (p95).
GN VAV1 OR VAV.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99323974; PubMed=10395673;
RA Song J.S., Halem-Smith H., Arudchandran R., Gomez J., Scott P.M.,
RA Mill J.F., Tan T.-H., Rivera J.;
RT "Tyrosine phosphorylation of Vav stimulates IL-6 production in mast
RL J. Immunol. 163:802-810(1999).
CC -!- FUNCTION: Couples tyrosine kinase signals with the activation of
CC the Rho/Rac GTPases, thus leading to cell differentiation and/or
CC proliferation.
CC -!- SUBUNIT: Interacts with SLA (By similarity).
CC -!- PTM: Phosphorylated on tyrosine residues.
CC -!- SIMILARITY: Contains 1 calponin-homology (CH) domain.
CC -!- SIMILARITY: Contains 1 DBL-homology (DH) domain.
CC -!- SIMILARITY: Contains 1 PH domain.
CC -!- SIMILARITY: Contains 1 zinc-dependent phosphol-ester and DAG
CC binding domain.
CC -!- SIMILARITY: Contains 1 SH2 domain.
CC -!- SIMILARITY: Contains 2 SH3 domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U939476; AAA98606.1; -.
DR HSSP; P29354; 1GRI.
DR InterPro; IPR001715; Calponin-like.
DR InterPro; IPR003247; CH type.
DR InterPro; IPR002219; DAG_PE_bind.
DR InterPro; IPR001331; GDS_CDC24.
DR InterPro; IPR001849; PH.
DR InterPro; IPR000219; RhoGEF.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR003096; SM22_calponin.
DR Pfam; PF00307; CH; 1.
DR Pfam; PF00130; DAG_PE_bind; 1.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00621; RhoGEF; 1.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 2.
DR PRINTS; PR00401; SH2DOMAIN.

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DR PRINTS; PR00452; SH3DOMAIN.
DR PRINTS; PR00886; SM22CALPONIN.
DR PRODOM; PD001527; CH type; 1.
DR PRODOM; PD000093; SH2; 1.
DR PRODOM; PD000066; SH3; 1.
DR SMART; SM00109; C1; 1.
DR SMART; SM00033; CH; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00325; RhoGEF; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 2.
DR PROSITE; PS00021; CH; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS00010; DH_2; 1.
DR PROSITE; PS00741; DH_1; 1.
DR PROSITE; PS50003; PH DOMAIN; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 2.
KW Proto-oncogene; Phorbol-ester binding; Zinc; SH2 domain; SH3 domain;
KW Guanine-nucleotide releasing factor; Repeat; Phosphorylation.
FT DOMAIN 1 119
FT DOMAIN 194 373
FT DOMAIN 402 504
FT DOMAIN 516 564
FT DOMAIN 615 658
FT DOMAIN 669 763
FT DOMAIN 780 840
SQ SEQUENCE 843 AA; 97953 MW; C4A5CACD45FCB80E CRC64;

Query Match          14.5%; Score 85.5; DB 1; Length 843;
Best Local Similarity 31.4%; Pred. No. 0.42;
Matches 2; Conservative 14; Mismatches 21; Indels 13; Gaps 3;

QY 26 ASAQEDYNAPCRFINVKKGQOIYVYSLVKENGAGFEWAGSVYGDQDENVGVYGFPRN 85
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 785 AKARYDFCARDRSELSLKEDII-----KILNKKGGQGWGEIYGR-----IGWPPSN 833

QY 86 LVKEQRYQE 95
    | : |
Db 834 YVEED--YSE 841

RESULT 13
VAV_MOUSE
ID -VAV_MOUSE STANDARD; PRT; 845 AA.
AC P27870;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Vav proto-oncogene.
GN VAV1 OR VAV.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92228488; PubMed=1565462;
RA Adams J.A., Houston H., Allen J., Lints T., Harvey R.;
RT "The hematopoietically expressed vav proto-oncogene shares homology
RT with the dbl GDP-GTP exchange factor, the bcr gene and a yeast gene
RT (CDC24) involved in cytoskeletal organization.";
RL Oncogene 7:611-618(1992).
RN [2]
RP SEQUENCE OF 1-93 FROM N.A.
RX MEDLINE=91172176; PubMed=2005887;
RA Katrav S., Cleveland J.L., Heslop H.E., Pulido D.;
RT "Loss of the amino-terminal helix-loop-helix domain of the vav proto-
RL oncogene activates its transforming potential.";
RL Mol. Cell. Biol. 11:1912-1920(1991).
RN [3]
RP INTERACTION WITH SLA.

```

RX MEDLINE=20130290; PubMed=10662792;  
 RA Sosinowski T., Pandey A., Dixit V.M., Weiss A.;  
 RT "Src-like adaptor protein (SLAP) is a negative regulator of T cell  
 RL receptor signaling.";  
 J. Exp. Med. 191:463-474(2000).  
 CC -|- FUNCTION: Couples tyrosine kinase signals with the activation of  
 CC the Rho/Rac GTPases, thus leading to cell differentiation and/or  
 CC proliferation.  
 CC -|- SUBUNIT: Interacts with SLA.  
 CC -|- TISSUE SPECIFICITY: Widely expressed in hematopoietic cells but  
 CC not in other cell types.  
 CC -|- PTM: Phosphorylated on tyrosine residues (By similarity).  
 CC -|- SIMILARITY: Contains 1 calponin-homology (CH) domain.  
 CC -|- SIMILARITY: Contains 1 DBL-homology (DH) domain.  
 CC -|- SIMILARITY: Contains 1 PH domain.  
 CC -|- SIMILARITY: Contains 1 zinc-dependent phorbol-ester and DAG  
 CC binding domain.  
 CC -|- SIMILARITY: Contains 1 SH2 domain.  
 CC -|- SIMILARITY: Contains 2 SH3 domains.  
 CC -----  
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 CC -----  
 DR EMBL; X64361; CAA45713.1; -;  
 DR EMBL; M59833; AAA63402.1; -;  
 DR PIR; A61187; TVMSV.  
 DR PDB; 1F5X; 15-SEP-00.  
 DR PDB; 1GCP; 28-JAN-03.  
 DR PDB; 1GCQ; 28-JAN-03.  
 DR PDB; 1K1Z; 18-DEC-02.  
 DR TRANSFAC; T01230; -;  
 DR MGD; MGI:98923; Vav1.  
 DR InterPro; IPR001715; Calponin-like.  
 DR InterPro; IPR003247; CH type.  
 DR InterPro; IPR002219; DAG\_PE-bind.  
 DR InterPro; IPR001331; GDS\_CDC24.  
 DR InterPro; IPR001849; PH.  
 DR InterPro; IPR000219; RhoGEF.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001452; SH3.  
 DR InterPro; IPR003096; SM22\_calponin.  
 DR Pfam; PF00307; CH; 1.  
 DR Pfam; PF00130; DAG\_PE-bind; 1.  
 DR Pfam; PF00169; PH; 1.  
 DR Pfam; PF00621; RhoGEF; 1.  
 DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00018; SH3; 2.  
 DR PRINTS; PR00401; SH2DOMAIN.  
 DR PRINTS; PR00452; SH3DOMAIN.  
 DR PRINTS; PR00888; SM22CALPONIN.  
 DR ProDom; PD001527; CH type; 1.  
 DR ProDom; PD000093; SH2; 1.  
 DR ProDom; PD000066; SH3; 1.  
 DR SMART; SM00109; C1; 1.  
 DR SMART; SM00033; CH; 1.  
 DR SMART; SM00233; PH; 1.  
 DR SMART; SM00325; RhoGEF; 1.  
 DR SMART; SM00252; SH2; 1.  
 DR SMART; SM00326; SH3; 2.  
 DR PROSITE; PS50021; CH; 1.  
 DR PROSITE; PS00479; DAG\_PE\_BIND\_DOM\_1; 1.  
 DR PROSITE; PS50081; DAG\_PE\_BIND\_DOM\_2; 1.  
 DR PROSITE; PS50010; DH\_2; 1.  
 DR PROSITE; PS00741; DH\_1; 1.  
 DR PROSITE; PS50003; PH\_DOMAIN; 1.  
 DR PROSITE; PS50001; SH2; 1.  
 DR PROSITE; PS50002; SH3; 2.  
 KW Proto-oncogene; Phorbol-ester binding; Zinc; SH2 domain; SH3 domain;

KW Guanine-nucleotide releasing factor; Repeat; Phosphorylation;  
 KW 3D-structure. 1 119 CH.  
 FT DOMAIN 194 373 DH.  
 FT DOMAIN 402 504 PH.  
 FT DOMAIN 516 564 PHORBOL-ESTER AND DAG BINDING.  
 FT DOMAIN 617 660 SH3 1.  
 FT DOMAIN 671 765 SH2.  
 FT DOMAIN 782 842 SH3 2.  
 FT CONFLICT 29 29 Q -> E (IN REF. 2).  
 SQ SEQUENCE 845 AA; 98136 MW; 3666DCCD1C5229DA CRC64;  
  
 Query Match 14.5%; Score 85.5; DB 1; Length 845;  
 Best Local Similarity 31.4%; Pred. No. 0.42;  
 Matches 22; Conservative 14; Mismatches 21; Indels 13; Gaps 3;  
  
 QY 26 ASAGEDYNAPDREFINVKKGQOIYVYKLVKENGAGFAGSVYGDQDEMGVVGYPN 85  
 DB 787 AKARYDFCARDSELSLKEGDII---KILNKKQQQWRRGEIYGR-----IGWFFPN 835  
 QY 86 LVKEQRVYQE 95  
 DB 836 YVEED--YSE 843  
  
 RESULT 14  
 VAV2 MOUSE STANDARD; PRT; 868 AA.  
 ID VAV2 MOUSE STANDARD; PRT; 868 AA.  
 AC Q60992;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Vav-2 protein.  
 GN VAV2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6;  
 RX MEDLINE=96313271; PubMed=8710375;  
 RA Schuebel K.E., Bustelo X.R., Nielsen D.A., Song B.J., Barbacid M.,  
 RT Goldman D., Lee I.J.;  
 RT "Isolation and characterization of murine vav2, a member of the vav  
 RL Oncogene 13:363-371(1996).  
 CC -|- FUNCTION: Guanine nucleotide exchange factor for the Rho family  
 CC of Ras-related GTPases (By similarity).  
 CC -|- SIMILARITY: Contains 1 calponin-homology (CH) domain.  
 CC -|- SIMILARITY: Contains 1 DBL-homology (DH) domain.  
 CC -|- SIMILARITY: Contains 1 PH domain.  
 CC -|- SIMILARITY: Contains 1 zinc-dependent phorbol-ester and DAG  
 CC binding domain.  
 CC -|- SIMILARITY: Contains 1 SH2 domain.  
 CC -|- SIMILARITY: Contains 2 SH3 domains.  
 CC -----  
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 CC -----  
 DR EMBL; U37017; AAC52761.1; -;  
 DR HSPB; Q60631; IGBQ.  
 DR MGD; MGI:102718; Vav2.  
 DR InterPro; IPR001715; Calponin-like.  
 DR InterPro; IPR003247; CH type.  
 DR InterPro; IPR002219; DAG\_PE-bind.  
 DR InterPro; IPR001331; GDS\_CDC24.  
 DR InterPro; IPR001849; PH.  
 DR InterPro; IPR000219; RhoGEF.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001452; SH3.  
 DR InterPro; IPR003096; SM22\_calponin.  
 DR Pfam; PF00307; CH; 1.  
 DR Pfam; PF00130; DAG\_PE-bind; 1.  
 DR Pfam; PF00169; PH; 1.  
 DR Pfam; PF00621; RhoGEF; 1.  
 DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00018; SH3; 2.  
 DR PRINTS; PR00401; SH2DOMAIN.  
 DR PRINTS; PR00452; SH3DOMAIN.  
 DR PRINTS; PR00888; SM22CALPONIN.  
 DR ProDom; PD001527; CH type; 1.  
 DR ProDom; PD000093; SH2; 1.  
 DR ProDom; PD000066; SH3; 1.  
 DR SMART; SM00109; C1; 1.  
 DR SMART; SM00033; CH; 1.  
 DR SMART; SM00233; PH; 1.  
 DR SMART; SM00325; RhoGEF; 1.  
 DR SMART; SM00252; SH2; 1.  
 DR SMART; SM00326; SH3; 2.  
 DR PROSITE; PS50021; CH; 1.  
 DR PROSITE; PS00479; DAG\_PE\_BIND\_DOM\_1; 1.  
 DR PROSITE; PS50081; DAG\_PE\_BIND\_DOM\_2; 1.  
 DR PROSITE; PS50010; DH\_2; 1.  
 DR PROSITE; PS00741; DH\_1; 1.  
 DR PROSITE; PS50003; PH\_DOMAIN; 1.  
 DR PROSITE; PS50001; SH2; 1.  
 DR PROSITE; PS50002; SH3; 2.  
 KW Proto-oncogene; Phorbol-ester binding; Zinc; SH2 domain; SH3 domain;



KW Guanine-nucleotide releasing factor; Repeat; Phosphorylation.  
FT DOMAIN 1 119 CH.  
FT DOMAIN 198 376 DH.  
FT DOMAIN 405 512 PH.  
FT DOMAIN 524 572 PHORBOL-ESTER AND DAG BINDING.  
FT DOMAIN 586 652 SH3 1.  
FT DOMAIN 673 767 SH2.  
FT DOMAIN 816 877 SH3 2.  
FT MOD\_RES 142 142 PHOSPHORYLATION (BY EGFR).  
FT MOD\_RES 159 159 PHOSPHORYLATION (BY EGFR).  
FT MOD\_RES 172 172 PHOSPHORYLATION (BY EGFR).  
SQ SEQUENCE 878 AA; 101256 MW; C8PF7681032146B4 CRC64;

Query Match 13.8%; Score 81.5; DB 1; Length 878;  
Best Local Similarity 26.3%; Pred. No. 1.1;  
Matches 20; Conservative 21; Mismatches 22; Indels 13; Gaps 3;  
QY 20 VVT---ISLSAQEDYNAPDCRFNVKGGQIYVYKLVKENGAGFEWAGSVYGDQDEM 76  
Db 812 VFTPRVIGTAVARYNFAARDMRELSLRSGDVVRIYSRIGDQG---WWKG-----ETN 861  
QY 77 GVVGYPFRNLVKEQV 92  
Db 862 GRIGWFPSTYVEEGI 877

Search completed: December 29, 2003, 16:04:13  
Job time : 4.31373 secs



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Db 26 MPKADWKLCADECSHPISNAVALQDVAFDCRFLTYRGQVYVFSKL---KGRGLF 82

QY 64 WAGSV 68

Db 83 WGSV 87

# RESULT 6

Q91ZV0 PRELIMINARY; PRT; 119 AA.  
AC Q91ZV0;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Melanoma inhibitory activity protein 2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RA Bosserhoff A.K., Buettner R.;  
RT "Characterization of the MIA gene family.";  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF390177; AAL26992.1; -;  
DR InterPro; IPR001452; SH3.  
DR SMART; SM00326; SH3; 1.  
SQ SEQUENCE 119 AA; 13397 MW; 589F390C0B49D1C7 CRC64;

Query Match 29.1%; Score 171.5; DB 11; Length 119;  
Best Local Similarity 39.2%; Pred. No. 5.7e-11;  
Matches 40; Conservative 14; Mismatches 39; Indels 9; Gaps 3;

QY 8 LASKKLCADCECVTISLQAQEDYNAPDRFINVKGQIYVYKLVKNGAGGEFWAGS 67

Db 26 LAHLKKGDLCEFTLSRVLALRDYTGDCRYLFTTGEISVYVYKLVGDR--EDLWAGS 83

QY 68 VYGDQDGMGVGVFPENLVKEQVYQATKEVPTTIDIDFFC 109

Db 84 ---KGKD----FGYFPRDAVQIEEVFISEIQMSTKESDFLC 118

# RESULT 7

Q90XF1 PRELIMINARY; PRT; 88 AA.  
AC Q90XF1;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Melanoma inhibitory activity protein (Fragment).  
OS Tetraodon nigroviridis (Green puffer).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
OC Tetraodontidae; Tetraodontidae; Tetraodon.  
OX NCBI\_TaxID=99883;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Bosserhoff A.K., Buettner R.;  
RT "Characterization of the MIA gene family.";  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF390176; AAL26991.1; -;  
DR InterPro; IPR001452; SH3.  
DR Pfam; PF00018; SH3; 1.  
DR SMART; SM00326; SH3; 1.  
FT NON\_TER 1  
SQ SEQUENCE 88 AA; 10080 MW; C355C1FE04DA22EA CRC64;

Query Match 28.6%; Score 168.5; DB 13; Length 88;  
Best Local Similarity 43.3%; Pred. No. 8.4e-11;  
Matches 39; Conservative 15; Mismatches 29; Indels 7; Gaps 4;

QY 23 ISLSAQEDYNAPDRFINVKGQIYVYKLVKNGAG--EFWAGSVYGD--QDEMGVV 79

Db 3 IMIARALQDYYPADCFIPRQGLIYVYAML---KGRGSQFWAGSVQDSYVQOE-ARI 58

QY 80 GYFPRNLVKEQVYQATKEVPTTIDIDFFC 109

Db 59 GHFPSSIVEETHPLMAAQTEVKTNSWDFYC 88

# RESULT 8

Q8C899 PRELIMINARY; PRT; 68 AA.  
AC Q8C899;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Otoraplin.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Head;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
DR EMBL; AK047965; BAC33202.1; -;  
SQ SEQUENCE 68 AA; 7431 MW; 3CBE75527D3CBF7F CRC64;

Query Match 16.9%; Score 100; DB 11; Length 68;  
Best Local Similarity 42.6%; Pred. No. 0.0019;  
Matches 20; Conservative 9; Mismatches 8; Indels 10; Gaps 2;

QY 1 HGIFMDRLASKKLCADCECV-----YTISLQAQEDYNA--PDC 37

Db 19 HGVFMDKLSKLCADCECVKALLTWFSLSFYHMGNLGKQPD 65

# RESULT 9

Q8R076 PRELIMINARY; PRT; 287 AA.  
AC Q8R076;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Hypothetical 32.7 kDa protein.  
GN VAV3.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BG027242; AAH27242.1; -;  
DR MGD; MGI:1888518; Vav3.  
DR InterPro; IPR000980; SH2.  
DR InterPro; IPR001452; SH3.  
DR Pfam; PF00017; SH2; 1.  
DR ProDom; PD000093; SH2; 1.  
DR ProDom; PD000066; SH3; 1.  
DR SMART; SM00325; SH2; 1.  
DR SMART; SM00326; SH3; 2.  
DR PROSITE; PS50001; SH2; 1.  
DR PROSITE; PS50002; SH3; 2.  
KW Hypothetical protein.  
SQ SEQUENCE 287 AA; 32662 MW; BF2850B8F921F048 CRC64;

```
Query Match      15.0%; Score 88.5; DB 11; Length 287;
Best Local Similarity 31.3%; Pred. No. 0.19;
Matches 21; Conservative 14; Mismatches 21; Indels 11; Gaps 2;

QY 23 ISLASAQEDYNAPDRCFRINVKKGQOIYVYSLVKENGAGERWAGSVYGDQDGMGVGVYF 82
Db 230 LGIAIARYDFCARDWRELKGLKGDVVKIYTKM-----SANGWWRGEVNGR-----VGMF 278
QY 83 PRLVKE 89
Db 279 PSTYVEE 285

RESULT 10
ID Q8UX6 PRELIMINARY; PRT; 846 AA.
AC Q8UX6;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DE GDP/GTP exchange factor VAV3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=11805146;
RA Inabe K., Ishiai M., Scharenberg A.M., Freshney N., Downward J.,
RA Kurosaki T.;
RT "Vav3 Modulates B Cell Receptor Responses by Regulating
RT Phosphoinositide 3-Kinase Activation.";
RL J. Exp. Med. 195;189-200(2002).
CC -!- SIMILARITY: CONTAINS 2 SH3 DOMAINS.
CC -!- SIMILARITY: CONTAINS 1 PH DOMAIN.
DR EMBL; AY046915; AL06249.1;
DR InterPro; IPR001715; Calponin-like.
DR InterPro; IPR003247; CH type.
DR InterPro; IPR002219; DAG PE-bind.
DR InterPro; IPR001331; GDS_CDC24.
DR InterPro; IPR001849; PH_1.
DR InterPro; IPR000219; RhGEF.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR003096; SM22_calponin.
DR Pfam; PF00307; CH; 1.
DR Pfam; PF00130; DAG PE-bind; 1.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00621; RhGEF; 1.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 1.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR PRINTS; PR00888; SM22CALPONIN.
DR ProDom; PD001527; CH type; 1.
DR ProDom; PD000093; SH2; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00109; C1; 1.
DR SMART; SM00033; CH; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00325; RhGEF; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 2.
DR PROSITE; PS50021; CH; 1.
DR PROSITE; PS00479; DAG PE BIND_DOM_1; 1.
DR PROSITE; PS50081; DAG PE BIND_DOM_2; 1.
DR PROSITE; PS00741; DH_1; 1.
DR PROSITE; PS50010; DH_2; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
DR PROSITE; PS50001; SH2; 1.

Query Match      15.0%; Score 88.5; DB 4; Length 1196;
Best Local Similarity 33.3%; Pred. No. 1.1;
Matches 27; Conservative 12; Mismatches 31; Indels 11; Gaps 4;

QY 20 VYTISLASAQEDYNAPDRCFRINVKKGQOIYVYSLVKENGAGERWAGSVYGDQDGMGV 79
Db 1050 VDTAPTVALVDYTNRSDELTIHRGDIIRVF---FXDN--EDWWYGSIGKQGE-----1098

Query Match      15.0%; Score 88.5; DB 4; Length 1196;
Best Local Similarity 33.3%; Pred. No. 1.1;
Matches 27; Conservative 12; Mismatches 31; Indels 11; Gaps 4;

QY 80 GYFPRNLVKEORVYQEAATKEV 100
Db 1099 GYFPAHVASETLVQELPPEI 1119

RESULT 12
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```
Q8N157
ID Q8N157 PRELIMINARY; PRT; 1196 AA.
AC Q8N157;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein FLJ34943.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RA Nanomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,
RA Katuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie K.,
RA Osuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,
RA Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.,
RA "NEDO human cDNA sequencing project";
RT Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
SEQUENCE FROM N.A.
RA Close J.P., Game I.G., Clark B., Thein S.L.;
RT "An integrated physical and transcript map of human 6q23 encompassing
RT a quantitative trait loci for foetal haemoglobin expression.";
RL Thesis (2002), Department of Clinical medicine, University of Oxford,
RL Oxford, United Kingdom.
CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR EMBL; AK092262; BAC03840.1; -.
DR EMBL; AJ459824; CAD30871.1; -.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 5.
DR PRINTS; PR00452; SH3DOMAIN.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS50002; SH3; 1.
DR PROSITE; PS50082; WD_REPEATS_2; 4.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Hypothetical protein; Repeat; SH3 domain; WD repeat.
SQ SEQUENCE 1196 AA; 137114 MW; 16A237C915DABF0F CRC64;

Query Match 15.0%; Score 88.5; DB 4; Length 1196;
Best Local Similarity 33.3%; Pred.No.1.1;
Matches 27; Conservative 12; Mismatches 31; Indels 11; Gaps 4;

QY 20 VYTIASAEQEDYNAPDCRFNVKKGQIYVYSLKLVKENGAGFAGSVYGDQDMGVV 79
DB 1050 VDTAPTVALYDYTNARSDLTTHRGDIIRVF---FKDN--EDWVYGS1-GKQE-----1098

QY 80 GYFPRNLVKEQRYQATKEV 100
DB 1099 GYFPANHVASATLYQLPEI 1119

RESULT 13
Q96D37 PRELIMINARY; PRT; 719 AA.
ID Q96D37;
AC Q96D37;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP SEQUENCE Placenta;
RC TISSUE=Placenta;
```

```
Strausberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RA Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 2 SH3 DOMAINS.
CC -!- SIMILARITY: CONTAINS 1 PH DOMAIN.
DR EMBL; BC013361; AAH13361.1; -.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR001331; GDS_CDC24.
DR InterPro; IPR001849; PH_CDC24.
DR InterPro; IPR000219; RHOGEF.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00130; DAG_PE-bind; 1.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00621; RHOGEF; 1.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 2.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR ProDom; PD000093; SH2; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00109; Cl; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00325; RHOGEF; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 2.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS00741; DH; 1; 1.
DR PROSITE; PS50010; DH; 2; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 2.
KW Hypothetical protein; SH3 domain.
SQ SEQUENCE 719 AA; 83727 MW; A51B757DAS43BA6C CRC64;

Query Match 14.7%; Score 86.5; DB 4; Length 719;
Best Local Similarity 32.9%; Pred.No.0.98;
Matches 23; Conservative 13; Mismatches 21; Indels 13; Gaps 3;

QY 26 ASAQEDYNAPDCRFNVKKGQIYVYSLKLVKENGAGFAGSVYGDQDMGVVGFPRN 85
DB 661 AKARYDFCARDSELSLKEGDI---KILNKGQQQWVRGEIYGR-----VGWFPAN 709

QY 86 LYKEQRYQOE 95
DB 710 YVEED--YSE 717

RESULT 14
O08526 PRELIMINARY; PRT; 166 AA.
ID O08526;
AC O08526;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Vav-T.
GN VAV.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=ddy; TISSUE=Testis;
RX MEDLINE=97190224; PubMed=9038379;
RA Okumura K., Kaneko Y., Nonoguchi K., Nishiyama H., Yokoi H.,
RA Higuchi T., Itoh K., Yoshida O., Miki T., Fujita J.;
RT "Expression of a novel isoform of Vav, Vav-T, containing a single
RT Src homology 3 domain in murine testicular germ cells.";
RL Oncogene 14:713-720(1997).
CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR EMBL; D83266; BAA18950.1; -.
DR HSP; Q60631; 1GBQ.
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DR MGD; MGI:98923; Vav.
DR InterPro; IPR000980; SH2.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 1.
DR PRINTS; PR00452; SH3DOMAIN.
DR ProDom; PD000093; SH2; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 1.
KW SH3 domain.
SQ SEQUENCE 166 AA; 19434 MW; 2C3AF1FF07A5018F CRC64;

Query Match 14.5%; Score 85.5; DB 11; Length 166;
Best Local Similarity 31.4%; Pred. No. 0.21;
Matches 22; Conservative 14; Mismatches 21; Indels 13; Gaps 3;

QY 26 ASAQEDYNAPDCRFINVKKGQIYVYSKLVKENGAGFEWAGSVYGDGDENGWVGYFPRN 85
Db 108 AKARYDFCARDRSELSLKEGDI-----KILNKKGQGGWWRGEIYGR-----IGWFFSN 156

QY 86 LVKEQRYVQE 95
Db 157 YVEED--YSE 164

RESULT 15
Q8VDU4 Q8VDU4 PRELIMINARY; PRT; 806 AA.
AC Q8VDU4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to vav oncogene.
GN VAV.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBTaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 PH DOMAIN.
DR EMBL; BC020487; AAH20487.1; -.
DR MGD; MGI:98923; Vav.
DR InterPro; IPR005613; AIP3.
DR InterPro; IPR001715; Calponin-like.
DR InterPro; IPR003247; CH type.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR001331; GDS_CDC24.
DR InterPro; IPR001849; PH_CDC24.
DR InterPro; IPR000219; RhGEF.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR003096; SM22_calponin.
DR Pfam; PF03915; AIP3; 1.
DR Pfam; PF00307; CH; 1.
DR Pfam; PF00130; DAG_PE-bind; 1.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00621; RhGEF; 1.
DR Pfam; PF00017; SH2; 1.
DR PRINTS; PR00452; SH3DOMAIN.
DR ProDom; PD001527; CH_type; 1.
DR ProDom; PD000093; SH2; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00109; C1; 1.
DR SMART; SM00033; CH; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00325; RhGEF; 1.

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DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 2.
DR PROSITE; PS50021; CH; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS00741; DH_1; 1.
DR PROSITE; PS50010; DH_2; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 2.
SQ SEQUENCE 806 AA; 93868 MW; F4368CD13A62D695 CRC64;

Query Match 14.5%; Score 85.5; DB 11; Length 806;
Best Local Similarity 31.4%; Pred. No. 1.4;
Matches 22; Conservative 14; Mismatches 21; Indels 13; Gaps 3;

QY 26 ASAQEDYNAPDCRFINVKKGQIYVYSKLVKENGAGFEWAGSVYGDGDENGWVGYFPRN 85
Db 748 AKARYDFCARDRSELSLKEGDI-----KILNKKGQGGWWRGEIYGR-----IGWFFSN 796

QY 86 LVKEQRYVQE 95
Db 797 YVEED--YSE 804

Search completed: December 29, 2003, 16:06:25
Job time : 16.9468 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2003, 16:03:18 ; Search time 21.5686 Seconds  
(without alignments)  
809.506 Million cell updates/sec

Title: US-10-019-455A-24

Perfect score: 590

Sequence: 1 HGIFMDRLASKKLCADCEV.....RVYQATKEVPTTDDIFFCE 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	590	100.0	110	22	Human MLP protein
2	590	100.0	128	22	Human growth regul
3	590	100.0	128	22	Human MLP protein
4	590	100.0	128	23	Human angiogenesis
5	590	100.0	128	23	Human PRO873 prot
6	590	100.0	128	23	Human PRO protein,
7	590	100.0	128	23	Novel human secret
8	561	95.1	105	22	Human growth regul
9	547	92.7	110	22	Mouse MLP protein

10	547	92.7	128	22	AA669125	Mouse MLP protein
11	541	91.7	110	22	AA669131	Rat MLP protein se
12	541	91.7	128	22	AA669130	Rat MLP protein se
13	417	70.7	87	22	AA669129	Rat MLP protein se
14	253.5	43.0	131	16	AA669811	Melanoma inhibitor
15	253.5	43.0	131	22	AA665614	Human MIA protein
16	251.5	42.6	137	22	AA665615	Recombinant human
17	231.5	39.2	130	16	AA669812	Melanoma inhibitor
18	226.5	38.4	138	22	AA665834	Human protein sequ
19	225.5	38.2	125	23	AA662120	Human TANGO 130 MI
20	225.5	38.2	410	21	AA662110	Human TANGO 130 pr
21	225.5	38.2	410	21	AA662118	Human TANGO 130 pa
22	225.5	38.2	1907	23	AA662127	Human TANGO 130 po
23	217	36.8	499	22	AA662119	Human PRO polypept
24	217	36.8	499	24	AA662119	Human PRO20088 pro
25	217	36.8	499	24	AA662119	Human secreted/tra
26	217	36.8	499	24	AA662119	Human secreted/tra
27	217	36.8	499	24	AA662119	Human secreted/tra
28	217	36.8	499	24	AA662119	Human PRO polypept
29	217	36.8	499	24	AA662119	Human PRO polypept
30	217	36.8	499	24	AA662119	Human secreted/tra
31	217	36.8	499	24	AA662119	Human PRO polypept
32	217	36.8	499	24	AA662119	Human secreted/tra
33	215	36.4	125	23	AA662119	Mouse TANGO 130 MI
34	215	36.4	303	22	AA662119	Human PRO polypept
35	215	36.4	303	22	AA662119	Human PRO polypept
36	215	36.4	303	23	AA662119	Human secreted/tra
37	215	36.4	303	23	AA662119	Human secreted/tra
38	215	36.4	303	23	AA662119	Human secreted/tra
39	215	36.4	303	24	AA662119	Human PRO19670 pro
40	215	36.4	303	24	AA662119	Human secreted pol
41	215	36.4	303	24	AA662119	Novel human secret
42	215	36.4	303	24	AA662119	Human PRO polypept
43	215	36.4	303	24	AA662119	Human secreted/tra
44	215	36.4	303	24	AA662119	Novel human secret
45	215	36.4	303	24	AA662119	Human secreted/tra

#### ALIGNMENTS

#### RESULT 1

AA669126  
ID AA669126 standard; Protein; 110 AA.

XX AA669126;

AC AA669126;  
XX 23-APR-2001 (first entry)

XX Human MLP protein sequence SEQ ID NO:24.

XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
XX joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
XX cardiant; gene therapy; secretory cell function regulator; promoter;  
XX inhibitor.

XX Homo sapiens.

XX WO200102564-A1.

XX 11-JAN-2001.

XX 29-JUN-2000; 2000WO-JP04278.

XX 30-JUN-1999; 99JP-0186718.

XX (TAKE ) TAKEDA CHEM IND LTD.

XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;

XX Tanaka H;

XX WPI; 2001-159271/16.

XX N-PSDB; AAF59079.



XX Safe, low-toxicity secretory cell function-regulatory protein and  
PT encoded DNA, applicable as drugs, in diagnosis and development of  
PT promoters and inhibitors for preventing or treating e.g. bone and joint  
PT diseases -  
XX  
XX Claim 1; Page 97-98; 111pp; Japanese.  
XX  
XX The present invention describes novel MLP proteins and their encoding  
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
CC activities, and can be used in gene therapy and as secretory cell  
CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
CC the diagnosis and development of promoters and inhibitors for preventing  
CC or treating bone and joint diseases as well as pathologic angiogenesis.  
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
CC in the exemplification of the present invention.  
XX  
XX Sequence 110 AA;  
SQ  
Query Match 100.0%; Score 590; DB 22; Length 110;  
Best Local Similarity 100.0%; Pred. No. 1.6e-68;  
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQIYVYSLVKENGA 60  
Db 1 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQIYVYSLVKENGA 60  
QY 61 GEFWAGSVYGDQDEMVGVPFRNLVKEQRVYQATKEVPTTIDDFCE 110  
Db 61 GEFWAGSVYGDQDEMVGVPFRNLVKEQRVYQATKEVPTTIDDFCE 110  
RESULT 2  
AAB82671  
ID AAB82671 standard; Protein; 128 AA.  
XX  
XX AAB82671;  
DT 02-OCT-2001 (first entry)  
XX  
XX Human growth regulatory-like polypeptide.  
XX  
XX Growth regulatory-like polypeptide; human; cartilage; melanoma;  
XX neuroectodermal tumour; glioma; cancer; therapy; diagnosis.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FT Peptide 1..23  
FT /label= Signal\_peptide  
FT Protein 24..128  
FT /label= Mature\_protein  
FT /note= "separately claimed in Claim 10"  
XX  
XX WO200155332-A2.  
XX  
XX 02-AUG-2001.  
XX  
XX 25-JAN-2001; 2001WO-US02455.  
XX  
XX 25-JAN-2000; 2000US-0491404.  
XX  
XX 02-MAY-2000; 2000US-0563786.  
XX  
XX (HYSE-) HYSEQ INC.  
XX  
XX Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;  
XX Drmanac RT;  
XX  
XX WPI; 2001-483233/52.  
XX  
XX N-PSDB; AAB26343.  
XX  
XX Isolated human growth regulatory-like polypeptide useful for treating  
XX e.g. Alzheimer's disease, cancer, autoimmune disorders,

PT hyperproliferative disorders, coagulation disorders, and nervous system  
PT disorders -  
XX  
XX Claim 10; Page 116-117; 119pp; English.  
XX  
XX The present sequence is that of a novel human growth regulatory-like  
CC polypeptide (GRLP). The amino acid sequence is predicted from a  
CC novel assembled cDNA (see AAB26343) based on Hyseq clone number  
CC 16372272. The protein has a mol.wt. of 14 kDa unglycosylated. GRLP  
CC belongs to the same protein family as growth regulatory proteins.  
CC growth factors, human melanoma derived growth regulatory protein,  
CC precursor (64% similarity and 45% identity over 111 amino acids)  
CC or melanoma inhibitory activity, cattle cartilage-derived  
CC retinoic acid sensitive protein (CD-RAP, 44% identity and 64%  
CC similarity over 126 amino acids) and other retinoic acid-sensitive  
CC proteins. GRLP polypeptides and polynucleotides of the invention  
CC can be used in the prophylaxis, treatment (including gene therapy)  
CC and diagnosis of disorders and diseases caused by, or involving,  
CC cartilage development and maintenance, inhibition of melanoma cell  
CC growth and tumours, including neuroectodermal tumours such as  
CC gliomas. The polypeptides, which include the GRLP mature protein,  
CC may also have nutritional uses, cytokine and cell proliferation  
CC or differentiation activity, stem cell growth factor activity,  
CC haematopoiesis regulating activity, tissue growth activity,  
CC immunosuppressive or immunostimulant activity, activin/inhibin  
CC activity, chemotactic/chemokinetic activity, haemostatic and  
CC thrombolytic activity, use in cancer diagnosis and therapy,  
CC drug screening, receptor/ligand activity, antiinflammatory  
CC activity, and treatment of leukaemia, nervous system disorders,  
XX arthritis and inflammation.  
XX  
XX Sequence 128 AA;  
SQ  
Query Match 100.0%; Score 590; DB 22; Length 128;  
Best Local Similarity 100.0%; Pred. No. 2e-68;  
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQIYVYSLVKENGA 60  
Db 19 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQIYVYSLVKENGA 78  
QY 61 GEFWAGSVYGDQDEMVGVPFRNLVKEQRVYQATKEVPTTIDDFCE 110  
Db 79 GEFWAGSVYGDQDEMVGVPFRNLVKEQRVYQATKEVPTTIDDFCE 128  
RESULT 3  
AAB69123  
ID AAB69123 standard; Protein; 128 AA.  
XX  
XX AAB69123;  
XX  
XX 23-APR-2001 (first entry)  
XX  
XX Human MLP protein sequence SEQ ID NO.6.  
XX  
XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
XX joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
XX cardiant; gene therapy; secretory cell function regulator; promoter;  
XX inhibitor.  
XX  
XX Homo sapiens.  
XX  
XX WO200102564-A1.  
XX  
XX 11-JAN-2001.  
XX  
XX 29-JUN-2000; 2000WO-JP04278.  
XX  
XX 30-JUN-1999; 99JP-0186718.  
XX  
XX (TAKE ) TAKEDA CHEM IND LTD.  
XX

PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
 PI Tanaka H;  
 XX WPI; 2001-159271/16.  
 DR N-PSDB; AAF59065.  
 XX  
 XX Safe, low-toxicity secretory cell function-regulatory protein and  
 PT encoded DNA, applicable as drugs, in diagnosis and development of  
 PT Promoters and inhibitors for preventing or treating e.g. bone and joint  
 PT diseases -  
 XX  
 XX Claim 2; Page 91-92; 111pp; Japanese.  
 PS  
 XX The present invention describes novel MLP proteins and their encoding  
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
 CC activities, and can be used in gene therapy and as secretory cell  
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
 CC the diagnosis and development of promoters and inhibitors for preventing  
 CC or treating bone and joint diseases as well as pathologic angiogenesis.  
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
 CC in the exemplification of the present invention.  
 XX  
 XX Sequence 128 AA;

Query Match 100.0%; Score 590; DB 22; Length 128;  
 Best Local Similarity 100.0%; Pred. No. 2e-68; Indels 0; Gaps 0;  
 Matches 110; Conservative 0; Mismatches 0;  
 QY 1 HGIFMDRLASKKLCADDECVYITISLASAQEDYNAPDCRFINVKKGQIYVYVKLVKNGA 60  
 DB 19 HGIFMDRLASKKLCADDECVYITISLASAQEDYNAPDCRFINVKKGQIYVYVKLVKNGA 78  
 QY 61 GEFWAGSVYGDQDGVGVYFPRNLVKEQRYQATKEVPTDIDFCE 110  
 DB 79 GEFWAGSVYGDQDGVGVYFPRNLVKEQRYQATKEVPTDIDFCE 128

RESULT 4  
 ABB95602  
 ID ABB95602 standard; Protein; 128 AA.

XX ABB95602;  
 AC  
 DT 19-JUL-2002 (first entry)  
 XX  
 DE Human angiogenesis related protein PRO9873 SEQ ID NO: 360.  
 XX  
 XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
 XX atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
 KW cardiatic; cytostatic; antiangiogenic; hypotensive; vulnerary;  
 KW antiarteriosclerotic.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WC200208284-A2.  
 XX  
 XX 31-JAN-2002.  
 XX  
 XX 09-JUL-2001; 2001WO-US21735.  
 XX  
 XX 20-JUL-2000; 2000US-219556P.  
 XX 25-JUL-2000; 2000US-220624P.  
 XX 25-JUL-2000; 2000US-220654P.  
 XX 28-JUL-2000; 2000WO-US20710.  
 XX 02-AUG-2000; 2000US-222695P.  
 XX 17-AUG-2000; 2000US-0643657.  
 XX 23-AUG-2000; 2000WO-US23322.  
 XX 24-AUG-2000; 2000US-23328P.  
 XX 07-SEP-2000; 2000US-230978P.  
 XX 15-SEP-2000; 2000US-000000P.  
 XX 18-SEP-2000; 2000US-0664610.  
 XX 18-SEP-2000; 2000US-0665350.  
 XX 24-OCT-2000; 2000US-242922P.

PR 08-NOV-2000; 2000US-0709238.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 10-NOV-2000; 2000WO-US30873.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000US-0747259.  
 PR 20-DEC-2000; 2000WO-US34956.  
 PR 22-JAN-2001; 2001US-0767609.  
 PR 28-FEB-2001; 2001US-0796498.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 01-MAR-2001; 2001WO-US06666.  
 PR 09-MAR-2001; 2001US-0802706.  
 PR 14-MAR-2001; 2001US-0808689.  
 PR 22-MAR-2001; 2001US-0816744.  
 PR 05-APR-2001; 2001US-0828366.  
 PR 10-MAY-2001; 2001US-0854208.  
 PR 10-MAY-2001; 2001US-0854280.  
 PR 25-MAY-2001; 2001US-0866028.  
 PR 25-MAY-2001; 2001US-0866034.  
 PR 25-MAY-2001; 2001WO-US17092.  
 PR 30-MAY-2001; 2001US-0870574.  
 PR 01-JUN-2001; 2001WO-US17443.  
 PR 20-JUN-2001; 2001WO-US17800.  
 PR 28-JUN-2001; 2001WO-US19692.  
 XX  
 XX (GETH ) GENENTECH INC.  
 PA (BAKE/) BAKER K P.  
 PA (FERR/) FERRARA N.  
 PA (GERB/) GERBER H.  
 PA (GERR/) GERRITSEN M E.  
 PA (GODD/) GODDARD A.  
 PA (GODO/) GODOWSKI P J.  
 PA (GURN/) GURNEY A L.  
 PA (HILL/) HILLAN K J.  
 PA (MARS/) MARSTERS S A.  
 PA (PANG/) PAN J.  
 PA (PAON/) PAONI N F.  
 PA (STEP/) STEPHAN J F.  
 PA (WATA/) WATANABE C K.  
 PA (WILL/) WILLIAMS P M.  
 PA (WOOD/) WOOD W I.  
 XX  
 XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;  
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
 XX  
 XX WPI: 2002-171999/22.  
 DR N-PSDB; ABL95740.  
 XX  
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 PT infarction), endothelial or angiogenic disorders in a mammal -  
 XX  
 XX Claim 11; Fig 360; 567pp; English.  
 PS  
 XX The present invention provides the protein and coding sequences of human  
 CC PRO proteins. These are useful for treating or diagnosing a  
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac  
 CC hypertrophy, trauma, cancer, age-related macular degeneration,  
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
 CC healing. The present sequence is a PRO protein of the invention.  
 XX  
 XX Sequence 128 AA;

Query Match 100.0%; Score 590; DB 23; Length 128;  
 Best Local Similarity 100.0%; Pred. No. 2e-68; Indels 0; Gaps 0;  
 Matches 110; Conservative 0; Mismatches 0;  
 QY 1 HGIFMDRLASKKLCADDECVYITISLASAQEDYNAPDCRFINVKKGQIYVYVKLVKNGA 60  
 DB 19 HGIFMDRLASKKLCADDECVYITISLASAQEDYNAPDCRFINVKKGQIYVYVKLVKNGA 78

QY 61 GEFWAGSVYGGQDEMGVGYFPPRLVKEQRYQVQATKEVPTTIDPFCE 110  
 DB |||||||||||||||||||||||||||||||||||||||||||||||||  
 79 GEFWAGSVYGGQDEMGVGYFPPRLVKEQRYQVQATKEVPTTIDPFCE 128

## RESULT 5

ABB84996  
 ID ABB84996 standard; Protein; 128 AA.

XX ABB84996;  
 AC

XX 16-MAY-2002 (first entry)

DE Human PR09873 protein sequence SEQ ID NO:360.

XX Human; angiogenesis; cardiant; cyostatic; antiangiogenic; hypotensive;  
 KW vulnary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
 KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
 KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
 KW age-related macular degeneration; arterial restenosis; angina;  
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
 KW wound healing; chromosome mapping; Gene mapping.

XX Homo sapiens.

OS WO200200690-A2.

PN 03-JAN-2002.

XX 20-JUN-2001; 2001WO-US19692.

XX 23-JUN-2000; 2000US-213637P.

PR 20-JUL-2000; 2000US-219556P.

PR 25-JUL-2000; 2000US-220624P.

PR 25-JUL-2000; 2000US-220654P.

PR 28-JUL-2000; 2000WO-US20710.

PR 02-AUG-2000; 2000US-222895P.

PR 17-AUG-2000; 2000US-0643657.

PR 23-AUG-2000; 2000WO-US23522.

PR 24-AUG-2000; 2000WO-US23328.

PR 07-SEP-2000; 2000US-230978P.

PR 18-SEP-2000; 2000US-0664610.

PR 18-SEP-2000; 2000US-0666350.

PR 24-OCT-2000; 2000US-242322P.

PR 08-NOV-2000; 2000US-0709238.

PR 10-NOV-2000; 2000WO-US30952.

PR 01-DEC-2000; 2000WO-US30873.

PR 20-DEC-2000; 2000US-0747259.

PR 22-JAN-2001; 2001US-0767609.

PR 28-FEB-2001; 2001US-0796498.

PR 01-MAR-2001; 2001WO-US06520.

PR 09-MAR-2001; 2001US-0802706.

PR 14-MAR-2001; 2001US-0808689.

PR 22-MAR-2001; 2001US-0816744.

PR 05-APR-2001; 2001US-0828366.

PR 10-MAY-2001; 2001US-0854208.

PR 10-MAY-2001; 2001US-0854280.

PR 25-MAY-2001; 2001US-0866028.

PR 25-MAY-2001; 2001US-0866034.

PR 25-MAY-2001; 2001WO-US17092.

PR 30-MAY-2001; 2001US-0870574.

PR 30-MAY-2001; 2001WO-US17443.

PR 01-JUN-2001; 2001WO-US17800.

XX (GETH ) GENENTECH INC.

XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;

PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;

PI Stephan JP, Watanabe CK, Williams PM, Wood WI, Ye W;

XX WPI; 2002-090516/12.

DR N-PSDB; ABL88251.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 PT infarction), endothelial or angiogenic disorders in a mammal -

XX Claim 11; Fig 360; 565pp; English.

XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to  
 CC ABB85003. The PRO proteins and polynucleotides have cardiant, cyostatic,  
 CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic  
 CC activities, and can be used in gene therapy. The PRO polynucleotides,  
 CC proteins, agonists and antagonists are useful for treating or diagnosing  
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal,  
 CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular  
 CC degeneration, atherosclerosis, hypertension, arterial restenosis,  
 CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,  
 CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver  
 CC carcinoma) and wound healing. The PRO polynucleotides have applications  
 CC in molecular biology, including use as hybridisation probes, and in  
 CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and  
 CC probes used in the exemplification of the present invention.

XX SQ Sequence 128 AA;

Query Match 100.0%; Score 590; DB 23; Length 128;

Best Local Similarity 100.0%; Pred. No. 2e-69; 0; Indels 0; Gaps 0;

Matches 110; Conservative 0; Mismatches 0;

QY 1 HGIFMDRLASKKLCADDECYTTISLASAQEDYNAPDCRFINVKGGQIYVYSLVKENGA 60  
 |||||||||||||||||||||||||||||||||||||||||||||||||

Db 19 HGIFMDRLASKKLCADDECYTTISLASAQEDYNAPDCRFINVKGGQIYVYSLVKENGA 78  
 |||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 GEFWAGSVYGGQDEMGVGYFPPRLVKEQRYQVQATKEVPTTIDPFCE 110  
 |||||||||||||||||||||||||||||||||||||||||||||||||

Db 79 GEFWAGSVYGGQDEMGVGYFPPRLVKEQRYQVQATKEVPTTIDPFCE 128  
 |||||||||||||||||||||||||||||||||||||||||||||||||

## RESULT 6

AJ -83627

ID AAU83627 standard; Protein; 128 AA.

XX AAU83627;

AC AAU83627;

XX 08-MAY-2002 (first entry)

DE Human PRO protein, Seq ID No 72.

XX Human; secreted protein; PRO; tumour; lung cancer; colon cancer;  
 KW breast cancer; prostate tumour; rectal tumour; liver tumour;  
 KW pericyte cell proliferation; chondrocyte cell proliferation;  
 KW tumour necrosis factor-alpha.

XX Homo sapiens.

XX WO200208288-A2.

XX 31-JAN-2002.

XX 29-JUN-2001; 2001WO-US21066.

XX 20-JUL-2000; 2000US-219556P.

XX 25-JUL-2000; 2000US-220585P.

XX 25-JUL-2000; 2000US-220605P.

XX 25-JUL-2000; 2000US-220607P.

XX 25-JUL-2000; 2000US-220624P.

XX 25-JUL-2000; 2000US-220638P.

XX 25-JUL-2000; 2000US-220664P.

XX 25-JUL-2000; 2000US-220666P.

XX 26-JUL-2000; 2000US-220893P.

PR 28-JUL-2000; 2000WO-US20710.  
 PR 23-AUG-2000; 2000WO-US23522.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 15-SEP-2000; 2000US-000000P.  
 PR 10-NOV-2000; 2000WO-US30873.  
 PR 28-NOV-2000; 2000US-253646P.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000US-0747259.  
 PR 28-DEC-2000; 2000WO-US34956.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 10-MAY-2001; 2001US-0854280.  
 PR 25-MAY-2001; 2001WO-US17092.

(GETH ) GENENTECH INC.

XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;  
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WT;  
 XX WPI; 2002-172001/22.  
 DR N-PSDB; ABK33571.

XX One hundred and twenty two nucleic acids encoding PRO polypeptides,  
 PT useful for treating a PRO related disorder and for diagnosing tumours  
 PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal  
 PT tumour or liver tumour -

PS Claim 11; Figure 72; 359pp; English.

XX The invention relates to one hundred and twenty two nucleic acids  
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides  
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,  
 CC agonists and antagonists are useful for treating a PRO related disorder.  
 CC The PRO polypeptides are useful for diagnosing tumours, especially lung  
 CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or  
 CC liver tumour. The PRO polypeptides are useful for stimulating the  
 CC proliferation of, or gene expression, in pericyte cells, for stimulating  
 CC the proliferation or differentiation of chondrocyte cells, for  
 CC stimulating the release of tumour necrosis factor-alpha from human blood,  
 CC for stimulating or inhibiting the proliferation of normal human dermal  
 CC fibroblast cells. The PRO polypeptide may also be used as molecular  
 CC weight markers and for tissue typing. The PRO nucleic acids have  
 CC applications in molecular biology, including use as hybridisation probes,  
 CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO  
 CC protein sequences of the invention.

XX Sequence 128 AA;

Query Match 100.0%; Score 590; DB 23; Length 128;  
 Best Local Similarity 100.0%; Pred. No. 2e-68;  
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGIFMDRLASKKLCADDECVTITSLASQEDYNAPDCRFINVKGGQIYVYSLVKENGA 60  
 DB 19 HGIFMDRLASKKLCADDECVTITSLASQEDYNAPDCRFINVKGGQIYVYSLVKENGA 78  
 QY 61 GEFWAGSVYGDQDEMGVGVYFPRNLVKEQRYQVQATKEVPTTIDIFFCE 110  
 DB 79 GEFWAGSVYGDQDEMGVGVYFPRNLVKEQRYQVQATKEVPTTIDIFFCE 128

RESULT 7

AAU09871  
 ID AAU09871 standard; Protein; 128 AA.

XX AAU09871;

XX 26-FEB-2002 (first entry)

XX Novel human secreted protein #12.

XX Secreted protein; cytostatic; immunosuppressive; vulnery; vaccine;  
 KW antiinflammatory; neuroprotective; nephrotropic; cardiovascular;  
 KW human; cancer; autoimmune disease; wound healing disorder; infection;

KW haematopoietic disorder; inflammatory disorder; infertility;  
 KW neurological disease; psychiatric disease; cardiovascular disease;  
 KW respiratory disease; renal; gastrointestinal.

OS Homo sapiens.

XX WO200179454-A1.

XX 25-OCT-2001.

XX 11-APR-2001; 2001WO-US11797.

XX 13-APR-2000; 2000US-196603P.

XX 24-APR-2000; 2000US-199417P.

XX (SMIK ) SMITHKLINE BEECHAM CORP.

XX (SMIK ) SMITHKLINE BEECHAM PLC.

XX Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;

XX WPI; 2002-061975/08.

XX N-PSDB; AAS17583.

XX New secreted proteins or polypeptides, useful for treating e.g. cancer,  
 PT autoimmune diseases, wound healing disorder, infections, haematopoietic  
 PT disorders, inflammatory disorders, infertility, cancer -

XX Claim 1; Page 73-74; 92pp; English.

XX The invention relates to an isolated novel secreted polypeptide (I) and  
 CC polynucleotide (II). (I) and (II) are useful for treating cancer.  
 CC autoimmune diseases, wound healing disorder, infections, haematopoietic  
 CC disorders, inflammatory disorders, infertility, respiratory and  
 CC psychiatric diseases, cardiovascular diseases, respiratory diseases,  
 CC renal diseases, or gastrointestinal diseases. These may also be used to  
 CC treat diseases, abnormalities and disorders caused by abnormal  
 CC expression, production, function and/or metabolism of the genes, as  
 CC vaccines for inducing immunological response in a mammal, and in  
 CC screening methods for detecting the effect of added compounds on the  
 CC production of mRNA and polypeptide in cells. The polypeptides can be used  
 CC as immunogens to produce antibodies immunospecific for the polypeptides,  
 CC and to identify membrane-bound or soluble receptors. The polynucleotides  
 CC may be used as diagnostic reagents, in chromosome localisation studies,  
 CC and in tissue expression studies. The present sequence represents the  
 CC amino acid sequence of novel human secreted protein #12.

XX Sequence 128 AA;

Query Match 100.0%; Score 590; DB 23; Length 128;  
 Best Local Similarity 100.0%; Pred. No. 2e-68;  
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGIFMDRLASKKLCADDECVTITSLASQEDYNAPDCRFINVKGGQIYVYSLVKENGA 60  
 DB 19 HGIFMDRLASKKLCADDECVTITSLASQEDYNAPDCRFINVKGGQIYVYSLVKENGA 78  
 QY 61 GEFWAGSVYGDQDEMGVGVYFPRNLVKEQRYQVQATKEVPTTIDIFFCE 110  
 DB 79 GEFWAGSVYGDQDEMGVGVYFPRNLVKEQRYQVQATKEVPTTIDIFFCE 128

RESULT 8

AA82672

ID AA82672 standard; Protein; 105 AA.

XX AA82672;

XX 02-OCT-2001 (first entry)

XX Human growth regulatory-like polypeptide (mature protein).

XX Growth regulatory-like polypeptide; human; cartilage; melanoma;  
 KW neuroectodermal tumour; glioma; cancer; therapy; diagnosis.

```

XX OS Homo sapiens.
XX PN WO200155332-A2.
XX PD 02-AUG-2001.
XX PF 25-JAN-2001; 2001WO-US02455.
XX PR 25-JAN-2000; 2000US-0491404.
XX PS 02-MAY-2000; 2000US-0563786.
XX PA (HYSE-) HYSEQ INC.
XX PI Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;
XX PI Dmanac RT;
XX PR WPI; 2001-483233/52.
XX PS N-PSDB; AAH26343.
XX PT Isolated human growth regulatory-like polypeptide useful for treating
XX PT e.g. Alzheimer's disease, cancer, autoimmune disorders,
XX PT hyperproliferative disorders, coagulation disorders, and nervous system
XX PT disorders -
XX PS Claim 10; Page 117; 119pp; English.
XX CC The present sequence is that of a novel human growth regulatory-like
XX CC polypeptide (GRLP) mature protein. The sequence is predicted from
XX CC a novel assembled cDNA (see AAH26343) based on Hyseq clone number
XX CC 1637272. The protein has a mol.wt. of 14 kDa unglycosylated. GRLP
XX CC belongs to the same protein family as growth regulatory proteins,
XX CC growth factors, human melanoma derived growth regulatory protein
XX CC precursor (64% similarity and 45% identity over 111 amino acids)
XX CC or melanoma inhibitory activity, (CD-RAP, 44% identity and 64%
XX CC retinoic acid sensitive protein (CD-RAP, 44% identity and 64%
XX CC similarity over 126 amino acids) and other retinoic acid-sensitive
XX CC proteins. GRLP polypeptides and polynucleotides of the invention
XX CC can be used in the prophylaxis and treatment (including gene therapy)
XX CC and diagnosis of disorders and diseases caused by, or involving,
XX CC cartilage development and maintenance, inhibition of melanoma cell
XX CC growth and tumours, including neuroectodermal tumours such as
XX CC gliomas. The polypeptides, which include the GRLP mature protein,
XX CC may also have nutritional uses, cytokine and cell proliferation,
XX CC or differentiation activity, stem cell growth factor activity,
XX CC hematopoiesis regulating activity, tissue growth activity,
XX CC immunosuppressive or immunostimulant activity, activin/inhibin
XX CC activity, chemotactic/chemokinetic activity, haemostatic and
XX CC thrombolytic activity, use in cancer diagnosis and therapy,
XX CC drug screening, receptor/ligand activity, antiinflammatory
XX CC activity, and treatment of leukaemia, nervous system disorders,
XX CC arthritis and inflammation.
XX PS Sequence 105 AA;
XX SQ
Query Match 95.1%; Score 561; DB 22; Length 105;
Best Local Similarity 100.0%; Pred. No. 8.9e-65;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQIYVYVKLVKENGAFWA 65
Db 1 DRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQIYVYVKLVKENGAFWA 60

QY 66 GSVYGDQDGMGVGYFPNRLVKRQRYVQATKEVPTTIDDFCE 110
Db 61 GSVYGDQDGMGVGYFPNRLVKRQRYVQATKEVPTTIDDFCE 105

RESULT 9
AAB69127
ID AAB69127 standard; Protein; 110 AA.
XX AC AAB69127;

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XX 23-APR-2001 (first entry)
XX DE Mouse MLP protein sequence SEQ ID NO:26.
XX KW MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
XX KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
XX KW cardiant; gene therapy; secretory cell function regulator; promoter;
XX KW inhibitor.
XX OS Mus musculus.
XX PN WO200102564-A1.
XX PD 11-JAN-2001.
XX PF 29-JUN-2000; 2000WO-JP04278.
XX PR 30-JUN-1999; 99JP-0186718.
XX PA (TAKE ) TAKEDA CHEM IND LTD.
XX PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
XX PI Tanaka H;
XX PS WPI; 2001-159271/16.
XX PS N-PSDB; AAF59080.
XX CC Safe, low-toxicity secretory cell function-regulatory protein and
XX CC encoded DNA, applicable as drugs, in diagnosis and development of
XX CC promoters and inhibitors for preventing or treating e.g. bone and joint
XX CC diseases -
XX PS Claim 3; Page 98-99; 111pp; Japanese.
XX CC The present invention describes novel MLP proteins and their encoding
XX CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
XX CC activities, and can be used in gene therapy and as secretory cell
XX CC function regulators. The MLP proteins and DNAs can be used in drugs, in
XX CC the diagnosis and development of promoters and inhibitors for preventing
XX CC or treating bone and joint diseases as well as pathologic angiogenesis.
XX CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
XX CC in the exemplification of the present invention.
XX SQ Sequence 110 AA;
XX SQ
Query Match 92.7%; Score 547; DB 22; Length 110;
Best Local Similarity 90.0%; Pred. No. 6.3e-63;
Matches 99; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 HGIEMDLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQIYVYVKLVKENG 60
Db 1 HGVFMDKLSKKLCADDECVYTISLASAQEDYNAPDCRFIDVKKGQIYVYVKLVTEGA 60

QY 61 GEFWAGSVYGDQDGMGVGYFPNRLVKRQRYVQATKEVPTTIDDFCE 110
Db 61 GEFWAGSVYGDQDGMGVGYFPNRLVKRQRYVQATKEVPTTIDDFCE 110

RESULT 10
AAB69125
ID AAB69125 standard; Protein; 128 AA.
XX AC AAB69125;
XX 23-APR-2001 (first entry)
XX DE Mouse MLP protein sequence SEQ ID NO:12.
XX KW MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
XX KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
XX KW cardiant; gene therapy; secretory cell function regulator; promoter;
XX KW inhibitor.

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XX OS Mus musculus.
XX PN WO200102564-A1.
XX PD 11-JAN-2001.
XX PF 29-JUN-2000; 2000WO-JP04278.
XX PR 30-JUN-1999; 99JP-0186718.
XX PA (TAKE ) TAKEDA CHEM IND LTD.
XX PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
XX PI Tanaka H;
XX DR WPI; 2001-159271/16.
XX DR N-PSDB; AAF59068.
XX PF Safe, low-toxicity secretory cell function-regulatory protein and
XX PT encoded DNA, applicable as drugs, in diagnosis and development of
XX PT promoters and inhibitors for preventing or treating e.g. bone and joint
XX PT diseases -
XX PS Claim 4; Page 93-94; 111pp; Japanese.
XX CC The present invention describes novel MLP proteins and their encoding
XX CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
XX CC activities, and can be used in gene therapy and as secretory cell
XX CC function regulators. The MLP proteins and DNAs can be used in drugs, in
XX CC the diagnosis and development of promoters and inhibitors for preventing
XX CC or treating bone and joint diseases as well as pathologic angiogenesis.
XX CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
XX CC in the exemplification of the present invention.
XX SQ Sequence 128 AA;
XX QY Query Match 92.7%; Score 547; DB 22; Length 128;
XX DB Best Local Similarity 90.0%; Pred. No. 7.8e-63;
XX M Matches 99; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
XX QY 1 HGFMRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYKLVKNGA 60
XX DB 19 HGVFMDKLSKKLCADDECVYTISLASAQEDYNAPDCRFIDVKGQQIYVYKLVKNGA 78
XX QY 61 GEFWAGSVYGDGDEMGVGVPEPNLVKEQRYQVQATKEVPTTDDIDFCE 110
XX DB 79 GEFWAGSVYGDGDEMGVGVPEPNLVKEQRYQVQATKEIPTTDDIDFCE 128
XX RESULT 11
XX AAB69131
XX ID AAB69131 standard; Protein; 110 AA.
XX AC AAB69131;
XX DT 23-APR-2001 (first entry)
XX DE Rat MLP protein sequence SEQ ID NO:49.
XX KW MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
XX KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
XX KW cardiant; gene therapy; secretory cell function regulator; promoter;
XX KW inhibitor.
XX OS Rattus sp.
XX PN WO200102564-A1.
XX PD 11-JAN-2001.
XX PF 29-JUN-2000; 2000WO-JP04278.
XX PR
XX PA (TAKE ) TAKEDA CHEM IND LTD.
XX PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
XX PI Tanaka H;
XX DR WPI; 2001-159271/16.
XX DR N-PSDB; AAF59098.
XX PF Safe, low-toxicity secretory cell function-regulatory protein and
XX PT encoded DNA, applicable as drugs, in diagnosis and development of
XX PT promoters and inhibitors for preventing or treating e.g. bone and joint
XX PT diseases -
XX PS Claim 5; Page 107; 111pp; Japanese.
XX CC The present invention describes novel MLP proteins and their encoding
XX CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
XX CC activities, and can be used in gene therapy and as secretory cell
XX CC function regulators. The MLP proteins and DNAs can be used in drugs, in
XX CC the diagnosis and development of promoters and inhibitors for preventing
XX CC or treating bone and joint diseases as well as pathologic angiogenesis.
XX CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
XX CC in the exemplification of the present invention.
XX SQ Sequence 110 AA;
XX QY Query Match 91.7%; Score 541; DB 22; Length 110;
XX DB Best Local Similarity 89.1%; Pred. No. 3.8e-62;
XX M Matches 98; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
XX QY 1 HGFMRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYKLVKNGA 60
XX DB 1 HGVFMDKLSKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYKLVKNGA 60
XX QY 61 GEFWAGSVYGDGDEMGVGVPEPNLVKEQRYQVQATKEVPTTDDIDFCE 110
XX DB 61 GEFWAGSVYGDGDEMGVGVPEPNLVKEQRYQVQATKEIPTTDDIDFCE 110
XX RESULT 12
XX AAB69130
XX ID AAB69130 standard; Protein; 128 AA.
XX AC AAB69130;
XX DT 23-APR-2001 (first entry)
XX DE Rat MLP protein sequence SEQ ID NO:47.
XX KW MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
XX KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
XX KW cardiant; gene therapy; secretory cell function regulator; promoter;
XX KW inhibitor.
XX OS Rattus sp.
XX PN WO200102564-A1.
XX PD 11-JAN-2001.
XX PF 29-JUN-2000; 2000WO-JP04278.
XX PR 30-JUN-1999; 99JP-0186718.
XX PA (TAKE ) TAKEDA CHEM IND LTD.
XX PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
XX PI Tanaka H;
XX DR WPI; 2001-159271/16.
XX DR N-PSDB; AAF59098.
XX PF Safe, low-toxicity secretory cell function-regulatory protein and
XX PT encoded DNA, applicable as drugs, in diagnosis and development of
XX PT promoters and inhibitors for preventing or treating e.g. bone and joint
XX PT diseases -
XX PS Claim 5; Page 107; 111pp; Japanese.
XX CC The present invention describes novel MLP proteins and their encoding
XX CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
XX CC activities, and can be used in gene therapy and as secretory cell
XX CC function regulators. The MLP proteins and DNAs can be used in drugs, in
XX CC the diagnosis and development of promoters and inhibitors for preventing
XX CC or treating bone and joint diseases as well as pathologic angiogenesis.
XX CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
XX CC in the exemplification of the present invention.
XX SQ Sequence 110 AA;
XX QY Query Match 91.7%; Score 541; DB 22; Length 110;
XX DB Best Local Similarity 89.1%; Pred. No. 3.8e-62;
XX M Matches 98; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
XX QY 1 HGFMRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYKLVKNGA 60
XX DB 1 HGVFMDKLSKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYKLVKNGA 60
XX QY 61 GEFWAGSVYGDGDEMGVGVPEPNLVKEQRYQVQATKEVPTTDDIDFCE 110
XX DB 61 GEFWAGSVYGDGDEMGVGVPEPNLVKEQRYQVQATKEIPTTDDIDFCE 110
XX RESULT 13
XX AAB69130
XX ID AAB69130 standard; Protein; 128 AA.
XX AC AAB69130;
XX DT 23-APR-2001 (first entry)
XX DE Rat MLP protein sequence SEQ ID NO:47.
XX KW MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
XX KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
XX KW cardiant; gene therapy; secretory cell function regulator; promoter;
XX KW inhibitor.
XX OS Rattus sp.
XX PN WO200102564-A1.
XX PD 11-JAN-2001.
XX PF 29-JUN-2000; 2000WO-JP04278.
XX PR 30-JUN-1999; 99JP-0186718.
XX PA (TAKE ) TAKEDA CHEM IND LTD.
XX PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
XX PI Tanaka H;
XX DR WPI; 2001-159271/16.
XX DR N-PSDB; AAF59098.
XX PF Safe, low-toxicity secretory cell function-regulatory protein and
XX PT encoded DNA, applicable as drugs, in diagnosis and development of
XX PT promoters and inhibitors for preventing or treating e.g. bone and joint
XX PT diseases -
XX PS Claim 5; Page 107; 111pp; Japanese.
XX CC The present invention describes novel MLP proteins and their encoding
XX CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
XX CC activities, and can be used in gene therapy and as secretory cell
XX CC function regulators. The MLP proteins and DNAs can be used in drugs, in
XX CC the diagnosis and development of promoters and inhibitors for preventing
XX CC or treating bone and joint diseases as well as pathologic angiogenesis.
XX CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
XX CC in the exemplification of the present invention.
XX SQ Sequence 110 AA;
XX QY Query Match 91.7%; Score 541; DB 22; Length 110;
XX DB Best Local Similarity 89.1%; Pred. No. 3.8e-62;
XX M Matches 98; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
XX QY 1 HGFMRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYKLVKNGA 60
XX DB 1 HGVFMDKLSKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYKLVKNGA 60
XX QY 61 GEFWAGSVYGDGDEMGVGVPEPNLVKEQRYQVQATKEVPTTDDIDFCE 110
XX DB 61 GEFWAGSVYGDGDEMGVGVPEPNLVKEQRYQVQATKEIPTTDDIDFCE 110

```

XX Safe, low-toxicity secretory cell function-regulatory protein and  
PT encoded DNA, applicable as drugs, in diagnosis and development of  
PT promoters and inhibitors for preventing or treating e.g. bone and joint  
PT diseases -  
XX  
PS Claim 6; Page 106; 111pp; Japanese.  
XX  
PS The present invention describes novel MLP proteins and their encoding  
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
CC activities, and can be used in gene therapy and as secretory cell  
CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
CC the diagnosis and development of promoters and inhibitors for preventing  
CC or treating bone and joint diseases as well as pathologic angiogenesis.  
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
CC in the exemplification of the present invention.  
XX  
XX Sequence 128 AA;  
Query Match 91.7%; Score 541; DB 22; Length 128;  
Best Local Similarity 89.1%; Pred. No. 4.7e-62;  
Matches 98; Conservative 7; Mismatches 5; Indels 0; Gaps 0;  
QY 1 HGIWDRLASXKLCADDECVYTTISASAQEDYNAPDCRFINVKKGQIYVYSKLVKNGA 60  
DB 19 HGMFMDKLSSKLCADDECVYTTISARAQEDYNAPDCRFINVKKGQIYVYSKLVTEGA 78  
QY 61 GEFWAGSVYGDQDEMGVGVFPFNLVKEQRYQVQATKEVPTDIDDFCE 110  
DB 79 GAFWAGSVYGDQDEMGVGVFPFNLVREQRYQVQATKEIPTDIDDFCE 128  
RESULT 13  
AAB69129  
ID AAB69129 standard; Protein; 87 AA.  
XX  
AC AAB69129;  
XX  
DT 23-APR-2001 (first entry)  
XX  
DE Rat MLP protein sequence SEQ ID NO:39.  
XX  
XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
KW cardiant; gene therapy; secretory cell function regulator; promoter;  
KW inhibitor.  
XX  
OS Rattus sp.  
XX  
XX WO200102564-A1.  
XX  
XX 11-JAN-2001.  
XX  
XX 29-JUN-2000; 2000WO-JP04278.  
XX  
XX 30-JUN-1999; 99JP-0186718.  
XX  
XX (TAKE ) TAKEDA CHEM IND LTD.  
XX  
XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
PI Tanaka H;  
XX  
XX WPI; 2001-159271/16.  
XX  
XX Safe, low-toxicity secretory cell function-regulatory protein and  
PT encoded DNA, applicable as drugs, in diagnosis and development of  
PT promoters and inhibitors for preventing or treating e.g. bone and joint  
PT diseases -  
XX  
XX Example 9; Page 103; 111pp; Japanese.  
XX  
XX The present invention describes novel MLP proteins and their encoding  
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
CC activities, and can be used in gene therapy and as secretory cell  
CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
CC the diagnosis and development of promoters and inhibitors for preventing  
CC or treating bone and joint diseases as well as pathologic angiogenesis.  
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
CC in the exemplification of the present invention.  
XX  
XX Sequence 87 AA;  
Query Match 70.7%; Score 417; DB 22; Length 87;  
Best Local Similarity 88.5%; Pred. No. 3.8e-46;  
Matches 77; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
QY 6 DRIASXKLCADDECVYTTISASAQEDYNAPDCRFINVKKGQIYVYSKLVKNGAGFWA 65  
DB 1 DKLSSKLCADDECVYTTISARAQEDYNAPDCRFINVKKGQIYVYSKLVTEGAGFWA 60  
QY 66 GSVYGDQDEMGVGVFPFNLVKEQRYV 92  
DB 61 GSVYGDQDEMGVGVFPFNLVREQRYV 87  
RESULT 14  
AAR69811  
ID AAR69811 standard; Protein; 131 AA.  
XX  
AC AAR69811;  
XX  
DT 25-MAR-2003 (updated)  
XX  
DT 26-OCT-1995 (first entry)  
XX  
XX Melanoma inhibiting protein (human).  
XX  
XX Melanoma; inhibition; cancer; melanoma; glioblastoma; neuroblastoma;  
KW small cell lung cancer; neuroectodermal tumours; immunosuppressant;  
KW phytohaemagglutinin; lymphocyte; interleukin 2; IL-2; detection;  
KW probe; fusion protein.  
XX  
XX Homo sapiens.  
XX  
XX WO9503328-A2.  
XX  
XX 02-FEB-1995.  
XX  
XX 19-JUL-1994; 94WO-EP02369.  
XX  
XX 20-JUL-1993; 93DE-4324247.  
XX  
XX (BOEF ) BOEHRINGER MANNHEIM GMBH.  
XX  
XX Bogdahn U, Buettner R, Kaluza B;  
XX  
XX WPI; 1995-075191/10.  
XX  
XX N-PSDB; AAQ84050, AAQ84051.  
XX  
XX New melanoma inhibiting protein and related nucleic acid -  
PT vectors, transformed cells, antibodies etc., useful for treating  
PT tumours and as immunosuppressant e.g. by gene therapy  
XX  
XX Claim 1; Page 54; 85pp; German.  
XX  
XX This protein has melanoma-inhibiting activity and can be used to  
CC treat cancer (melanoma, glioblastoma, neuroblastoma, small cell  
CC lung cancer, neuroectodermal tumours) or as an immunosuppressant  
CC (it inhibits IL-2 or phytohaemagglutinin induced proliferation of  
CC peripheral blood lymphocytes). Antibodies raised against the  
CC protein can be used to detect cell producing the protein and also  
CC for protein purification. Probes derived from DNA encoding the  
CC protein (AAQ84050, AAQ84051) can be used to detect sequences encoding  
CC the protein or related proteins. The protein may be expressed as  
CC a fusion protein (conjugated with dihydrofolate reductase (DHFR)).  
XX (Updated on 25-MAR-2003 to correct PN field.)  
XX



SQ Sequence 131 AA;  
Query Match 43.0%; Score 253.5; DB 16; Length 131;  
Best Local Similarity 45.4%; Pred. No. 1.3e-24;  
Matches 49; Conservative 21; Mismatches 33; Indels 5; Gaps 3;  
QY 5 MDRASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQOIYVYVKLVKENGAGE-F 63  
DB 27 MPKLAADRLKCADQECSPISNAVALQDYMAPDCRFILTHRGQVYVFSKL---KGRGLRF 83  
QY 64 WAGSVYGDQDEMGV-VGYFPRNLVKEQRYOEATKEVPTTIDDFCE 110  
DB 84 WGGSVQGDYGDLAARLGYPSSIVREDQTLKPGKVDVKTDKWDFYQ 131

RESULT 15  
AAG65614  
ID AAG65614 standard; Protein; 131 AA.  
XX  
AC AAG65614;  
XX  
XX 07-JAN-2002 (first entry)  
XX  
DE Human MIA protein sequence.  
XX  
KW MIA; melanoma inhibiting activity protein; antiinflammatory; human;  
KW antiarthritic; antirheumatic; antithyroid; osteopathic; nephrotropic;  
KW immunosuppressive; ophthalmological; dermatological; antidiabetic;  
KW neuroprotective; immune tolerance; T-cell tolerance.  
XX  
OS Homo sapiens.  
XX  
XX WO200170253-A1.  
XX  
XX 27-SEP-2001.  
XX  
XX 15-MAR-2001; 2001WO-EP02991.  
XX  
XX 23-MAR-2000; 2000EP-0201063.  
XX  
XX (ALKU ) AKZO NOBEL NV.  
XX  
XX Nelissen RLH, Verheijden GFM;  
XX  
XX WPI; 2001-611446/70.  
XX  
XX DR N-PSDB; AAH47783.  
XX

Use of melanoma inhibiting activity protein or its derivatives as  
immune modulatory agents for the treatment of inflammatory diseases,  
specifically rheumatoid arthritis -  
Example 4; Page 34; 4lpp; English.  
XX  
XX The invention relates to the use of melanoma inhibiting activity (MIA)  
XX protein and/or its fragments that have anti-inflammatory effects and  
XX induce systemic immune tolerance or specific T-cell tolerance to MIA  
XX antigen, for manufacturing a preparation against inflammatory diseases  
XX and for induction of systemic immune tolerance or specific T-cell  
XX tolerance in patients suffering from or susceptible to inflammatory  
XX diseases. A fragment of MIA is useful as a therapeutic substance and is  
XX useful for manufacture of pharmaceutical preparations against  
XX inflammatory diseases such as an immune-cell mediated cartilage  
XX destruction disease, specifically rheumatoid arthritis, autoimmune  
XX diseases like Graves' disease, juvenile arthritis, primary  
XX glomerulonephritis, polyarthritis, osteoarthritis, Sjogren's syndrome,  
XX myasthenia gravis, Addison's disease, primary biliary sclerosis,  
XX uveitis, systemic lupus erythematosus, inflammatory bowel disease,  
XX multiple sclerosis or diabetes. The MIA polypeptides have specific  
XX effect on the autoreactive T-cells thus leaving the other components of  
XX the immune system intact as compared to the non-specific suppressive  
XX effect of immunosuppressive drugs. The present sequence represents a  
XX human MIA protein.

SQ Sequence 131 AA;  
Query Match 43.0%; Score 253.5; DB 22; Length 131;  
Best Local Similarity 45.4%; Pred. No. 1.3e-24;  
Matches 49; Conservative 21; Mismatches 33; Indels 5; Gaps 3;  
QY 5 MDRASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQOIYVYVKLVKENGAGE-F 63  
DB 27 MPKLAADRLKCADQECSPISMAVALQDYMAPDCRFILTHRGQVYVFSKL---KGRGLRF 83  
QY 64 WAGSVYGDQDEMGV-VGYFPRNLVKEQRYOEATKEVPTTIDDFCE 110  
DB 84 WGGSVQGDYGDLAARLGYPSSIVREDQTLKPGKVDVKTDKWDFYQ 131

Search completed: December 29, 2003, 16:09:03  
Job time : 22.5686 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2003, 16:09:08 ; Search time 15.098 Seconds  
(without alignments)  
1449.984 Million cell updates/sec

Title: US-10-019-455A-24

Perfect score: 590

Sequence: 1 HGIFMDRLASKKLCADDECV.....RVYQATKEVPTTIDIFFCE 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 724715 seqs, 199017464 residues

Total number of hits satisfying chosen parameters: 724715

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications AA.\*  
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2: /cgn2\_6/ptodata/2/pubaa/PCT\_NEW\_PUB.pep.\*  
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11: /cgn2\_6/ptodata/2/pubaa/US09C\_PUBCOMB.pep.\*  
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18: /cgn2\_6/ptodata/2/pubaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	590	100.0	128	12	US-10-216-163-72
2	590	100.0	128	12	US-10-218-765-72
3	590	100.0	128	12	US-10-219-063-72
4	590	100.0	128	12	US-10-219-066-72
5	590	100.0	128	12	US-10-219-067-72
6	590	100.0	128	12	US-10-219-068-72
7	590	100.0	128	12	US-10-219-069-72
8	590	100.0	128	12	US-10-219-073-72
9	590	100.0	128	12	US-10-219-475-72
10	590	100.0	128	12	US-10-219-480-72
11	590	100.0	128	12	US-10-219-483-72
12	590	100.0	128	12	US-10-219-525-72
13	590	100.0	128	12	US-10-219-526-72
14	590	100.0	128	12	US-10-219-530-72
15	590	100.0	128	12	US-10-219-531-72

16	590	100.0	128	12	US-10-219-532-72	Sequence 72, Appl
17	590	100.0	128	12	US-10-219-533-72	Sequence 72, Appl
18	590	100.0	128	12	US-10-223-081-360	Sequence 360, Appl
19	590	100.0	128	12	US-10-230-437-72	Sequence 72, Appl
20	590	100.0	128	12	US-10-232-228-72	Sequence 72, Appl
21	590	100.0	128	12	US-10-232-082-360	Sequence 360, Appl
22	590	100.0	128	15	US-10-227-884-72	Sequence 72, Appl
23	590	100.0	128	15	US-10-230-163-72	Sequence 72, Appl
24	590	100.0	128	15	US-10-230-338-72	Sequence 72, Appl
25	590	100.0	128	15	US-10-218-631-72	Sequence 72, Appl
26	590	100.0	128	15	US-10-230-414-72	Sequence 72, Appl
27	590	100.0	128	15	US-10-216-159A-72	Sequence 72, Appl
28	590	100.0	128	15	US-10-218-849-72	Sequence 72, Appl
29	590	100.0	128	15	US-10-227-873-72	Sequence 72, Appl
30	590	100.0	128	15	US-10-227-883-72	Sequence 72, Appl
31	590	100.0	128	15	US-10-219-076-72	Sequence 72, Appl
32	590	100.0	128	15	US-10-230-434-72	Sequence 72, Appl
33	590	100.0	128	15	US-10-219-003-72	Sequence 72, Appl
34	590	100.0	128	15	US-10-219-075-72	Sequence 72, Appl
35	590	100.0	128	15	US-10-219-464-72	Sequence 72, Appl
36	590	100.0	128	15	US-10-219-466-72	Sequence 72, Appl
37	590	100.0	128	15	US-10-219-479-72	Sequence 72, Appl
38	590	100.0	128	15	US-10-219-481-72	Sequence 72, Appl
39	590	100.0	128	15	US-10-230-260-72	Sequence 72, Appl
40	590	100.0	128	15	US-10-232-231-72	Sequence 72, Appl
41	590	100.0	128	15	US-10-232-233-72	Sequence 72, Appl
42	590	100.0	128	15	US-10-216-165-72	Sequence 72, Appl
43	590	100.0	128	15	US-10-218-956-72	Sequence 72, Appl
44	590	100.0	128	15	US-10-219-468-72	Sequence 72, Appl
45	590	100.0	128	15	US-10-219-478-72	Sequence 72, Appl

## ALIGNMENTS

### RESULT 1

US-10-216-163-72  
; Sequence 72, Application US/10216163  
; Publication No. US20030149239A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3530PIC3  
; CURRENT APPLICATION NUMBER: US/10/216,163  
; CURRENT FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: 10/119,480  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/069873  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656

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; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-163-72

Query Match      100.0%; Score 590; Dk 12; Length 128;
Best Local Similarity 100.0%; Pred. No. 5e-64;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQIYVYSKLVKNGA 60
    |||||||
Db 19 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQIYVYSKLVKNGA 78
    |||||||

QY 61 GEFWAGSVYGDQDGMGVGVFPRLNVKEQRYQEQATKEVPTTDDFFCE 110
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Db 79 GEFWAGSVYGDQDGMGVGVFPRLNVKEQRYQEQATKEVPTTDDFFCE 128
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RESULT 2
US-10-218-765-72
; Sequence 72, Application US/10218765
; Publication No. US20030187201A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C19
; CURRENT APPLICATION NUMBER: US/10/218,765
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
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; PRIOR FILING DATE: 1998-06-18
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; PRIOR FILING DATE: 1998-06-24
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; PRIOR APPLICATION NUMBER: 60/090691
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/095302
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095318
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095916
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/096146
; PRIOR FILING DATE: 1998-08-11
; PRIOR APPLICATION NUMBER: 60/096791
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/097986
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: 60/098544
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099803
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099811
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100038
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101786
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101922
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/106178
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US-10-219-067-72  
; Sequence 72, Application US/10219067  
; Publication No. US20030187204A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3530P1C51  
; CURRENT APPLICATION NUMBER: US/10/219,067  
; CURRENT FILING DATE: 2002-08-14  
; PRIOR APPLICATION NUMBER: 10/119,480  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/069873  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 246  
; SEQ ID NO 72  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-219-067-72  
Query Match 100.0%; Score 590; DB 12; Length 128;  
Best Local Similarity 100.0%; Pred. No. 5e-64;  
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HGFMRLASKKLCADDECVYVITSLASAEQEDYNAPDCRFINVKKGQOIYVYSKLVKNGA 60  
DB 19 HGFMRLASKKLCADDECVYVITSLASAEQEDYNAPDCRFINVKKGQOIYVYSKLVKNGA 78  
QY 61 GEFWAGSVYGDQDEMGVGYFPRNLVKEQRYVQATKEVPTTIDDFCE 110  
DB 79 GEFWAGSVYGDQDEMGVGYFPRNLVKEQRYVQATKEVPTTIDDFCE 128  
RESULT 6  
US-10-219-068-72  
; Sequence 72, Application US/10219068  
; Publication No. US20030187205A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.

US-10-219-066-72  
; Sequence 72, Application US/10219066  
; Publication No. US20030187203A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3530P1C27  
; CURRENT APPLICATION NUMBER: US/10/219,066  
; CURRENT FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: 10/119,480  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/069873  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 246  
; SEQ ID NO 72  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-219-066-72  
Query Match 100.0%; Score 590; DB 12; Length 128;  
Best Local Similarity 100.0%; Pred. No. 5e-64;  
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HGFMRLASKKLCADDECVYVITSLASAEQEDYNAPDCRFINVKKGQOIYVYSKLVKNGA 60  
DB 19 HGFMRLASKKLCADDECVYVITSLASAEQEDYNAPDCRFINVKKGQOIYVYSKLVKNGA 78  
QY 61 GEFWAGSVYGDQDEMGVGYFPRNLVKEQRYVQATKEVPTTIDDFCE 110  
DB 79 GEFWAGSVYGDQDEMGVGYFPRNLVKEQRYVQATKEVPTTIDDFCE 128  
RESULT 5

APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3530PIC31  
CURRENT APPLICATION NUMBER: US/10/219,068  
CURRENT FILING DATE: 2002-08-13  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 246  
SEQ ID NO 72  
LENGTH: 128  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-219-068-72

Query Match 100.0%; Score 590; DB 12; Length 128;  
Best Local Similarity 100.0%; Pred. No. 5e-64;  
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HGIFMDRLASKKLCADDECVVTISLASAQEDYNAPDCRFINVKKGQIYVYSKLVKNGA 60  
Db 19 HGIFMDRLASKKLCADDECVVTISLASAQEDYNAPDCRFINVKKGQIYVYSKLVKNGA 78

Qy 61 GEFWAGSVYGDQDEMGVGFPRNLVKEQRYQVQATKEVPTTIDIDFCE 110  
Db 79 GEFWAGSVYGDQDEMGVGFPRNLVKEQRYQVQATKEVPTTIDIDFCE 128

RESULT 7  
US-10-219-069-72  
Sequence 72, Application US/10219069  
Publication No. US20030187206A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Desnoyers, Luc  
APPLICANT: Gerritsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3530PIC40  
CURRENT APPLICATION NUMBER: US/10/219,069  
CURRENT FILING DATE: 2002-08-13  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09

PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 246  
SEQ ID NO 72  
LENGTH: 128  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-219-069-72

Query Match 100.0%; Score 590; DB 12; Length 128;  
Best Local Similarity 100.0%; Pred. No. 5e-64;  
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HGIFMDRLASKKLCADDECVVTISLASAQEDYNAPDCRFINVKKGQIYVYSKLVKNGA 60  
Db 19 HGIFMDRLASKKLCADDECVVTISLASAQEDYNAPDCRFINVKKGQIYVYSKLVKNGA 78

Qy 61 GEFWAGSVYGDQDEMGVGFPRNLVKEQRYQVQATKEVPTTIDIDFCE 110  
Db 79 GEFWAGSVYGDQDEMGVGFPRNLVKEQRYQVQATKEVPTTIDIDFCE 128

RESULT 8  
US-10-219-073-72  
Sequence 72, Application US/10219073  
Publication No. US20030187207A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Desnoyers, Luc  
APPLICANT: Gerritsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3530PIC52  
CURRENT APPLICATION NUMBER: US/10/219,073  
CURRENT FILING DATE: 2002-08-14  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910



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; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-475-72

Query Match      100.0%; Score 590; DB 12; Length 128;
Best Local Similarity 100.0%; Pred. No. 5e-64;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HGIFMDRLASKKLCADDECVTITSLASAOEDYNAPDCRFINVKKGQOIYVYSLVKVNGA 60
    |||||||
Db 19 HGIFMDRLASKKLCADDECVTITSLASAOEDYNAPDCRFINVKKGQOIYVYSLVKVNGA 78
    |||||||

Qy 61 GEFWAGSVYGDQDEMGVGFPRNLVKEQRYQATKEVPTTIDIDFFCE 110
    |||||||
Db 79 GEFWAGSVYGDQDEMGVGFPRNLVKEQRYQATKEVPTTIDIDFFCE 128
    |||||||

RESULT 9
US-10-219-475-72
; Sequence 72, Application US/10219475
; Publication No. US20030187208A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC49
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-073-72

Query Match      100.0%; Score 590; DB 12; Length 128;
Best Local Similarity 100.0%; Pred. No. 5e-64;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HGIFMDRLASKKLCADDECVTITSLASAOEDYNAPDCRFINVKKGQOIYVYSLVKVNGA 60
    |||||||
Db 19 HGIFMDRLASKKLCADDECVTITSLASAOEDYNAPDCRFINVKKGQOIYVYSLVKVNGA 78
    |||||||

Qy 61 GEFWAGSVYGDQDEMGVGFPRNLVKEQRYQATKEVPTTIDIDFFCE 110
    |||||||
Db 79 GEFWAGSVYGDQDEMGVGFPRNLVKEQRYQATKEVPTTIDIDFFCE 128
    |||||||

RESULT 9
US-10-219-475-72
; Sequence 72, Application US/10219475
; Publication No. US20030187208A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC49
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-480-72

Query Match      100.0%; Score 590; DB 12; Length 128;
Best Local Similarity 100.0%; Pred. No. 5e-64;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HGIFMDRLASKKLCADDECVTITSLASAOEDYNAPDCRFINVKKGQOIYVYSLVKVNGA 60
    |||||||
Db 19 HGIFMDRLASKKLCADDECVTITSLASAOEDYNAPDCRFINVKKGQOIYVYSLVKVNGA 78
    |||||||

Qy 61 GEFWAGSVYGDQDEMGVGFPRNLVKEQRYQATKEVPTTIDIDFFCE 110
    |||||||
Db 79 GEFWAGSVYGDQDEMGVGFPRNLVKEQRYQATKEVPTTIDIDFFCE 128
    |||||||

RESULT 10
US-10-219-480-72
; Sequence 72, Application US/10219480
; Publication No. US20030187209A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC38
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-480-72

Query Match      100.0%; Score 590; DB 12; Length 128;
Best Local Similarity 100.0%; Pred. No. 5e-64;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HGIFMDRLASKKLCADDECVTITSLASAOEDYNAPDCRFINVKKGQOIYVYSLVKVNGA 60
    |||||||
Db 19 HGIFMDRLASKKLCADDECVTITSLASAOEDYNAPDCRFINVKKGQOIYVYSLVKVNGA 78
    |||||||
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QY 61 GEFWAGSVYGDQDEMGVGFPRNLVKEQRYVQYQATKEVPTTDDIFFCE 110  
Db 79 GEFWAGSVYGDQDEMGVGFPRNLVKEQRYVQYQATKEVPTTDDIFFCE 128

## RESULT 11

US-10-219-483-72  
; Sequence 72, Application US/10219483  
; Publication No. US20030187210A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3530P1C43  
; CURRENT APPLICATION NUMBER: US/10/219,483  
; CURRENT FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: 10/119,480  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/069873  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 246  
; SEQ ID NO 72  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-219-483-72

Query Match 100.0%; Score 590; DB 12; Length 128;  
Best Local Similarity 100.0%; Pred. No. 5e-64;  
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKGQOIYVYSLVKENGA 60  
Db 19 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKGQOIYVYSLVKENGA 78  
QY 61 GEFWAGSVYGDQDEMGVGFPRNLVKEQRYVQYQATKEVPTTDDIFFCE 110  
Db 79 GEFWAGSVYGDQDEMGVGFPRNLVKEQRYVQYQATKEVPTTDDIFFCE 128

## RESULT 12

US-10-219-525-72  
; Sequence 72, Application US/10219525  
; Publication No. US20030187211A1  
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3530P1C29  
; CURRENT APPLICATION NUMBER: US/10/219,525  
; CURRENT FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: 10/119,480  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/069873  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 246  
; SEQ ID NO 72  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-219-525-72

Query Match 100.0%; Score 590; DB 12; Length 128;  
Best Local Similarity 100.0%; Pred. No. 5e-64;  
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKGQOIYVYSLVKENGA 60  
Db 19 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKGQOIYVYSLVKENGA 78  
QY 61 GEFWAGSVYGDQDEMGVGFPRNLVKEQRYVQYQATKEVPTTDDIFFCE 110  
Db 79 GEFWAGSVYGDQDEMGVGFPRNLVKEQRYVQYQATKEVPTTDDIFFCE 128

## RESULT 13

US-10-219-526-72  
; Sequence 72, Application US/10219526  
; Publication No. US20030187212A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.

```

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC41
; CURRENT APPLICATION NUMBER: US/10/219,526
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-526-72

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Query Match 100.0%; Score 590; DB 12; Length 128;
Best Local Similarity 100.0%; Pred. No. 5e-64;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQOIYVYSKLVKNGA 60
DB 19 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQOIYVYSKLVKNGA 78

QY 61 GEFWAGSVYGDQDEMGVGVYPRNLVKEQRYVQATKEVPTTIDIDFFCE 110
DB 79 GEFWAGSVYGDQDEMGVGVYPRNLVKEQRYVQATKEVPTTIDIDFFCE 128

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RESULT 14
US-10-219-530-72
; Sequence 72, Application US/10219530
; Publication No. US20030187213A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC54
; CURRENT APPLICATION NUMBER: US/10/219,530
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17

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; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-530-72

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```

Query Match 100.0%; Score 590; DB 12; Length 128;
Best Local Similarity 100.0%; Pred. No. 5e-64;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQOIYVYSKLVKNGA 60
DB 19 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQOIYVYSKLVKNGA 78

QY 61 GEFWAGSVYGDQDEMGVGVYPRNLVKEQRYVQATKEVPTTIDIDFFCE 110
DB 79 GEFWAGSVYGDQDEMGVGVYPRNLVKEQRYVQATKEVPTTIDIDFFCE 128

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RESULT 15
US-10-219-531-72
; Sequence 72, Application US/10219531
; Publication No. US20030187214A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC66
; CURRENT APPLICATION NUMBER: US/10/219,531
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656

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Tue Dec 30 10:20:40 2003

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; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-531-72

Query Match      100.0%; Score 590; DB 12; Length 128;
Best Local Similarity 100.0%; Pred. No. 5e-64;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HGIFMDRLASKKLCADDECVYTTISLASAQEDYNAPDCRFINVKKGQQIYVYVKLVKNGA 60
Db      19 HGIFMDRLASKKLCADDECVYTTISLASAQEDYNAPDCRFINVKKGQQIYVYVKLVKNGA 78

Qy      61 GEFWAGSYVYGDQDEMGMVGVYFPRNLVKEQRYQVQVATKEVPTTIDIDFCE 110
Db      79 GEFWAGSYVYGDQDEMGMVGVYFPRNLVKEQRYQVQVATKEVPTTIDIDFCE 128
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Search completed: December 29, 2003, 16:26:15  
Job time : 15.098 secs





Tue Dec 30 10:20:40 2003

Db 27 MPKLADKRLCADQBCSHPI5MAVALQDYMADPCRFLLTHRGQVVVFSKL---KGRGLF 83  
QY 64 WAGSVYGGQDGMGV-VGYPRNLVKEQRYVQATKEVPTTDDIFFCE 110  
Db 84 WGSVQGDYGDLAARLGYFPSSIVREDQTLKPGKVDKDKWDFYCYQ 131

RESULT 2

US-08-578-649-5  
; Sequence 5, Application US/08578649  
; Patent No. 5770366  
; GENERAL INFORMATION:  
; APPLICANT: Ulrich Bogdan  
; APPLICANT: Reinhard Buttner  
; APPLICANT: Brigitte Kaluza  
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felfe & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: Wordperfect  
; CURRENT APPLICATION DATA:  
; FILING DATE: 29-July-1994  
; FILING DATE: 29-July-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE P 43 24 247.2  
; FILING DATE: 20-July-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Andrew L. Tiajolo  
; REGISTRATION NUMBER: 31.575  
; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 688-9200  
; TELEFAX: (212) 838-3884  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 130 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-578-649-5

Query Match 39.2%; Score 231.5; DB 1; Length 130;  
Best Local Similarity 43.5%; Pred. No. 2.2e-22;  
Matches 47; Conservative 21; Mismatches 35; Indels 5; Gaps 3;

QY 5 MDRLASKKLCADECVYTTISLASAQEDYNAPDCRFNLVKKGGQIYVYKLVKENGAGE-R 63  
Db 26 MPKLADKRLCADQBCSHPI5MAVALQDYMADPCRFLLTHRGQVVVFSKL---KGRGLF 82  
QY 64 WAGSVYGGQDGMGV-VGYPRNLVKEQRYVQATKEVPTTDDIFFCE 110  
Db 83 WGSVQGDYGDLAARLGYFPSSIVREDQTLKPGKVDKDKWDFYCYQ 130

RESULT 3

US-07-646-537B-2  
; Sequence 2, Application US/07646537B  
; Patent No. 5348864  
; GENERAL INFORMATION:  
; APPLICANT: Barbacid, Mariano  
; TITLE OF INVENTION: Vav Proto-Oncogene Protein  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Bristol-Myers Squibb Company  
; STREET: P.O. Box 4000  
; CITY: Princeton  
; STATE: New Jersey  
; COUNTRY: U.S.A.  
; ZIP: 08543-4000  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/646,537B  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gaul, Timothy J.  
; REGISTRATION NUMBER: 33,111  
; REFERENCE/DOCKET NUMBER: DC10  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (609) 921-5901  
; TELEFAX: (609) 921-4526  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 844 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-646-537B-2

Query Match 14.5%; Score 85.5; DB 1; Length 844;  
Best Local Similarity 31.4%; Pred. No. 0.032;  
Matches 22; Conservative 14; Mismatches 21; Indels 13; Gaps 3;  
QY 26 ASAQEDYNAPDCRFNLVKKGGQIYVYKLVKENGAGEFWAGSVYGGQDGMGVYFPFRN 85  
Db 786 AKARYDFCARDSELSLKEGDII----KILNKGQGGWWRGEIYGR-----IGWFFPSN 834  
QY 86 LVKEQRYVQOE 95  
Db 835 YVEED--YSE 842

RESULT 4

US-09-346-510B-21  
; Sequence 21, Application US/09346510B  
; Patent No. 6281014  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, Timothy J.  
; TITLE OF INVENTION: SH3-Containing Protein, DNA and Uses Thereof  
; FILE REFERENCE: D6221CIP  
; CURRENT APPLICATION NUMBER: US/09/346,510B  
; CURRENT FILING DATE: 1999-07-01  
; PRIOR APPLICATION NUMBER: 08/871,732  
; PRIOR FILING DATE: 1997-06-09  
; NUMBER OF SEQ ID NOS: 32  
; SEQ ID NO 21  
; TYPE: PRT  
; LENGTH: 54  
; ORGANISM: unknown  
; FEATURE:  
; NAME/KEY: Domain  
; OTHER INFORMATION: amino acid sequence of Vav SH3 domain  
US-09-346-510B-21

Query Match 13.8%; Score 81.5; DB 3; Length 54;  
Best Local Similarity 32.3%; Pred. No. 0.0023;  
Matches 20; Conservative 13; Mismatches 18; Indels 11; Gaps 2;  
QY 28 AQEDYNAPDCRFNLVKKGGQIYVYKLVKENGAGEFWAGSVYGGQDGMGVYFPFRNLV 87  
Db 1 ARYDFCARDSELSLKEGDII----KILNKGQGGWWRGEIYGR-----VGWFFPANYV 49







; INFORMATION FOR SEQ ID NO: 135:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 62 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-630-915A-135

Query Match 11.3%; Score 66.5; DB 4; Length 62;  
Best Local Similarity 26.6%; Pred. No. 0.25;  
Matches 17; Conservative 11; Mismatches 29; Indels 7; Gaps 2;

Qy 25 LASAQEDYNADCRFINVKKQOIYVYKLVKENGAGFEFWAGSVYGGODEMGVGYEPR 84  
Db 4 IAQVIASYATGTPQLTAPGQLI-----LIRKKNPGGWEGELQARKKQ--IGWFFA 56

Qy 85 NLVK 88  
Db 57 NYVK 60

RESULT 11  
US-08-245-511-48  
; Sequence 48, Application US/08245511  
; Patent No. 5928900

; GENERAL INFORMATION:  
; APPLICANT: Masure, H Robert  
; APPLICANT: Pearce, Barbara J  
; APPLICANT: Tuomanen, Elaine  
; TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND  
; TITLE OF INVENTION: ACCELLULAR VACCINES BASED THEREON  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/245,511  
; FILING DATE: 18-MAY-1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/116,541  
; FILING DATE: 01-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 600-1-069 CIP  
; TELEPHONE: 201 487-5800  
; TELEFAX: 201 343-1684  
; TELEX: 133521

; INFORMATION FOR SEQ ID NO: 48:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 642 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Streptococcus pneumoniae  
; IMMEDIATE SOURCE:  
; CLONE: amia  
; FEATURE:

; OTHER INFORMATION: NOTE: the reference contains a  
; OTHER INFORMATION: sequence error; the correct sequence shown below is obtained  
; PUBLICATION INFORMATION:  
; AUTHORS: Allouing, et al.  
; JOURNAL: Mol. Microbiol.  
; VOLUME: 4  
; PAGES: 633-644  
; DATE: 1990  
US-08-245-511-48

Query Match 11.3%; Score 66.5; DB 2; Length 642;  
Best Local Similarity 22.5%; Pred. No. 6.5;  
Matches 27; Conservative 20; Mismatches 44; Indels 29; Gaps 4;

Qy 6 DRLASKKLCADDECVTYITSLASAQEDYNAPDCRFINVKKQOIYVYKLVKEN-----58  
Db 309 EKVATKKALLNKDPQALNFALDRSAYSAQ-----INGKDGAAALAVRNLFVKPDPFVSAGEK 364

Qy 59 -----GAGEFWAGSVYGGODEMGVGYEPRNLVKEQRYQEATKEVPTTIDF 107  
Db 365 TFGDLVAAQLPAYGDWKGVNLADQD-----GLF--NADKAKAEFRKAKKALEADGVQF 417

RESULT 12

US-08-600-993A-48  
; Sequence 48, Application US/08600993A  
; Patent No. 5981229

; GENERAL INFORMATION:  
; APPLICANT: Masure, H Robert  
; APPLICANT: Pearce, Barbara J  
; APPLICANT: Tuomanen, Elaine  
; TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND  
; TITLE OF INVENTION: ACCELLULAR VACCINES BASED THEREON  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/600,993A  
; FILING DATE: 1-MAR-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/245,511  
; FILING DATE: 18-MAY-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/116,541  
; FILING DATE: 01-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 600-1-069 US  
; TELEPHONE: 201 487-5800  
; TELEFAX: 201 343-1684  
; TELEX: 133521

; INFORMATION FOR SEQ ID NO: 48:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 642 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO

ANTI-SENSE: NO  
ORIGINAL SOURCE: Streptococcus pneumoniae  
IMMEDIATE SOURCE: amia  
FEATURE: amia  
OTHER INFORMATION: the reference contains a sequence error; the correct sequence shown below is obtained from GENBANK  
PUBLICATION INFORMATION:  
AUTHORS: Allouing, et al.  
JOURNAL: Mol. Microbiol.  
VOLUME: 4  
PAGES: 633-644  
DATE: 1990  
US-08-600-993A-48

Query Match 11.3%; Score 66.5; DB 2; Length 642;  
Best Local Similarity 22.5%; Pred. No. 6.5;  
Matches 27; Conservative 20; Mismatches 44; Indels 29; Gaps 4;  
QY 6 DRLASKKLCADCECVYTISLASAQEDYNAPDCRFNVKKGQIYVYKLVKEN----- 58  
Db 309 EKVATKALLNKDFQALNFALDRSAYSQAQ-----INGKDGALAVRNLFVKPDPFVSAGEK 364  
QY 59 -----GAGFEWAGSVVYGGQDGMGVVGYFPNVLVKEQRYQVQATKEVPTTIDF 107  
Db 365 TFGDLVAAQLPAYGDWKGVLNADGQD-----GLF--NADKAEFRKAKKALEADGVQF 417

RESULT 13  
US-08-630-915A-40  
; Sequence 40, Application US/08630915A  
; Patent No. 6309820  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: HOFFMAN, No. 6309820h  
; APPLICANT: KAY, Brian K.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: MCCONNELL, Stephen J.  
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL  
; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND  
; TITLE OF INVENTION: USING SAME  
; NUMBER OF SEQUENCES: 227  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/630,915A  
; FILING DATE: 03-APR-1996  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-174  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 40:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 248 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown

MOLECULE TYPE: peptide  
US-08-630-915A-40  
Query Match 11.2%; Score 66; DB 4; Length 248;  
Best Local Similarity 30.4%; Pred. No. 2;  
Matches 24; Conservative 7; Mismatches 24; Indels 24; Gaps 3;  
QY 28 AOEDYNAPDCRFNVKKGQIYVYKLVKENGAGFEWAGSVVYGGQDGMGVVGYFPNVLV 87  
Db 190 AMYDYANNDELSFGQLINVMNK-----DDPDWMQGEI-----NGVTGLFPSNYV 237  
QY 88 KEQRYQVQATKEVPTTID 106  
Db 238 K-----MTTSD 244

RESULT 14  
US-08-434-255-8  
; Sequence 8, Application US/08434255  
; Patent No. 5621089  
; GENERAL INFORMATION:  
; APPLICANT: Sloma, Alan P.  
; APPLICANT: Outtrup, Helle  
; APPLICANT: Dambmann, Claus  
; APPLICANT: Aaslyng, Dorric  
; TITLE OF INVENTION: ALKALINE PROTEASE  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 5621089o No. 5621089disk of No. 5621089th America, Inc.  
; STREET: 405 Lexington Avenue, 64th Floor  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10174-6401  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/434,255  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Agis Dr., Cheryl H.  
; REGISTRATION NUMBER: 34,086  
; REFERENCE/DOCKET NUMBER: 3764.400-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-867-0123  
; TELEFAX: 212-878-9655  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 280 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-434-255-8

Query Match 11.2%; Score 66; DB 1; Length 280;  
Best Local Similarity 29.6%; Pred. No. 2.4;  
Matches 21; Conservative 11; Mismatches 39; Indels 0; Gaps 0;  
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QY 82 FPNLVKEQRY 92  
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RESULT 15  
US-08-459-967-8

; Sequence 8, Application US/08459967  
; Patent No. 5622841  
; GENERAL INFORMATION:  
; APPLICANT: Sloma, Alan P.  
; APPLICANT: Outtrup, Helle  
; APPLICANT: Dammann, Claus  
; APPLICANT: Aaslyng, Dorrit  
; TITLE OF INVENTION: ALKALINE PROTEASE  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 5622841o No. 5622841disk of No. 5622841th America, Inc.  
; STREET: 405 Lexington Avenue, 64th Floor  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10174-6401  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/459,967  
; FILING DATE: 02-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/434,255  
; FILING DATE: 03-MAY-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Agtis Dr., Cheryl H.  
; REGISTRATION NUMBER: 34,086  
; REFERENCE/DOCKET NUMBER: 3764.400-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-867-0123  
; TELEFAX: 212-878-9655  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 280 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-459-967-8

Query Match 11.2%; Score 66; DB 1; Length 280;  
Best Local Similarity 25.6%; Pred. No. 2.4;  
Matches 21; Conservative 11; Mismatches 39; Indels 0; Gaps 0;

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Db 34 TVAVLDGVDYNDHFDLARKVIKGYDFIDRDNNPMDLNGHGHVAGTVAADTNGIGVAGM 93  
|::: : ||| | : : : | : : : | : : : |  
Qy 82 FPNLVKEQRV 92  
| : : |  
Db 94 APDTKILAVRV 104  
| : : |

Search completed: December 29, 2003, 16:11:50  
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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 29, 2003, 16:11:59 ; Search time 1810.69 Seconds  
(without alignments)  
2485.278 Million cell updates/sec

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Perfect score: 590  
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Fgapop 6.0 , Fgapext 7.0  
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Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Database :

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- 2: gb\_hug.\*
- 3: gb\_in.\*
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- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*

RESULT 1

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- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htg\_mus.\*
- 34: em\_htg\_pln.\*
- 35: em\_htg\_rnd.\*
- 36: em\_htg\_mam.\*
- 37: em\_htg\_vrt.\*
- 38: em\_sy.\*
- 39: em\_htgo\_hum.\*
- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	590	100.0	330	6	BD010816 Novel pol
2	590	100.0	330	6	BD093117 Novel pol
3	590	100.0	384	6	BD010802 Novel pol
4	590	100.0	384	6	BD093103 Novel pol
5	590	100.0	521	6	AX358818 Sequence
6	590	100.0	521	6	AX362311 Sequence
7	590	100.0	521	6	AX454774 Sequence
8	590	100.0	521	6	AX491252 Sequence
9	590	100.0	846	9	AF233261 Homo sapi
10	590	100.0	865	9	AF243505 Homo sapi
11	590	100.0	923	6	BD010820 Novel pol
12	590	100.0	923	6	BD093121 Novel pol
13	590	100.0	1422	9	HS242552 Homo sapi
14	547	92.7	330	6	BD010817 Novel pol
15	547	92.7	330	6	BD093118 Novel pol
16	547	92.7	384	6	BD010805 Novel pol
17	547	92.7	384	6	BD093106 Novel pol
18	547	92.7	929	10	AF243504 Mus muscu
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20	547	92.7	947	6	BD093122 Novel pol
21	547	92.7	958	10	MMU243939 Mus muscu
22	547	92.7	1054	10	AF233333 Mus muscu
23	541	91.7	330	6	BD010836 Novel pol
24	541	91.7	330	6	BD093137 Novel pol
25	541	91.7	384	6	BD010835 Novel pol
26	541	91.7	384	6	BD093136 Novel pol
27	477.5	80.9	484	5	AF233518 Gallus ga
28	471	79.8	307	6	BD010830 Novel pol
29	471	79.8	307	6	BD093131 Novel pol
30	413	70.0	261	6	BD010829 Novel pol
31	413	70.0	261	6	BD093130 Novel pol
32	390	66.1	466	5	AF233519 Rana cate
33	269	45.6	121151	9	HS705D16 Human DNA
34	266.5	45.2	144765	2	EX510362 Mus muscu
C 35	285.5	45.0	215581	2	AC106161 Rattus no
C 36	254.5	43.1	442	6	AX331430 Sequence
C 37	254.5	43.1	442	6	AX331840 Sequence
38	253.5	43.0	330	6	A42959 Sequence 18
39	253.5	43.0	330	6	AX016802 Sequence
40	253.5	43.0	396	9	BT007044 Homo sapi
41	253.5	43.0	396	12	BT007775 Synthetic
42	253.5	43.0	459	6	A42942 Sequence 1
43	253.5	43.0	459	6	AX016785 Sequence
C 44	253.5	43.0	459	6	AX252508 Sequence
C 45	253.5	43.0	459	6	AX287209 Sequence

ALIGNMENTS





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RESULT 3
LOCUS      BD010802              384 bp    DNA          linear    PAT 31-JAN-2002
DEFINITION Novel polypeptide and DNA thereof.
ACCESSION  BD010802
VERSION     BD010802.1 GI:18639175
KEYWORDS    JP 2001069994-A/3.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens

REFERENCE   1 (bases 1 to 384)
AUTHORS     Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y.,
            Yoshimura,K. and Tanaka,H.
TITLE       Patent: JP 2001069994-A 3 21-MAR-2001;
JOURNAL     TAKEDA CHEMICAL INDUSTRIES LTD
COMMENT     OS Homo sapiens (human)
            PN JP 2001069994-A/3
            PD 21-MAR-2001
            PR 29-JUN-2000 JP 2000195911

PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI
SHINICHI MOGI,
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC
A61P19/08,
PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC
G01N33/53//
PC C12P21/08, C12N15/00, A61K37/02, C12N5/00
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FT /db_xref='taxon:9606'

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BASE COUNT  99 a 70 c 106 g 109 t
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Pred. No.:      7.69e-66      Length:      384
Score:          590.00      Matches:      110
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             6      Gaps:      0

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QY      1 HisGlyIlePheMetAspArgIleuAlaSerLysLysLysCysAlaAspGluCysVal 20
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      55 CATGGAATATTATGACCGCTCTAGCTTCCAGAAAGCTCTGTGCAGATGATGAGTGTGTC 114

QY      21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
      |||
      115 TATACTATTCTCTGCGTAGTGTCTCAAGAAGATTATTAATGCCCGGACTGTAGATTCAAT 174

QY      41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 60
      |||
      175 AACGTTAAAAAGGGCAGCAGATCTATGTGTACTCAAAAGCTGTGTAAGAAAGAAATGGAGCT 234

QY      61 GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80
      |||
      235 GGAGAATTTTGGCTGGCAGTGTATTATGGTGTATGGCCAGACAGATGGAGTCTGGTGGGT 294

QY      81 TyrPheProArgAsnLeuValLysGluGlnAcqValTyrGlnGluAlaThrLysGluVal 100
      |||
      295 TATTTCCTCCAGGAACCTTGGTCAAGGAACACGCGTGTGTACCAAGGAGCTACCAAGGAAGTT 354

QY      101 ProThrAspIleAspPhePheCysGlu 110
      |||
      355 CCCACCACGGATATTGACTTCTTCTCGGAG 384

RESULT 4
LOCUS      BD093103              384 bp    DNA          linear    PAT 27-AUG-2002
DEFINITION Novel polypeptide and its DNA.
ACCESSION  BD093103
VERSION     BD093103.1 GI:22638691
KEYWORDS    WO 0102564-A/3.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens

REFERENCE   1 (bases 1 to 384)
AUTHORS     Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y.,
            Yoshimura,K. and Tanaka,H.
TITLE       Patent: WO 0102564-A 3 11-JAN-2001;
JOURNAL     TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO
            OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,
            HIDEYUKI TANAKA
COMMENT     OS Homo sapiens (human)
            PN WO 0102564-A/3
            PD 11-JAN-2001
            PR 29-JUN-2000 WO 2000JP004278
            PR 30-JUN-1999 JP 99P 186718
            PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
            MOGI,
            PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
            PC C12N15/12, C12N5/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC
            A61K38/17,
            PC A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7088// (C12P21/
            PC 02, C12R1:19)
            CC
            FH Key      Location/Qualifiers
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            FT /mol_type="genomic DNA"
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BASE COUNT  99 a 70 c 106 g 109 t
ORIGIN

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Pred. No.:      7.69e-66      Length:      384
Score:          590.00      Matches:      110
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
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QY      21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
      |||
      115 TATACTATTCTCTGCGTAGTGTCTCAAGAAGATTATTAATGCCCGGACTGTAGATTCAAT 174

QY      41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 60
      |||
      175 AACGTTAAAAAGGGCAGCAGATCTATGTGTACTCAAAAGCTGTGTAAGAAAGAAATGGAGCT 234

QY      61 GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80
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Db 235 GGAGAAATTTGGCTGGCAGGTTTATGGTGATGCCAGGACGAGATGGGAGTCGTGGGT 294
Qy 81 TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100
Db 295 TATTTCCCGAGAACTTGGTCAAGAACAGCGTGTGTACCAAGGAAGCTACCAAGGAAGTT 354
Qy 101 ProThrThrAspIleAspPheCysGlu 110
Db 355 CCCACCGGATATTGACTTCTTCTGCGAG 384

RESULT 5
AX358818
LOCUS AX358818 521 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 71 from Patent WO0193983.
ACCESSION AX358818
VERSION AX358818.1 GI:18675310
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
Watanabe, C.K., and Wood, W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0193983-A 71 13-DEC-2001;
Genentech Inc. (US)
FEATURES
source
Location/Qualifiers
1..521
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BASE COUNT 167 a 86 c 131 g 137 t
ORIGIN

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Pred. No.: 1..65 Length: 521
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

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Qy 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
Db 152 TATACTATTTCTCTGGCTAGTGTCTCAAGAGATTATTAATGCCCGGAGCTGTAGATTCA 211
Qy 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLysLeuValLysGluAsnGlyAla 60
Db 212 AACGTTAAAAAAGGCGACGAGATCTATGTCTCAAAAGCTGTGTAAGAAATAATGGAGCT 271
Qy 61 GlyCluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80
Db 272 GGAGAAATTTGGCTGGCAGTGTATGTTATGTTGTCAGGACGAGATGGGAGTCGTGGGT 331
Qy 81 TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100
Db 332 TATTTCCCGAGAACTTGGTCAAGAACAGCGTGTGTACCAAGGAAGCTACCAAGGAAGTT 391
Qy 101 ProThrThrAspIleAspPheCysGlu 110
Db 392 CCCACCGGATATTGACTTCTTCTGCGAG 421

RESULT 6
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LOCUS AX358818 521 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 71 from Patent WO0193983.
ACCESSION AX358818
VERSION AX358818.1 GI:18675310
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
Watanabe, C.K., and Wood, W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0193983-A 71 13-DEC-2001;
Genentech Inc. (US)
FEATURES
source
Location/Qualifiers
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/mol_type="genomic DNA"
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BASE COUNT 167 a 86 c 131 g 137 t
ORIGIN

Alignment Scores:
Pred. No.: 1..65 Length: 521
Score: 590.00 Matches: 110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-019-455A-24 (1-110) x AX358818 (1-521)
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Qy 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
Db 152 TATACTATTTCTCTGGCTAGTGTCTCAAGAGATTATTAATGCCCGGAGCTGTAGATTCA 211
Qy 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLysLeuValLysGluAsnGlyAla 60
Db 212 AACGTTAAAAAAGGCGACGAGATCTATGTCTCAAAAGCTGTGTAAGAAATAATGGAGCT 271
Qy 61 GlyCluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80
Db 272 GGAGAAATTTGGCTGGCAGTGTATGTTATGTTGTCAGGACGAGATGGGAGTCGTGGGT 331
Qy 81 TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100
Db 332 TATTTCCCGAGAACTTGGTCAAGAACAGCGTGTGTACCAAGGAAGCTACCAAGGAAGTT 391
Qy 101 ProThrThrAspIleAspPheCysGlu 110
Db 392 CCCACCGGATATTGACTTCTTCTGCGAG 421
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AX362311
LOCUS AX362311 521 bp DNA linear PAT 15-FEB-2002
DEFINITION Sequence 71 from Patent WO0208288.
ACCESSION AX362311
VERSION AX362311.1 GI:18694613
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
Watanabe, C.K., and Wood, W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0208288-A 71 31-JAN-2002;
Genentech, Inc. (US)
FEATURES
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BASE COUNT 167 a 86 c 131 g 137 t
ORIGIN

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Percent Similarity: 100.00% Conservative: 0
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Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

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Db 92 CATGGAATATTATGGACCGCTAGCTTCCAAGAGCTCTGTCAGATGATGAGTGTGTC 151
Qy 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
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Db 392 CCCACCGGATATTGACTTCTTCTGCGAG 421

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DEFINITION Sequence 359 from Patent WO0208284.
ACCESSION AX454774
VERSION AX454774.1 GI:21714011
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,
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Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J., Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I. and Ye, W.

Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis

Patent: WO 0208284-A 359 31-JAN-2002;  
Genentech, Inc. (US); Baker, Kevin P. (US); Ferrara, Napoleone (US); Gerber, Hanspeter (US); Gerritsen, Mary E. (US); Goddard, Audrey (US); Godowski, Paul J. (US); Gurney, Austin L. (US); Hillan, Kenneth J. (US); Marsters, Scott A. (US); Pan, James (US); Paoni, Nicholas F. (US); Stephan, Jean-Philippe F. (US); Watanabe, Colin K. (US); Williams, P. Mickey (US); Wood, William I. (US)

#### FEATURES

source

Location/Qualifiers

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/organism="Homo sapiens"

/mol\_type="genomic DNA"

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BASE COUNT 167 a 86 c 131 g 137 t

ORIGIN

#### Alignment Scores:

Pred. No.: 1..65 Length: 521  
Score: 590.00 Matches: 110  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

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Db 152 TATACATTTCTCTGGCTAGTCTCAAGAAGATTATAATGCCCGGACTGTAGATTCA 211

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QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 60

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Db 212 AACGTTAAAAAAGGGCAGCAGATCTATGTCTCAAGAGCTGTAAAGAAATGGAGCT 271

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QY 61 GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80

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QY 101 ProThrThrAspIleAspPheCysGlu 110

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Db 392 CCACACCGAATATTGACTTCTTCGCGAG 421

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RESULT 8

AX491252

LOCUS AX491252 521 bp DNA linear PAT 16-AUG-2002

DEFINITION Sequence 359 from Patent WO200690.

ACCESSION AX491252

VERSION AX491252.1 GI:22323963

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1

Baker, K.P., Ferrara, N., Gerber, H., Gerecht, M.E., Goddard, A.,

Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,

Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.

and Ye, W.

Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis

#### JOURNAL

Patent: WO 020690-A 359 03-JAN-2002;

Genentech, Inc. (US)

FEATURES

source

Location/Qualifiers

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/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

BASE COUNT 167 a 86 c 131 g 137 t

ORIGIN

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Pred. No.: 1..65 Length: 521  
Score: 590.00 Matches: 110  
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US-10-019-455A-24 (1-110) x AX491252 (1-521)

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Db 152 TATACATTTCTCTGGCTAGTCTCAAGAAGATTATAATGCCCGGACTGTAGATTCA 211

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QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 60

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QY 101 ProThrThrAspIleAspPheCysGlu 110

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Db 392 CCACACCGAATATTGACTTCTTCGCGAG 421

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RESULT 9

AF233261

LOCUS Homo sapiens otopaplin (OTOR) mRNA, complete cds. PRI 06-JUL-2000

DEFINITION AF233261

ACCESSION AF233261.1 GI:8927427

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 846)

Robertson, N.G., Heller, S., Lin, J.S., Resendes, B.L., Weremowicz, S.,

Denis, C.S., Bell, A.M., Hudspeth, A.J. and Morton, C.C.

A novel conserved cochlear gene, OTOR: identification, expression

analysis, and chromosomal mapping

Genomics 66 (3), 242-248 (2000)

JOURNAL

MEDLINE

PUBMED

REFERENCE

2 (bases 1 to 846)

Robertson, N.G., Heller, S., Lin, J.S., Resendes, B.L., Weremowicz, S.,

Denis, C.S., Bell, A.M., Hudspeth, A.J. and Morton, C.C.

Direct Submission

Submitted (09-FEB-2000) Pathology, Brigham and Women's Hospital, 75

Francis Street, Boston, MA 02115, USA

Location/Qualifiers

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DB: 9 Gaps: 0

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QY 101 ProThrThrAspIleAspPheCysGlu 110  
Db 399 CCCACCGGATATTGACTTCTTCGCGAG 428

RESULT 10  
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DEFINITION Homo sapiens fibrocyte-derived protein (FDP) mRNA, complete cds.  
ACCESSION AF243505  
VERSION AF243505.1 GI:11991843  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM

REFERENCE  
AUTHORS Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 865)  
Cohen-Salmon,M., Frenz,D., Verpy,E., Voegeling,S. and  
Petit,C.  
TITLE Fdp, a new fibrocyte-derived protein related to MIA/CD-RAP, has an  
in vitro effect on the early differentiation of the inner ear  
mesenchyme  
J. Biol. Chem. 275 (51), 40036-40041 (2000)  
20568254

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REFERENCE 2 (bases 1 to 865)  
AUTHORS Cohen-Salmon,M., Frenz,D., Verpy,E., Voegeling,S. and Petit,C.  
TITLE Direct Submission  
JOURNAL Submitted (09-MAR-2000) Biotechnologies, Institut Pasteur, 25 rue  
du Dr. Roux, Paris 75015, France  
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LOCUS BD010820 923 bp DNA linear PAT 31-JAN-2002  
DEFINITION Novel polypeptide and DNA thereof.  
ACCESSION BD010820  
VERSION BD010820.1 GI:18639193  
KEYWORDS JP 2001069994-A/21.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 923)

AUTHORS Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y., Yoshimura, K. and Tanaka, H.  
 TITLE Novel polypeptide and DNA thereof  
 JOURNAL TAKEDA CHEMICAL INDUSTRIES LTD  
 COMMENT OS Homo sapiens (human)  
 PN JP 2001069994-A/21  
 PF 21-MAR-2001  
 PD 29-JUN-2000 JP 2000195911  
 PR YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI SHINICHI MOGI,  
 PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA  
 PC C12N15/09, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC A61P19/08,  
 PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC G01N33/53//  
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 DEFINITION Novel polypeptide and its DNA.  
 ACCESSION BD093121  
 VERSION BD093121.1 GI:22638709  
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 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 923)  
 AUTHORS Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y., Yoshimura, K. and Tanaka, H.  
 TITLE Novel polypeptide and its DNA  
 JOURNAL Patent: WO 0102564-A 21 11-JAN-2001;  
 TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA  
 COMMENT OS Homo sapiens (human)  
 PN WO 0102564-A/21  
 PD 11-JAN-2001  
 PF 29-JUN-2000 WO 2000JP004278  
 PP 30-JUN-1999 JP 99P 186718  
 PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI MOGI,  
 PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA  
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 Score: 590.00 Matches: 110  
 Percent Similarity: 100.00% Conservative: 0  
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 Qy 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40  
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 Qy 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyVala 60  
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 Db 388 CCCACACCGGATATTGACTTCTTCTCGGAG 417  
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 LOCUS HSA242552 1422 bp mRNA linear PRI 29-JAN-2001  
 DEFINITION Homo sapiens mRNA for melanoma inhibitory activity like protein (MIAL gene).  
 ACCESSION AJ242552

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VERSION      AJ242552.1 GI:12619172
KEYWORDS     melanoma inhibitory activity like protein; Mial gene.
SOURCE       Homo sapiens
ORGANISM     Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
AUTHORS      Rendtorff,N.D., Prodin,M., Attie-Bitach,T., Vekemans,M. and
              Tommerup,N.
TITLE        Identification and characterization of an inner ear-expressed human
              melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent
              polymorphism that abolishes translation
JOURNAL      Genomics 71 (1), 40-52 (2001)
MEDLINE      21100875
PUBMED       11161796
REFERENCE    2 (bases 1 to 1422)
AUTHORS      Rendtorff,N.D.
TITLE        Direct Submission
JOURNAL      Submitted (21-MAY-1999) Rendtorff N.D., Department of Medical
              Genetics, Institute of Medical Biochemistry and Genetics,
              Blegdamsvej 3, 2200 Copenhagen N, DENMARK
REMARK       Revisited by author 03-AUG-1999
COMMENT       Related sequences: AJ243939 (Mus musculus mRNA)
              Related sequences: AJ252324 to AJ252327 (genomic sequence).
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exon         /gene="MIAL"
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exon         258..363
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exon         /number=3
exon         257*258
exon         /gene="MIAL"
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exon         364..387
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exon         /number=4
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BASE COUNT   417 a 220 c 306 g 479 t
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Score:        590.00       Matches: 110
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Best Local Similarity: 100.00%  Mismatches: 0
Query Match:  100.00%      Indels: 0
DB:           9           Gaps: 0
US-10-019-455A-24 (1-110) x HSA242552 (1-1422)
QY           1 HisGlyIlePheMetAspArgLeuAlaSerIlysLysLeuCysAlaAspGluCysVal 20
              |||||
Db           55 CATGAATATTATGGACCGCTAGCTTCCAGAGAGCTCTGTGCAGATGATGATGTGTC 114
QY           21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
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Db           115 TATACTATTCTCTGGCTAGTGCTCAGAAGATTATAATGCCCGGACTGTAGATTCAAT 174
QY           41 AsnValIlysGlyGlnGlnIleTyrValTyrSerIlysLeuValIlysGluAsnGlyAla 60
              |||||
Db           175 AACGTTAAAAAGGCGCAGCATCTATGTGTACTCAAAAGCTGGTAAAAAGAAATGGAGCT 234
QY           61 GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80
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Db           235 GGAGAAATTTGGGCTGGCAGTGTTATTGTGTATGCCAGGACGACATGGGAGTCGTGGGT 294
QY           81 TyrPheProArgAsnLeuValIlysGluGlnArgValTyrGlnGluAlaThrIlysGluVal 100
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Db           295 TATTTCGCCAGGAACCTTGTCAAGGAACAGCGTGTGTACCAAGAAAGTACCAAGGAAGTT 354
QY           101 ProThrThrAspIleAspPhePheCysGlu 110
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Db           355 CCCACCCAGGATATTGACTTCTTCGCGAG 384

RESULT 14
BD010817
LOCUS       BD010817
DEFINITION Novel polypeptide and DNA thereof.
ACCESSION   BD010817
VERSION     BD010817.1 GI:18639190
KEYWORDS    JP 2001069994-A/18.
SOURCE      Mus sp.
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (Bases 1 to 330)
              Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y.,
              Yoshimura,K. and Tanaka,H.
              Patent: JP 2001069994-A 18 21-MAR-2001;
              TAKEDA CHEMICAL INDUSTRIES LTD
              OS Mus sp. (mouse)
              PN JP 2001069994-A/18
              PF 21-MAR-2001
              PP 29-JUN-2000 JP 2000195911
              PR
              PI YASUAKI ITO,KAZUNORI NISHI,KAZUHIRO OGI,SHOICHI OKUBO,PI
              SHINICHI MOGI,
              PI YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA
              PC C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P9/00,A61P19/02,PC
              A61P19/08,
              PC C07K14/47,C07K16/18,C12N1/21,C12N5/10,G01N33/15,G01N33/50,PC
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              PC C12P21/08,C12N15/00,A61K37/02,C12N5/00
              CC
              FH Key Location/Qualifiers
              FT source 1..330
              FT /organism="Mus sp. (mouse)".

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FEATURES             Location/Qualifiers
source               1..330
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BASE COUNT          91 a 60 c 92 g 87 t
ORIGIN
Alignment Scores:   1.88e-60      Length: 330
Pred. No.:          547.00      Matches: 99
Score:              96.36%      Conservative: 7
Percent Similarity: 90.00%      Mismatches: 4
Best Local Similarity: 92.71%   Indels: 0
Query Match:        6          Gaps: 0
DB:
US-10-019-455A-24 (1-110) x BD010817 (1-330)
Qy 1 HisGlyIlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspGluCysVal 20
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Db 1 CATGGTGATATTATGGATAAACCTTCTCTAAGAAGTTGTGCGGATGAGGAGTGTGTC 60
Qy 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 61 TATACTATTCTCTGGCAAGACAGACAGAAATTACAAATGCCCCAGACTGTAGGTTTCATC 120
Qy 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 60
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Db 121 GATGTCGAAGAAGCGCAGCAGATCTATGTTTACTCCAAAGCTGGTAAACAGAAACGGAGCT 180
Qy 61 GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80
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Db 181 GGAGAGTTTGGGCTGCGAGTGTTTATGGTGACCCAGGATGAGATGGGAATTGTAGGT 240
Qy 81 TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100
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Db 241 TATTTCCCAAGCAACTTGGTGAAGGAGCAGCGTGTATACCAGGAGGCCCAAGGAGATC 300
Qy 101 ProThrThrAspIleAspPheCysGlu 110
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Db 301 CCAACCAAGGATATTGACTTCTTCTGTGAA 330

RESULT 15
BD093118
LOCUS              330 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION         Novel polypeptide and its DNA.
ACCESSION          BD093118
VERSION            BD093118.1 GI:22638706
KEYWORDS           WO 0102564-A/18.
SOURCE             Mus sp.
ORGANISM           Mus sp.
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS            Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y.,
                  Yoshimura,K. and Tanaka,H.
TITLE              Novel polypeptide and its DNA
JOURNAL            Patent: WO 0102564-A 18 11-JAN-2001;
                  TAKEDA CHEMICAL INDUSTRIES LTD,YASUAKI ITO,KAZUNORI NISHI, KAZUHIRO
                  OGI, SHOICHI OKUBO,SHINICHI MOGI,YUKO NOGUCHI,KOJI YOSHIMURA,
                  HIDEYUKI TANAKA
COMMENT
OS Mus sp. (mouse)
PN WO 0102564-A/18
PD 11-JAN-2001
PF 29-JUN-2000 WO 2000JP004278
PR 30-JUN-1999 JP 99P 186718
PI YASUAKI ITO,KAZUNORI NISHI,KAZUHIRO OGI,SHOICHI OKUBO,SHINICHI
PI MOGI,
PI YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA
PC C12N15/12,C12N5/10,C12P21/02,C07K14/47,C07K16/18,A61K45/00, PC
A61K38/17,
PC A61K39/395,A61K49/16,A61P19/02,A61P19/08,A61K31/7088/(C12P21/

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Search completed: December 29, 2003, 19:57:18  
Job time : 1812.69 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 29, 2003, 16:23:14 ; Search time 1138.05 Seconds  
(without alignments)  
2349.180 Million cell updates/sec

Title: US-10-019-455a-24

Perfect score: 590

Sequence: 1 HGFMDELASKKLCADDEC.....RVYQATKEVPTTIDPFCE 110

Scoring table:

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delep 6.0 , Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O=/cgn2\_1/USPRO\_spool/US10019455/runat\_29122003\_160347\_254/app.query.fasta\_1.1770  
-DB=EST -QFMT=fastap -SUFFIX=irst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
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-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
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Database :

EST:  
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2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_estl:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	547	92.7	398	13	BQ570035
2	547	92.7	488	13	BQ564607
3	547	92.7	514	13	BQ568498
4	547	92.7	534	13	BQ564134
5	547	92.7	560	13	BQ569741
6	547	92.7	608	13	BQ564944
7	547	92.7	630	13	BQ568471
8	547	92.7	684	13	BQ563768
9	547	92.7	696	10	BB611549
10	542	91.9	474	13	BQ565637
11	521	88.3	409	13	BQ566932
12	515	87.3	490	13	BQ565411
13	502	85.1	604	13	BQ567343
14	457	77.5	365	13	BY232622
15	442	74.9	527	10	BE236443
16	413	70.0	485	13	BQ565179
17	410.5	69.6	795	13	BU748241
18	353.5	59.9	533	9	AL925854
19	343	58.1	588	13	BQ566776
20	335	56.8	280	13	BQ568785
21	285	48.3	349	9	AW023324
22	275.5	46.7	633	14	CD360404
23	266.5	45.2	677	13	BQ563227
24	266.5	45.2	3240	11	AK047965
25	254.5	43.1	442	9	AA282143
26	244.5	43.1	929	13	BU195892
27	233.5	43.0	473	14	CA433401
28	233.5	43.0	480	12	BM715936
29	233.5	43.0	492	12	BM856478
30	233.5	43.0	507	12	BM674250
31	233.5	43.0	515	13	BQ892734
32	233.5	43.0	522	13	BQ681978
33	233.5	43.0	522	13	BU157778
34	233.5	43.0	529	13	BU194561
35	233.5	43.0	609	12	BM791767
36	233.5	43.0	890	12	BG766328
37	233.5	43.0	1140	12	BG765502
38	232.5	42.8	437	9	AV592759
39	232.5	42.8	453	9	AA627297
40	252.5	42.8	517	10	BE665724
41	251	42.5	544	13	BQ208982
42	250.5	42.5	594	14	CA509768
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# ALIGNMENTS

RESULT 1

BQ570035

LOCUS

DEFINITION

BQ570035 398 bp mRNA linear EST 19-JUN-2002  
gil143b10.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA  
clone gil143b10 5', mRNA sequence.

ACCESSION

BQ570035

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 398)  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## AUTHORS

Kachar,B.  
EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing

## JOURNAL

## COMMENT

Unpublished

Contact: Kachar,B.

Structural Cell Biology

National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA

Tel: 301-402-1599

Fax: 301-402-1765

Email: kacharbenid@nih.gov

Plate: 143 row: b column: 10

Seq primer: M13RPl reverse primer (ABI).

Location/Qualifiers

## FEATURES

source

1..398

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="BALB/c"

/db\_xref="taxon:10090"

/clone="gii43b10"

/sex="male and female"

/dev\_stage="Post natal day 5 to 13"

/clone\_lib="Mouse Organ of Corti cDNA pBluescript"

/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bulla capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning Kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold end, upon titration on XL1 Blue MRF<sup>-</sup> cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACACCTATGACC) and 25<sup>st</sup> strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster

City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 105 a 69 c 116 g 108 t

## ORIGIN

## Alignment Scores:

Pred. No.:	1.2e-64	Length:	398
Score:	547.00	Matches:	99
Percent Similarity:	96.36%	Conservative:	7
Best Local Similarity:	90.00%	Mismatches:	4
Query Match:	92.71%	Indels:	0
DB:	13	Gaps:	0

US-10-019-455A-24 (1-110) x BQ570035 (1-398)

QY	1	HisGlyIlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspGluCysVal	20
DB	67	CATGGTGATTATGGATAAACTTTCTTAAGAAGTTGTGGGATGAGGAGTGTC	126
QY	21	TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle	40
DB	127	TATATCTATTCTCTGGCAAGAGCACAGAGATTACAAATGCCCCAGACTGTAGGTTTCATC	186
QY	41	AsnVallyLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla	60
DB	187	GATGTCAAGAAGGCGACGACATCTATGTTTACTCCAAGCTGGTAAACAGAAACCGAGCT	246
QY	61	GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly	80
DB	247	GGAGAGTTTTGGGTGGCAGTGTATTATGTCCACCACGAGGATGAGATGGGATTTAGGT	306
QY	81	TyrPheProArgAnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal	100
DB	307	TATTTCCCAACCACTTTGGTGAAGGAGCAGCGTGATATACAGGAGGCCACCAAGGAGATC	366
QY	101	ProThrThrAspIleAspPhePheCysGlu	110
DB	367	CCAAACCGGATATTGACTTCTCTGTGAA	396

## RESULT 2

BQ564607

## LOCUS

gii9h02.yl Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA  
Clone gii9h02 5', mRNA sequence.

## ACCESSION

BQ564607

## VERSION

BQ564607.1 GI:21467924

## KEYWORDS

## SOURCE

Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Kachar,B.

## REFERENCE

## TITLES

## AUTHORS

## JOURNAL

## COMMENT

## FEATURES

## source

## 1..488

## /organism="Mus musculus"

## /mol\_type="mRNA"



(catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's Exassist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTATGACC) and 25x strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 147 a 85 c 143 g 139 t  
ORIGIN

Alignment Scores:  
Pred. No.: 1,71e-64 Length: 514  
Score: 547.00 Matches: 99  
Percent Similarity: 96.36% Conservative: 7  
Best Local Similarity: 90.00% Mismatches: 4  
Query Match: 92.71% Indels: 0  
DB: 13 Gaps: 0

US-10-019-455A-24 (1-110) x BQ568498 (1-514)

QY 1 HisGlyIlePheMetAspArgLeuAlaSerLysLeuCysAlaAspGluCysVal 20  
Db 59 CATGGTGTATTATGATTAACCTTCTCTAAGAGTTGTGTCGATGAGGAGTGTGTC 118  
QY 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40  
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QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyVala 60  
Db 179 GATGTCAGAAAGGGCAGCAGAGATCTATGTTTACTCCAGCTGTTACAGAAACCGAGCT 238  
QY 61 GlyGluPheTrpIaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80  
Db 239 GGAGAGTTTGGGCTGGCAGTGTATTATGTTGACCCAGCAGATGAGATGGGAATTTAGCT 298

QY 81 TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100  
Db 299 TATTTCCCGACCACTTGGTAGAGGACGAGCTGTATACCGAGGCGCCACCAAGGATC 358  
QY 101 ProThrThrAspIleAspPhePheCysGlu 110  
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LOCUS BQ564134 534 bp mRNA linear EST 19-JUN-2002  
DEFINITION gi11401.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone gi11401 5', mRNA sequence.  
ACCESSION BQ564134  
VERSION BQ564134.1 GI:21467451  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 534)  
AUTHORS Kachar, B.  
TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing  
JOURNAL Unpublished  
COMMENT Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kachar@nidcd.nih.gov  
Plate: 11 row: d column: 01  
Seq primer: M13Rpl reverse primer (ABI).  
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/clone="gi11401"  
/sex="male and female"  
/dev\_stage="Post natal day 5 to 13"  
/clone\_lib="Mouse Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden)





strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 160 a 92 c 154 g 153 t

ORIGIN

Alignment Scores:  
Pred. No.: 1.92e-64 Length: 560  
Score: 547.00 Matches: 99  
Percent Similarity: 96.36% Conservative: 7  
Best Local Similarity: 90.00% Mismatches: 4  
Query Match: 92.71% Indels: 0  
DB: 13 Gaps: 0

US-10-019-455A-24 (1-110) x BQ569741 (1-560)

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QY 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40  
DB 120 TATACTATTTCTTGGCAGAGACACAGGAAGATTACATGCCAGCTGTAGTTTCATC 179  
QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 60  
DB 180 GATGTCAAGAAAGGCGAGCAGATCTATGTTTACTTCCAGCTGTTAACAAGAAACGAGCT 239  
QY 61 GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValGly 80  
DB 240 GGAGAGTTTGGCGTGGCAGTGTATGTTGACACAGATGAGATGGGAATTTGTAGGT 299  
QY 81 TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100  
DB 300 TATTTCCCGCAGCACTTGGTGAAGAGCAGCGGTATATCCAGGAGGCCACCAAGGAGATC 359  
QY 101 ProThrThrAspIleAspPheCysGlu 110  
DB 360 CAACACCGGATATTGACTTCTTCTGTGAA 389

RESULT 6  
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DEFINITION gi27909.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA  
clone gi27909 5', mRNA sequence.  
ACCESSION BQ564944  
VERSION BQ564944.1 GI:21468261  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 608)  
AUTHORS Kachar.B.  
TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing  
JOURNAL Unpublished  
COMMENT Contact: Kachar.B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kachar@nidcd.nih.gov  
Plate: 27 row: g column: 09

Seq primer: M13RP1 reverse primer (ABI).

FEATURES  
source

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/clone="gi27909"  
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/clone\_lib="Mouse Organ of Corti cDNA pBluescript"  
/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bulla capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on xli Blue MRF<sup>+</sup> cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 169 a 107 c 166 g 166 t

ORIGIN

Alignment Scores:  
Pred. No.: 2.15e-64 Length: 508  
Score: 547.00 Matches: 99



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|||||  
Db 247 GGAGAGTTTTGGCGTGCGAGTGTATTATGTTGACCCACAGGATGAGATGGGAATTGTAGGT 306  
|||||

Qy 81 TyrPheProArgAsnLeuVallyysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100  
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Db 307 TATTTCCCGAGCACTTGGTGAAGGAGCAGCGGTATACCGAGGAGGCCACCAAGGAGATC 366  
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Qy 101 ProThrThrAspIleAspPheCysGlu 110  
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Db 367 CCAACCCAGGATATTGACTTCTTCTGTGAA 396  
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RESULT 8  
BQ563768  
LOCUS  
DEFINITION  
BQ563768  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 684)  
Kachar.B.  
EST analysis of gene expression in the mouse Organ of Corti at the  
onset of hearing  
Unpublished  
Contact: Kachar, B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kachar@nidcd.nih.gov  
Plate: 06 row: C column: 09  
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Location/Qualifiers  
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/db\_xref="taxon:10090"  
/clone="gi06c09"  
/sex="male and female"  
/dev\_stage="Post natal day 5 to 13"  
/clone\_lib="Mouse Organ of Corti cDNA pBluescript"  
/note="Organ: Organ of Corti; Vector: pBluescript; The  
organ of Corti (OC) was fine dissected from a total of 386  
OC as follows: 102 samples from post-natal (P) day 5; 72  
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;  
14 from P12 and 24 from P13. After killing animals by  
cervical dislocation followed by decapitation, the bulla  
was removed and opened in Leibowitz medium. The bony  
capsule of the cochlea was chipped away, stria vascularis  
and spiral ligament were removed and the sensory  
epithelium was carefully dissected out of the modiolus.  
Total RNA was extracted using the micro Fasttrack kit  
(catalog # K1593-02; Invitrogen, Carlsbad, CA), according  
to manufacturer's instructions. Reverse transcription and  
library construction were carried out with the Uni-Zap XR  
vector kit (catalog # 237211, Stratagene) and Uni-Zap XR  
Gigapack III Gold Cloning kit (catalog # 237612), both  
from Stratagene (La Jolla, CA, USA), according to  
manufacturer's instructions. Briefly: 1.5 ug mRNA was  
reverse transcribed using a hybrid oligo(dT) linker-primer  
that contains an Xho I site. First strand synthesis was  
primed with the linker- primer and transcribed using  
Moloney murine leukemia virus reverse transcriptase  
(MMLV-RT) and 5-methyl dCTP. The second strand was

BASE COUNT 194 a 120 c 178 g 192 t  
ORIGIN

Alignment Scores:  
Pred. No.: 2,548-64 Length: 684  
Score: 547.00 Matches: 99  
Percent Similarity: 96.36% Conservativeness: 7  
Best Local Similarity: 90.00% Mismatches: 4  
Query Match: 92.71% Indels: 0  
DB: 13 Gaps: 0

US-10-019-455A-24 (1-110) x BQ563768 (1-684)

Qy 1 HisGlyIlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspGluCysVal 20  
|||||  
Db 67 CATGGTGTATTATGGATAAACTTTCTTCTAAGAAGTTGTGCGGATGAGGAGTGTGTC 126  
|||||

Qy 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40  
|||||

Db 127 TATACATTTCTCTGGCAGAGACACAGGAAGATTACATGCCCCAGACTGTAGGTTCATC 186  
|||||

Qy 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 60  
|||||

Db 187 GATGTCAAGAAAGGGCAGCAGATCTATGTTTACTCCAGCTGGTAACAGAAAACGAGCT 246  
|||||

Qy 61 GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80  
|||||

Db 247 GGAGAGTTTTGGCGTGCGCAGTGTATTATGTCACCCAGGATGAGATGTAGGT 306  
|||||

Qy 81 TyrPheProArgAsnLeuVallyysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100  
|||||

Db 307 TATTTCCCGAGCACTTGGTGAAGGAGCAGCGGTATACCGAGGAGGCCACCAAGGAGATC 366  
|||||

Qy 101 ProThrThrAspIleAspPheCysGlu 110  
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Db 367 CCAACCCAGGATATTGACTTCTTCTGTGAA 396  
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RESULT 9  
B8611549  
LOCUS

BB611549 696 bp mRNA linear EST 31-AUG-2001



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/dev stage="Post natal day 5 to 13"
/clone_lib="Mouse Organ of Corti cDNA pBluescript"
/notes="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XLI Blue MRF+ cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTATGACC) and 25x strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."
```

145 a 78 c 131 g 120 t

BASE COUNT

ORIGIN

Alignment Scores:

Pred. No.:	7,38e-64	Length:	474
Score:	542.00	Matches:	98
Percent Similarity:	95.45%	Conservative:	7
Best Local Similarity:	89.09%	Mismatches:	5
Query Match:	91.86%	Indels:	0
DB:	13	Gaps:	0

US-10-019-455A-24 (11-110) x BQ565637 (11-474)

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Db 68 CATGGTGTATTTATGGATAAACTTCTCTTAATAAGTTGTGTGGATGAGAGGTGTGTC 127  
QY 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40  
Db 128 TATACTATTCTCTGGCAGACGACACAGGAGATTACATGCCCCAGACTGTAGGTTTCATC 187  
QY 41 AsnValLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 60  
Db 188 GATGTCAAGAAAGGGCAGCAGATCTATGTTTACTCAAGCTGTATCAAGAAACCGAGCT 247  
QY 61 GlyGluPheThrAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValGly 80  
Db 248 GGAGAGTTTGGCTGGCAGTGTATTATGTGACCCAGGATGATGGGAATTAGGT 307  
QY 81 TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100  
Db 308 TATTCCCCAGCAACTTGTGAAGGAGCAGCGTGTATACAGGAGGCGCCACCAAGGAGATC 367  
QY 101 ProThrThrAspIleAspPheCysGlu 110  
Db 368 CCAACCCAGGATATTGACTTCTTCTGTGAA 397

RESULT 11  
BQ566932  
LOCUS  
DEFINITION  
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ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
CONTACT: Kachar, B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kachar@nidcd.nih.gov  
Plate: 73 row 9 column: 09  
Seq primer: M13RPL reverse primer (ABI).  
Location/Qualifiers  
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/clone="gi73909"  
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/dev stage="Post natal day 5 to 13"  
/notes="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit

(catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's EXAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGAAACAGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Watham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 102 a 75 c 121 g 111 t

# Alignment Scores:

Pred. No.:	4.5e-61	Length:	409
Score:	521.00	Matches:	97
Percent Similarity:	94.55%	Conservative:	7
Best Local Similarity:	88.18%	Mismatches:	5
Query Match:	88.31%	Indels:	1
DB:	13	Gaps:	0

US-10-019-455a-24 (1-110) x BQ566932 (1-409)

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Qy	20	lTyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheI	40
Db	141	CTATACTATTCTTCGCAAGACACAGGAGATTACATGCCCCAGCTGTAGTTCAT	200
Qy	40	aAsnValIlyslsGlyGlnIlelTyrValTyrSerIlyslsIleuValIlyslsGlyAl	60
Db	201	CGATGTCGAAGAAAGGCGACAGATCTATGTTTACTCCAAAGCTGGTAACAGAAACCGAGC	260
Qy	60	aGlyGluPheIrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValG	80
Db	261	TGGAGAGTTTGGGCTGGCAGTGTATTATGGTACCACCAGGATGAGTGGGAATTGTAGG	320

Qy	80	YTyR-PheProArgAenLeuValIlyslsGluGlnArgValTyrGlnGluAlaThrIlyslsGluVa	100
Db	321	TATTTTCCCGACGACTGTGTGAAGGAGCAGCGTGTATACCGAGGCGCCACCAAGAGAT	380
Qy	100	1ProThrThrAspIleAspPhePheCys	109
Db	381	CCCAACACACGGCTATTGACTTCTTCTGT	408
RESULT 12			
BQ565411			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FEATURES			
source			

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/strain="BALB/c"  
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/clone="gi37b12"  
/sex="male and female"  
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/clone\_lib="Mouse Organ of Corti cDNA pBluescript"  
/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden)







strength BigDye terminator sequencing chemistry (Applied Biosystems Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Watham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified.

BASE COUNT 178 a 108 c 152 g 166 t

ORIGIN

Alignment Scores:  
Pred. No.: 3 08e-58 Length: 604  
Score: 502.00 Matches: 92  
Percent Similarity: 96.00% Conservatives: 4  
Best Local Similarity: 92.00% Mismatches: 4  
Query Match: 85.08% Indels: 0  
DB: 13 Gaps: 0

US-10-019-455A-24 (1-110) x B0567343 (1-604)

QY 11 LysLysLeuCysAlaAspAspGluCysValTyThrIleSerLeuAlaSerIaGlu 30  
Db 1 AAGAAGTTGTGCGGATGAGGAGTGTCTATCTATCTCTGCGAAGACGAGGAA 60  
QY 31 AspTyAsnAlaProAspCysArgPheIleAsnValLysGlyGlnIleTyVal 50  
Db 61 GATTACATGCCACAGCTGTAGTTTCATCGATGTCACAGAGGCGAGATCTATGTT 120  
QY 51 TySerLysLeuValLysGluLysGlyAlaGlyGluPheTrpAlaGlySerValTyGly 70  
Db 121 TACTCCAAAGCTGTACACAGAAACGAGCTGCGAGAGTTTGGCTGGCAGTGTATGCT 180  
QY 71 AspGlyGlnAspGluMetGlyValValGlyTyPheProArgAsnLeuValLysGluGln 90  
Db 181 GACCACAGATGAGATGGGAATGTAGGTATTTCCACAGCACTTGTGTGAGAGCAG 240  
QY 91 ArgValTyGlnGluAlaThrLysGluValProThrAspIleAspPheCysGlu 110  
Db 241 CGTGTTATACAGAGGCCACCAAGAGAGATCCCAACACGAGATTTGACTTCTCTGTGAA 300

RESULT 14

BY232622

LOCUS

DEFINITION

CDNA clone F930026720 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

BY232622 365 bp mRNA linear EST 10-DEC-2002  
CDNA clone F930026720 5', mRNA sequence.  
BY232622  
BY232622.1 GI:26413732  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 365)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,  
Nikaido, I., Otsu, N., Saito, R., Suzuki, H., Yamana, A., Schonbach, C.,  
Yegi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Bult, C., Hume, D.A.,  
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Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M.,  
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M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale,  
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Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura,  
M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,  
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii,  
Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata,  
K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander,  
E.S., Rogers, J., Birney, E. and Hayashizaki, Y.  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

12466851

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URL: http://genome.res.riken.go.jp/

Arizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane

T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A.,

Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K.,

Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami

M., Waki, K., Watabiki, A., Muramatsu, M. and Hayashizaki, Y. Direct

Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with

Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a

nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN

Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues.

Tissues were provided by Kirk W. Beisel (Boys Town National

Research Hospital 555 North 30th Street Omaha, NE 68131 USA) whose

assistance we gratefully acknowledge. Please visit our web site

(http://genome.gsc.riken.go.jp) for further details.

FEATURES

Location/Qualifiers

1..365

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="F930026720"

/tissue\_type="inner ear"

/dev\_stage="adult"

/clone\_lib="RIKEN full-length enriched, adult inner ear"

BASE COUNT 97 a 60 c 110 g 98 t

ORIGIN

Alignment Scores:

Pred. No.: 2.22e-52 Length: 365

Score: 457.00 Matches: 85

Percent Similarity: 94.79% Conservatives: 6

Best Local Similarity: 88.54% Mismatches: 5

Query Match: 77.46% Indels: 0

DB: 13 Gaps: 0

US-10-019-455A-24 (1-110) x BY232622 (1-365)

QY 1 HisGlyIlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysVal 20  
 Db 78 CATGGGTGATTTATGATAAACTTTCTTAAAGAGTGTGTGGATGAGGAGTGTGTC 137  
 QY 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40  
 Db 138 TATACTATTTCCTGGCAGAGACAGAGAGATTACAATGCCACAGACTGTAGTTTCATC 197  
 QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 60  
 Db 198 GATGTCCAAGAAAGGGCAGCAGATCTATGTTTACTCCAAGCTGCTTAACAGAAAACCGAGCT 257  
 QY 61 GlyGluPheTyrAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80  
 Db 258 GGAGAGTTTGGGCTGGCGAGTGTTTATGTGTGACACAGATGAGATGGGAATTGTAGGT 317  
 QY 81 TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAla 96  
 Db 318 TATTTTCCCCAGCAACTTGGTGAAGGAGCAGCGGTGTATACCAGGAGGCC 365

## RESULT 15

BE236443 527 bp mRNA linear EST 25-APR-2001  
 LOCUS 144645 MARC 4BOV Bos taurus CDNA 5', mRNA sequence.  
 DEFINITION BE236443  
 ACCESSION BE236443  
 VERSION BE236443.1 GI:9021161  
 KEYWORDS EST

## SOURCE

Bos taurus (cow)

## ORGANISM

Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovidae; Bovinae; Bos.

## REFERENCE

1 (bases 1 to 527)

## AUTHORS

Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,  
 Casas,E., Wray,J.E., White,J., Cho,J., Fahrrenkrug,S.C., Bennett  
 ,G.L., Heaton,M.P., laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,  
 Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and  
 Keefe,J.W.

## TITLE

Sequence evaluation of four pooled-tissue normalized bovine cDNA  
 libraries and construction of a gene index for cattle

## JOURNAL

Genome Res. 11 (4), 626-630 (2001)

## MEDLINE

21180013

## PUBMED

11282978

## COMMENT

Contact: Smith TPL  
 USDA, ARS, US Meat Animal Research Center  
 PO Box 166, Clay Center, NE 68933-0166, USA  
 Tel: 402 762 4366  
 Fax: 402 762 4390  
 Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt trimmed with phred

v0.980904.e. Vector identified by cross\_match with the -minscore 18

and -minmatch 12 options.

## PCR Primers

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTCACGTCAGCAGC

Plate: 54 row: C column: 18

Seq primer: ATTAGGTGACACTATAG.

Location/Qualifiers

1..527

/organism="Bos taurus"

/mol\_type="mRNA"

/db\_xref="taxon:9913"

/tissue\_type="pooled"

/lab\_host="DH10B"

/clone\_lib="MARC 4BOV"

/note="vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;

Library made from pooled tissue from day 20 and day 40

embryos."

BASE COUNT 173 a 94 c 126 g 134 t

ORIGIN

Alignment Scores:

Pred. No.: 4.17e-50 Length: 527

Score: 442.00 Matches: 87  
 Percent Similarity: 81.08% Conservative: 3  
 Best Local Similarity: 78.38% Mismatches: 7  
 Query Match: 74.92% Indels: 14  
 DB: 10 Gaps: 2

US-10-019-455A-24 (1-110) x BE236443 (1-527)

QY 1 HisGlyIlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysVal 20  
 Db 89 CATGGATATTTATGACACAGACTTGGTTCAGAAAGCTGTGTCCAGATGATGATGTGC 148  
 QY 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40  
 Db 149 TATACTATTTCCTGGCCAGAGCTCAAGAAGATTACAATGCTCCGACTGTAGATTCAIT 208  
 QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 60  
 Db 209 AACGTTAAAAAAGGACAGTGGATCTATGTTTACTCAAGCTG----- 250  
 QY 61 GlyGluPheTyrAlaGlySerValTyrGlyAsp---GlyGlnAspGluMetGlyValVal 79  
 Db 251 -----GTCATATGGCAATCAGTCTGAGATGAAATGGAAACCGTG 289  
 QY 80 GlyTyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGlu 99  
 Db 290 GGTATTATTTCCAGCAACTTGGTCCAGGAACAACATGTGTACCAAGAAGCCACCAAGGAA 349  
 QY 100 ValProThrThrAspIleAspPhePheCysGlu 110  
 Db 350 GTTCCTACCACGGATATTGACTTTTTCGCGAG 382

Search completed: December 29, 2003, 22:00:48

Job time : 1140.05 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 29, 2003, 16:10:49 ; Search time 132.647 Seconds  
(without alignments)  
2238.558 Million cell updates/sec

Title: US-10-019-455a-24

Perfect score: 590

Sequence: 1 HGFMRLASKKLCADCEV.....RVQEQATKEVPTDIDFFCE 110

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh  
-Q=/cgn2\_1/USPRO\_pool/US10019455/runat\_29122003\_160347\_230/app\_query.fasta\_1.1770  
-DB=N Geneseq 19Jun03 -QPM=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS-human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10019455 -CGN 1.0 -runat\_29122003\_160347\_230 -NCPU=6 -ICPU=3  
-NO\_WMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSFBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq 19Jun03:  
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23: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.\*  
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25: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match %	Length	DB	ID	Description
1	590	100.0	330	22	AAF59079	Human MLP nucleoti
2	590	100.0	384	22	AAF59065	Human MLP nucleoti
3	590	100.0	387	24	AA517583	DNA encoding novel
4	590	100.0	426	22	AAH26341	Human growth regul
5	590	100.0	521	24	ABL95740	Human angiogenesis
6	590	100.0	521	24	ABL8251	Human PRO9873 cDNA
7	590	100.0	521	24	ABK33571	cDNA encoding huma
8	590	100.0	891	22	AAH98228	Human EST-derived
9	590	100.0	891	22	AAH26342	Human growth regul
10	590	100.0	923	22	AAF59083	Human MLP nucleoti
11	590	100.0	1201	22	AAH26343	Human growth regul
12	547	92.7	330	22	AAF59080	Mouse MLP nucleoti
13	547	92.7	384	22	AAF59068	Mouse MLP nucleoti
14	547	92.7	947	22	AAF59084	Mouse MLP nucleoti
15	541	91.7	330	22	AAF59099	Rat MLP nucleotide
16	541	91.7	384	22	AAF59098	Rat MLP nucleotide
17	471	79.8	307	22	AAF59093	Rat MLP nucleotide
18	413	70.0	261	22	AAF59092	Rat MLP nucleotide
C 19	254.5	43.1	442	24	ABL61602	Breast cancer rela
C 20	254.5	43.1	442	24	ABL64012	Breast cancer rela
21	253.5	43.0	330	16	AAQ84061	Sequence encoding
22	253.5	43.0	459	16	AAQ84050	Sequence encoding
C 23	253.5	43.0	459	22	AAI70083	Melanoma inhibitor
C 24	253.5	43.0	459	22	AAI18732	Human antisense ol
25	253.5	43.0	555	23	ABV59229	Human prostate exp
26	251.5	42.6	433	22	AAH47783	Recombinant human
27	231.5	39.2	581	16	AAQ84052	Sequence encoding
28	226.5	38.4	417	22	AAH99775	Human protein enco
29	225.5	38.2	884	22	AA522459	Human cDNA encodi
30	225.5	38.2	1230	24	ABQ79850	Human TANGO 130 pa
31	225.5	38.2	1263	21	AAZ51245	Human TANGO 130 cd
32	225.5	38.2	1263	24	ABQ79849	Human TANGO 130 po
33	225.5	38.2	4409	23	ABV21035	Human prostate exp
34	225.5	38.2	4409	23	ABV23751	Human prostate exp
35	225.5	38.2	4409	23	ABV26878	Human prostate exp
36	225.5	38.2	4409	23	ABV29625	Human prostate exp
37	225.5	38.2	5724	24	ABQ79852	Human TANGO 130 po
38	225.5	38.2	8121	24	ABQ79851	Human TANGO 130 po
39	217	36.8	2037	22	AA546220	Human DNA encoding
40	217	36.8	2037	25	ACA57978	Human cDNA encodi
41	217	36.8	2037	25	ABX98448	Human cDNA encodi
42	217	36.8	2037	25	ABX98950	Novel human secret
43	217	36.8	2037	25	ACA05995	Human secreted/tra
44	217	36.8	2037	25	ABX98039	Human PRO polynucl
45	217	36.8	2037	25	ABX78823	Human PRO polynucl

ALIGNMENTS

RESULT 1  
AAF59079  
ID AAF59079 standard; DNA; 330 BP.  
XX  
AC AAF59079;  
XX  
DT 23-APR-2001 (first entry)  
XX  
DE Human MLP nucleotide sequence SEQ ID NO:23.  
XX

KW MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
KW cardiant; gene therapy; secretory cell function regulator; promoter;  
KW inhibitor; ds.  
XX  
OS Homo sapiens.  
XX

```

PN WO200102564-A1.
XX 11-JAN-2001.
XX 29-JUN-2000; 2000WO-JP04278.
XX 30-JUN-1999; 99JP-0186718.
XX (TAKE ) TAKEDA CHEM IND LTD.
XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
XX Tanaka H;
XX WPI: 2001-159271/16.
XX P-PSDB; AAB69126.
XX Safe, low-toxicity secretory cell function-regulatory protein and
XX encoded DNA, applicable as drugs, in diagnosis and development of
XX promoters and inhibitors for preventing or treating e.g. bone and joint
XX diseases -
XX Claim 8; Page 97; 111pp; Japanese.
XX The present invention describes novel MLP proteins and their encoding
XX DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
XX activities, and can be used in gene therapy and as secretory cell
XX function regulators. The MLP proteins and DNAs can be used in drugs, in
XX the diagnosis and development of promoters and inhibitors for preventing
XX or treating bone and joint diseases as well as pathologic angiogenesis.
XX AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
XX in the exemplification of the present invention.
XX Sequence 330 BP; 91 A; 60 C; 91 G; 88 T; 0 other;

Alignment Scores:
Pred. No.: 1-95e-75 Length: 330
Score: 590.00 Matches: 110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0
US-10-019-455A-24 (1-110) x AAF59079 (1-330)

QY 1 HisGlyIlePheMetAspArgLeuAlaSerLysLeuCysAlaAspGluCysVal 20
DB 1 CATGGAAATATTTATGGACCGTCTAGCTTCAAGAAGCTCTGTGCAGATGATGAGTGTGC 60
QY 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheile 40
DB 61 TATACTATTTCTCTGGCTAGTGTCTCAAGAAGATTATATGTCCTCCCGGACTGTAGATTCA 120
QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 60
DB 121 AACGTTAAAAAGGGGAGGAGATCTATGTGTACTCAAGCTGGTAAAAAGAAATCGAGCT 180
QY 61 GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80
DB 181 GGAGATTTTGGCTGGCAGTGTATTATGTGTATGTCGACGAGAGATGGAGTCTGTGGGT 240
QY 81 TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100
DB 241 TATTTCCCGGGAACCTTGGTCAAGGAACAGCGTGTGTACCAAGAGCTACCAAGGAAGTT 300
QY 101 ProThrThrAspIleAspPheCysGlu 110
DB 301 CCCACACCGGATATTGACTTCTCTCGGAG 330

RESULT 2
AAF59065
ID AAF59065 standard; DNA; 384 BP.
XX
AC AAF59065;

XX 23-APR-2001 (first entry)
XX Human MLP nucleotide sequence SEQ ID NO:4.
XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
XX joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
XX cardiant; gene therapy; secretory cell function regulator; promoter;
XX inhibitor; ds.
XX Homo sapiens.
XX WO200102564-A1.
XX 11-JAN-2001.
XX 29-JUN-2000; 2000WO-JP04278.
XX 30-JUN-1999; 99JP-0186718.
XX (TAKE ) TAKEDA CHEM IND LTD.
XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
XX Tanaka H;
XX WPI: 2001-159271/16.
XX P-PSDB; AAB69123.
XX Safe, low-toxicity secretory cell function-regulatory protein and
XX encoded DNA, applicable as drugs, in diagnosis and development of
XX promoters and inhibitors for preventing or treating e.g. bone and joint
XX diseases -
XX Example 1; Page 91; 111pp; Japanese.
XX The present invention describes novel MLP proteins and their encoding
XX DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
XX activities, and can be used in gene therapy and as secretory cell
XX function regulators. The MLP proteins and DNAs can be used in drugs, in
XX the diagnosis and development of promoters and inhibitors for preventing
XX or treating bone and joint diseases as well as pathologic angiogenesis.
XX AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
XX in the exemplification of the present invention.
XX Sequence 384 BP; 99 A; 70 C; 106 G; 109 T; 0 other;

Alignment Scores:
Pred. No.: 2.41e-75 Length: 384
Score: 590.00 Matches: 110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0
US-10-019-455A-24 (1-110) x AAF59065 (1-384)

QY 1 HisGlyIlePheMetAspArgLeuAlaSerLysLeuCysAlaAspGluCysVal 20
DB 55 CATGGAAATATTTATGGACCGTCTAGCTTCAAGAAGCTCTGTGCAGATGATGAGTGTGC 114
QY 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheile 40
DB 115 TATACTATTTCTCTGGCTAGTGTCTCAAGAAGATTATATGTCCTCCCGGACTGTAGATTCA 174
QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 60
DB 175 AACGTTAAAAAGGGGAGGAGATCTATGTGTACTCAAGCTGGTAAAAAGAAATGGAGCT 234
QY 61 GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80
DB 235 GGAGATTTTGGCTGGCAGTGTATTATGTGTATGTCGACGAGATGGAGTCTGTGGGT 294
QY 81 TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100

```

```

Db      295 TATTCCCAAGCACTGGTCAAGAACACGGTGTGTACCAAGAGCTACCAAGGAAGTT 354
QY      101 ProThrThrAspPhePheCysGlu 110
Db      355 CCCACCACGGATATTGACTTCTTCTGCGAG 384

RESULT 3
AAS17583
ID      AAS17583 standard; cDNA; 387 BP.
AC      AAS17583;
XX
DT      26-FEB-2002 (first entry)
DE      DNA encoding novel secreted protein #12.
XX
KW      Secreted protein; cytostatic; immunosuppressive; vulnary; vaccine;
KW      anti-inflammatory; neuroprotective; nephrotropic; cardiovascular;
KW      human; cancer; autoimmune disease; wound healing disorder; infection;
KW      haematopoietic disorder; inflammatory disorder; infertility;
KW      neurological disease; psychiatric disease; cardiovascular disease;
KW      respiratory disease; renal; gastrointestinal; ss.
XX
OS      Homo sapiens.
XX
FH      Key Location/Qualifiers
FT      1..387
FT      CDS /*tag= a
FT      /product= "Human secreted protein"
XX
PW      WO200179454-A1.
XX
XX      25-OCT-2001.
XX
XX      11-APR-2001; 2001WO-US11797.
XX
XX      13-APR-2000; 2000US-196503P.
XX      24-APR-2000; 2000US-199417P.
XX
XX      (SMIK ) SMITHKLINE BEECHAM CORP.
XX      (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX      Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;
XX
XX      WPI; 2002-061975/08.
XX      P-PSDB; AAU09671.
XX
XX      New secreted proteins or polypeptides, useful for treating e.g. cancer,
XX      autoimmune diseases, wound healing disorder, infections, haematopoietic
XX      disorders, inflammatory disorders, infertility, cancer -
XX
XX      Claim 2; Page 44; 92pp; English.
XX
XX      The invention relates to an isolated novel secreted polypeptide (I) and
XX      polynucleotide (II). (I) and (II) are useful for treating cancer,
XX      autoimmune diseases, wound healing disorder, infections, haematopoietic
XX      disorders, inflammatory disorders, infertility, neurological and
XX      psychiatric diseases, cardiovascular diseases, respiratory diseases,
XX      renal diseases, or gastrointestinal diseases. These may also be used to
XX      treat diseases, abnormalities and disorders caused by abnormal
XX      expression, production, function and/or metabolism of the genes, as
XX      vaccines for inducing immunological response in a mammal, and in
XX      screening methods for detecting the effect of added compounds on the
XX      production of mRNA and polypeptide in cells. The polypeptides can be used
XX      as immunogens to produce antibodies immunospecific for the polypeptides,
XX      and to identify membrane-bound or soluble receptors. The polynucleotides
XX      may be used as diagnostic reagents, in chromosome localisation studies,
XX      and in tissue expression studies. The present sequence represents the
XX      coding sequence of novel human secreted protein #12.
XX
XX      Sequence 387 BP; 101 A; 70 C; 106 G; 110 T; 0 other;

```

```

Alignment Scores:
Score: 2.44e-75 Length: 387
Pred. No.: 590.00 Matches: 110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0

US-10-019-455a-24 (1-110) x AAS17583 (1-387)
QY      1 HisGlyIlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspCysVal 20
Db      55 CATGAATATTATGACCGCTAGCTTCCAGAAAGCTCTGTGCAGATGATGATGTC 114
QY      21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
Db      115 TATACTATTCTCTGGCTAGTGTCTCAAGAGATTATAATATATATATATATATATAT 174
QY      41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 60
Db      175 AACGTTAAAAAGGCGCAGCATCTATGTGTACTCAAAAGCTGGTAAAGAAATGGAGCT 234
QY      61 GlyGluPheTyrAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80
Db      235 CGAGATTTTGGCTGGCAGTGTATGTATGTCAGCCAGGACGAGATGGAGTCTGCGGT 294
QY      81 TyrPheProArgAsnLeuValLysGlnGlnArgValTyrGlnGluAlaThrLysGluVal 100
Db      295 TATTTTCCCGAGAACTTGTGTCAAGGAACAGCGGTGTGTACCGAGAGCTTACCAAGGAAGTT 354
QY      101 ProThrThrAspPhePheCysGlu 110
Db      355 CCCACCACGGATATTGACTTCTTCTGCGAG 384

RESULT 4
AAH26341
ID      AAH26341 standard; cDNA; 426 BP.
XX
XX      AC      AAH26341;
XX
XX      DT      02-OCT-2001 (first entry)
XX      DE      Human growth regulatory-like polypeptide clone 16372272.
XX      KW      Growth regulatory-like polypeptide; human; cartilage; melanoma;
XX      neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;
XX      ss.
XX
XX      OS      Homo sapiens.
XX      EN      WO200155332-A2.
XX      PD      02-AUG-2001.
XX
XX      PF      25-JAN-2001; 2001WO-US02455.
XX      PR      25-JAN-2000; 2000US-0491404.
XX      PR      02-MAY-2000; 2000US-0563786.
XX      PA      (HYSE-) HYSEQ INC.
XX      PI      Mize NK, Boyle BJ, Ford JB, Arterburn MC, Tang YT, Liu C;
XX      Drmanac RT;
XX      WPI; 2001-483233/52.
XX
XX      Isolated human growth regulatory-like polypeptide useful for treating
XX      e.g. Alzheimer's disease, cancer, autoimmune disorders,
XX      hyperproliferative disorders, coagulation disorders, and nervous system
XX      disorders -
XX
XX      Example 1; Page 114; 119pp; English.

```

CC The present sequence is that of Hyseq clone identification number  
 CC 16372272, which was obtained from a human thymus cDNA library  
 CC using standard PCR with primers specific for vector sequence  
 CC flanking the inserts, sequencing by hybridisation sequence  
 CC signature analysis, and Sanger sequencing techniques. This  
 CC expressed sequence tag was used in the assembly of a full-length  
 CC cDNA sequence (see AAH26343) encoding a novel human growth  
 CC regulatory-like polypeptide (GRLP, see AAB82671). The GRLP  
 CC belongs to the same protein family as growth regulatory proteins,  
 CC growth factors, human melanoma derived growth regulatory protein  
 CC precursor (64% similarity and 45% identity over 111 amino acids)  
 CC or melanoma inhibitory activity, cattle cartilage-derived  
 CC retinoic acid sensitive protein (CD-RAP, 44% identity and 64%  
 CC similarity over 126 amino acids) and other retinoic acid-sensitive  
 CC proteins. GRLP polypeptides and polynucleotides of the invention  
 CC can be used in the prophylaxis, treatment (including gene therapy)  
 CC and diagnosis of disorders and diseases caused by, or involving,  
 CC cartilage development and maintenance, inhibition of melanoma cell  
 CC growth and tumours, including neuroectodermal tumours such as  
 CC gliomas. The polynucleotides can also be used to design probes  
 CC and primers, for chromosome and gene mapping, in the recombinant  
 CC production of protein, in the generation of antisense, ribozyme and  
 CC peptide-nucleic acid molecules, and to produce transgenic animals.

XX SQ Sequence 426 BP; 119 A; 73 C; 113 G; 120 T; 1 other;

#### Alignment Scores:

Pred. No.: 2.79e-75 Length: 426  
 Score: 590.00 Matches: 110  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 22 Gaps: 0

US-10-019-455A-24 (1-110) x AAH26341 (1-426)

QY 1 HisGlyIlePheMetAspArgLeuAlaSerIysLysLeuCysAlaAspGluCysVal 20  
 Db CATGGAATATTTATGGACCGCTAGCTTCCAAGAAGCTCTGTCAGATGATGAGTGTGTC 132  
 QY 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40  
 Db TATACATATTTCTCTGGCTAGTGTCTCAAGAAGATTATTAATCCCGGACTGTAGATTCATT 192  
 QY 41 AsnValIysLysGlyGlnGlnIleTyrValTyrSerLysLeuValIysGluAsnGluVala 60  
 Db AAGCTTAAAAAGGCGACGACATCTATGTTACTCAAAAGCTGTTAAAGAAATGGAGCT 252  
 QY 61 GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80  
 Db GGAGAATTTTGGGCTGGCAGTGTATGTTGATGGCCAGGACGAGATGGGAGTCGTGGT 312  
 QY 81 TyrPheProArgAsnLeuValIysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100  
 Db TATTTCCCGAGGAACCTGGTCAGGAACACGCTGTGTACCAAGCTGTTAAAGAAATGGAGTT 372  
 QY 101 ProThrThrAspIleAspPhePheCysGlu 110  
 Db CCCACACGAGATATTGACTTCTTCTCGCAG 402

#### RESULT 5

ABL95740  
 ID ABL95740 standard; cDNA; 521 BP.  
 XX  
 AC ABL95740;

DT 19-JUL-2002 (first entry)

DE Human angiogenesis related cDNA PRO9873 SEQ ID NO: 359.  
 XX

XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
 KW cardiac; cyostatic; antiangiogenic; hypotensive; vulnary;

KW antiarteriosclerotic; gene; ss.  
 XX Homo sapiens.  
 XX WO200208284-A2.  
 XX 31-JAN-2002.  
 XX 09-JUL-2001; 2001WO-US21735.  
 XX 20-JUL-2000; 2000US-219556P.  
 XX 25-JUL-2000; 2000US-220624P.  
 XX 25-JUL-2000; 2000US-220664P.  
 XX 28-JUL-2000; 2000WO-US20710.  
 XX 02-AUG-2000; 2000US-222695P.  
 XX 17-AUG-2000; 2000US-064357.  
 XX 23-AUG-2000; 2000WO-US23522.  
 XX 24-AUG-2000; 2000WO-US23328.  
 XX 07-SEP-2000; 2000US-230978P.  
 XX 15-SEP-2000; 2000US-000000P.  
 XX 18-SEP-2000; 2000US-0664610.  
 XX 18-SEP-2000; 2000US-0665350.  
 XX 24-OCT-2000; 2000US-242922P.  
 XX 08-NOV-2000; 2000US-0709238.  
 XX 10-NOV-2000; 2000WO-US30873.  
 XX 01-DEC-2000; 2000WO-US32678.  
 XX 20-DEC-2000; 2000US-0747259.  
 XX 22-JAN-2001; 2001US-076509.  
 XX 28-FEB-2001; 2001US-0796498.  
 XX 28-FEB-2001; 2001WO-US06520.  
 XX 01-MAR-2001; 2001WO-US06666.  
 XX 09-MAR-2001; 2001US-0802706.  
 XX 14-MAR-2001; 2001US-0808689.  
 XX 05-APR-2001; 2001US-0828366.  
 XX 10-MAY-2001; 2001US-0854208.  
 XX 25-MAY-2001; 2001US-0866028.  
 XX 25-MAY-2001; 2001US-0866034.  
 XX 30-MAY-2001; 2001WO-US17092.  
 XX 30-MAY-2001; 2001US-0870574.  
 XX 01-JUN-2001; 2001WO-US17443.  
 XX 20-JUN-2001; 2001WO-US17800.  
 XX 28-JUN-2001; 2001WO-US19692.  
 XX (GETH ) GENENTECH INC.  
 PA (BAKE/) BAKER K P.  
 PA (FERR/) FERRARA N.  
 PA (GERB/) GERBER H.  
 PA (GERB/) GERRITSEN M E.  
 PA (GODD/) GODDARD A.  
 PA (GODO/) GODOWSKI P J.  
 PA (GURN/) GURNEY A L.  
 PA (HILL/) HILLAN K J.  
 PA (MARS/) MARSTERS S A.  
 PA (PANG/) PAN J.  
 PA (PAON/) PAONI N F.  
 PA (STEP/) STEPHAN J P.  
 PA (WATA/) WATANABE C K.  
 PA (WILL/) WILLIAMS P M.  
 PA (WOOD/) WOOD W I.

XX (GETH ) GENENTECH INC.

PA (BAKE/) BAKER K P.

PA (FERR/) FERRARA N.

PA (GERB/) GERBER H.

PA (GERB/) GERRITSEN M E.

PA (GODD/) GODDARD A.

PA (GODO/) GODOWSKI P J.

PA (GURN/) GURNEY A L.

PA (HILL/) HILLAN K J.

PA (MARS/) MARSTERS S A.

PA (PANG/) PAN J.

PA (PAON/) PAONI N F.

PA (STEP/) STEPHAN J P.

PA (WATA/) WATANABE C K.

PA (WILL/) WILLIAMS P M.

PA (WOOD/) WOOD W I.

XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;

PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;

PI Stephan JF, Watanabe CK, Williams PW, Wood WI, Ye W;

XX WPI; 2002-171999/22.

DR P-PSDB; ABB95602.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,

PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 PT infarction), endothelial or angiogenic disorders in a mammal -  
 XX  
 PS Claim 1; Fig 359; 567pp; English.  
 XX  
 CC The present invention provides the protein and coding sequences of human  
 CC PRO proteins. These are useful for treating or diagnosing a  
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac  
 CC hypertrophy, trauma, cancer, age-related macular degeneration,  
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
 CC healing. The present sequence is a coding sequence of the invention.  
 XX  
 SQ Sequence 521 BP; 167 A; 86 C; 131 G; 137 T; 0 other;

Alignment Scores:  
 Pred. No.: 3,71e-75 Length: 521  
 Score: 590.00 Matches: 110  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 24 Gaps: 0

US-10-019-455A-24 (1-110) x ABL95740 (1-521)

QY 1 HisGlyIlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspGluCysVal 20  
 Db CATGGAATATTTATGACCGCTAGCTTCCAGAGAGCTCTGTGCAGATGATGATGTC 151  
 QY 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheTle 40  
 Db TATACATATTTCTGGCTAGTGTCTCAAGAGATTAATATGCTCCGAGCTGTAGATTTCAT 211  
 QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 60  
 Db AACGTTAAAAAGGCGACGACATCTATGTGTACTCAAGAGCTGGTAAAAAGAAATGGAGCT 271  
 QY 61 GlyGluPheThrAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80  
 Db CGAGAAATTTTGGCGTGGCAGTGTATGTGTATGTCGCGAGGAGAGATGGGAGTCTGGGT 331  
 QY 81 TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100  
 Db TATTTCCCGAGAACTTGTCTCAGGAAACAGCGTGTGTACCAAGAGCTACCAAGAGATT 391  
 QY 101 ProThrThrAspIleAspPheCysGlu 110  
 Db CCCACACGAGATTTGACTTCTCTCTGCGAG 421

RESULT 6

ID ABL88251

AC ABL88251; standard; cDNA; 521 BP.

XX

XX

DT 16-MAY-2002 (first entry)

XX

XX

DE Human PRO9873 cDNA sequence SEQ ID NO:359.

XX

KW Human; angiogenesis; cardiant; cystostatic; antiangiogenic; hypotensive;  
 KW vulnery; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
 KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
 KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
 KW age-related macular degeneration; arterial restenosis; angina;  
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
 KW wound healing; chromosome mapping; Gene mapping; Gene; ss.

OS Homo sapiens.

XX

XX WO200200690-A2.

XX

PD 03-JAN-2002.  
 XX  
 PF 20-JUN-2001; 2001WO-US19692.  
 XX  
 PR 23-JUN-2000; 2000US-213637P.  
 PR 20-JUL-2000; 2000US-219556P.  
 PR 25-JUL-2000; 2000US-220624P.  
 PR 28-JUL-2000; 2000US-220664P.  
 PR 02-AUG-2000; 2000WO-US20710.  
 PR 17-AUG-2000; 2000US-222695P.  
 PR 23-AUG-2000; 2000US-0643657.  
 PR 24-AUG-2000; 2000WO-US23522.  
 PR 07-SEP-2000; 2000US-230978P.  
 PR 18-SEP-2000; 2000US-0664610.  
 PR 24-OCT-2000; 2000US-0665350.  
 PR 08-NOV-2000; 2000US-0709238.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 10-NOV-2000; 2000WO-US30873.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000US-0747259.  
 PR 20-DEC-2000; 2000WO-US34956.  
 PR 22-JAN-2001; 2001US-0767609.  
 PR 28-FEB-2001; 2001US-0796498.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 01-MAR-2001; 2001WO-US06666.  
 PR 09-MAR-2001; 2001US-0802706.  
 PR 14-MAR-2001; 2001US-0808689.  
 PR 22-MAR-2001; 2001US-0816744.  
 PR 05-APR-2001; 2001US-0828366.  
 PR 10-MAY-2001; 2001US-0854208.  
 PR 25-MAY-2001; 2001US-0866028.  
 PR 25-MAY-2001; 2001US-0866034.  
 PR 30-MAY-2001; 2001WO-US17092.  
 PR 30-MAY-2001; 2001US-0870574.  
 PR 01-JUN-2001; 2001WO-US17443.  
 XX  
 XX (GETH ) GENENTECH INC.

Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;  
 Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
 Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

WPI; 2002-090516/12.

P-PSDB; ABB84996.

One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
 useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 infarction), endothelial or angiogenic disorders in a mammal -

Claim 2; Fig 359; 565pp; English.

ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to  
 ABB85003. The PRO proteins and polynucleotides have cardiant, cystostatic,  
 antiangiogenic, hypotensive, vulnery and antiarteriosclerotic  
 activities, and can be used in gene therapy. The PRO polynucleotides,  
 proteins, agonists and antagonists are useful for treating or diagnosing  
 a cardiovascular, endothelial or angiogenic disorder in a mammal,  
 e.g. cardiac hypertrophy, trauma, cancer, age-related macular  
 degeneration, atherosclerosis, hypertension, arterial restenosis,  
 rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,  
 lymphangitis, tumour angiogenesis (such as breast carcinoma and liver  
 carcinoma) and wound healing. The PRO polynucleotides have applications  
 in molecular biology, including use as hybridisation probes, and in  
 chromosome and gene mapping. ABL88259 to ABL88267 represent primers and  
 probes used in the exemplification of the present invention.

Sequence 521 BP; 167 A; 86 C; 131 G; 137 T; 0 other;

Alignment Scores:





```

RESULT 8
AAH98228
ID AAH98228 standard; cDNA; 891 BP.
XX
AC AAH98228;
XX
DT 12-OCT-2001 (first entry)
XX
DE Human EST-derived coding sequence SEQ ID NO: 85.
XX
KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder;
KW biodiversity; gene therapy; nutrition; ss.
XX
OS Homo sapiens.
XX
PN WO200154477-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US02687.
XX
PR 25-JAN-2000; 2000US-0491404.
PR 17-JUL-2000; 2000US-0617746.
PR 03-AUG-2000; 2000US-0631451.
PR 15-SEP-2000; 2000US-0663870.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX
DR WPI; 2001-476164/51.
DR P-ESDB; AAM23569.
XX
PT Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use -
XX
PS Claim 1; Page 236; 1275pp; English.
XX
CC The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics.
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a cDNA
CC of the invention.
XX
SQ Sequence 891 BP; 272 A; 146 C; 214 G; 259 T; 0 other;

Alignment Scores:
Pred. No.: 7,92e-75 Length: 891
Score: 590.00 Matches: 110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-10-019-455A-24 (1-110) x AAH98228 (1-891)

QY 1 HisGlyIlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspGluCysVal 20
DB 73 CATGGAATATTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGATGTGTC 132
QY 21 TyrThrIleSerLeuAlaSerAlaGluAspPyrHisAlaProAspCysArgPheIle 40
DB 133 TATATATTCTCTGGCTAGTGTCTCAGAGAGATTATATGCCCGGAGCTGTAGATTCAAT 192
QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyVala 60
DB 193 AACGTTAAAAAGGCGCAGCAGATCTATCTGTACTCAAGAGCTGGTAAAGAAATGGAGCT 252

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QY 61 GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80
DB 253 GGAGAAATTTGGGCTGGCAGTGTATTATGGTATGCCAGGACGAGATGGAGTCTGTGGGT 312
QY 81 TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100
DB 313 TATTTCCCGCAGAACTTGTCTCAGGAAACAGCGTGTGTACCGAGAGCTTACCAAGAAAGTT 372
QY 101 ProThrThrAspIleAspPhePheCysGlu 110
DB 373 CCACACACGGATATTGACTTCTTCTGGCAG 402
RESULT 9
AAH26342
ID AAH26342 standard; cDNA; 891 BP.
XX
AC AAH26342;
XX
DT 02-OCT-2001 (first entry)
XX
DE Human growth regulatory-like polypeptide partial cDNA clone.
XX
KW Growth regulatory-like polypeptide; human; cartilage; melanoma;
KW neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200155332-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US02455.
XX
PR 25-JAN-2000; 2000US-0491404.
PR 02-MAY-2000; 2000US-0563786.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;
PI Drmanac RT;
XX
DR WPI; 2001-483233/52.
XX
PT Isolated human growth regulatory-like polypeptide useful for treating
PT e.g. Alzheimer's disease, cancer, autoimmune disorders,
PT hyperproliferative disorders, coagulation disorders, and nervous system
PT disorders -
XX
PS Claim 1; Page 115; 119pp; English.
XX
CC The present sequence is that of a novel nucleic acid that was
CC assembled from human thymus cDNA library-derived Hyseq clone
CC identification number 16372272 (see AAH26341). A recursive
CC algorithm was used to extend the clone by pulling additional
CC sequences from different databases. A full-length sequence (see
CC AAH26343) encoding novel human growth regulatory-like polypeptide
CC (GRLP, see AAB82671) was subsequently obtained. Human GRLP
CC belongs to the same protein family as growth regulatory proteins,
CC growth factors, human melanoma derived growth regulatory protein,
CC precursor (64% similarity and 45% identity over 111 amino acids)
CC or melanoma inhibitory activity, cattle cartilage-derived
CC retinoic acid sensitive protein (CD-RAP, 44% identity and 64%
CC similarity over 126 amino acids) and other retinoic acid-sensitive
CC proteins. GRLP polypeptides and polynucleotides of the invention
CC can be used in the prophylaxis, treatment (including gene therapy)
CC and diagnosis of disorders and diseases caused by, or involving,
CC cartilage development and maintenance, inhibition of melanoma cell
CC growth and tumours, including neuroectodermal tumours such as
CC gliomas. The polynucleotides can also be used to design probes
CC and primers, for chromosome and gene mapping, in the recombinant
CC production of protein, in the generation of antisense, ribozyme and

```

CC peptide-nucleic acid molecules, and to produce transgenic animals.

SQ Sequence 891 BP; 272 A; 146 C; 214 G; 259 T; 0 other;

#### Alignment Scores:

Pred. No.: 7.92e-75 Length: 891  
Score: 590.00 Matches: 110  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 22 Gaps: 0

US-10-019-455A-24 (1-110) x AAH26342 (1-891)

QY 1 HisGlyIlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysVal 20  
DB 73 CATGGAATATTATGGACCGCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGTGTGTC 132  
QY 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40  
DB 133 TATACATATTTCTGTGGCTAGTGTCTCAAGAAGATTATATGCCCGGACTGTAGATTCATT 192  
QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 60  
DB 193 AACGTTAAAAAAGCGCAGCAGATCTATGTCTACTCAAAAGCTGGTAAAGAATAATGGAGCT 252  
QY 61 GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80  
DB 253 GGAGAATTTTGGGCTGGCAGTGTATGTTATGGTGGCCAGGACGAGATGGGAGTCGTGGGT 312  
QY 81 TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100  
DB 313 TATTTCCCAAGAACTTGGTCAAGAACACAGCTGTGTACCAAGAGCTACCAAGGAAGTT 372  
QY 101 ProThrThrAspIleAspPheCysGlu 110  
DB 373 CCCACCACGGATATTGACTTCTTCTCGCAG 402

#### RESULT 10

AAH59083  
ID AAH59083 standard; DNA; 923 BP.

XX AAH59083;

DT 23-APR-2001 (first entry)

XX Human MLP nucleotide sequence SEQ ID NO:29.

XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
KW Joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
KW cardiant; gene therapy; secretory cell function regulator; promoter;  
KW inhibitor; ds.

XX Homo sapiens.

XX WO200102564-A1.

XX 11-JAN-2001.

XX 29-JUN-2000; 2000WO-JP04278.

XX 30-JUN-1999; 99JP-0186718.

XX (TAKE ) TAKEDA CHEM IND LTD.

XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
PI Tanaka H;

XX WPI; 2001-159271/16.

XX Safe, low-toxicity secretory cell function-regulatory protein and  
PT encoded DNA, applicable as drugs, in diagnosis and development of  
PT promoters and inhibitors for preventing or treating e.g. bone and joint

#### PT diseases -

XX Example 1; Page 99-100; 111pp; Japanese.

XX The present invention describes novel MLP proteins and their encoding  
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
CC activities, and can be used in gene therapy and as secretory cell  
CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
CC the diagnosis and development of promoters and inhibitors for preventing  
CC or treating bone and joint diseases as well as pathologic angiogenesis.  
CC AAH59063 to AAH59099 and AAH69122 to AAH69132 represent sequences used  
CC in the exemplification of the present invention.

SQ Sequence 923 BP; 303 A; 147 C; 213 G; 260 T; 0 other;

#### Alignment Scores:

Pred. No.: 8.32e-75 Length: 923  
Score: 590.00 Matches: 110  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 22 Gaps: 0

US-10-019-455A-24 (1-110) x AAH59083 (1-923)

QY 1 HisGlyIlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysVal 20

DB 88 CATGGAATATTATGGACCGCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGTGTGTC 147

QY 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40

DB 148 TATACATATTTCTGTGGCTAGTGTCTCAAGAAGATTATATGCCCGGACTGTAGATTCATT 207

QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 60

DB 208 AACGTTAAAAAAGCGCAGCAGATCTATGTTATGGTGGCCAGGACGAGATGGGAGTCGTGGGT 267

QY 61 GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80

DB 268 GGAGAATTTTGGGCTGGCAGTGTATGTTATGGTGGCCAGGACGAGATGGGAGTCGTGGGT 327

QY 81 TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100

DB 328 TATTTCCCAAGAACTTGGTCAAGAACACAGCTGTGTACCAAGAGCTACCAAGGAAGTT 387

QY 101 ProThrThrAspIleAspPheCysGlu 110

DB 388 CCCACCACGGATATTGACTTCTTCTCGCAG 417

#### RESULT 11

AAH26343  
ID AAH26343 standard; cDNA; 1201 BP.

XX AAH26343;

XX 02-OCT-2001 (first entry)

XX Human growth regulatory-like polypeptide cDNA.

XX Growth regulatory-like polypeptide; human; cartilage; melanoma;  
KW neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;  
KW ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 33..419

FT sig\_peptide /\*tag= a

FT mat\_peptide /\*tag= b

FT /\*tag= c

PN WO200155332-A2.  
 XX 02-AUG-2001.  
 XX 25-JAN-2001; 2001WO-US02455.  
 XX 25-JAN-2000; 2000US-0491404.  
 XX 02-MAY-2000; 2000US-0563786.  
 XX (HYSE-) HYSEQ INC.  
 XX Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;  
 PI Drmanac RT;  
 XX WPI; 2001-483233/52.  
 XX P-PSDB; AAB82671.  
 XX Isolated human growth regulatory-like polypeptide useful for treating  
 PT e.g. Alzheimer's disease, cancer, autoimmune disorders, and nervous system  
 PT hyperproliferative disorders, coagulation disorders, and nervous system  
 PT disorders -  
 XX  
 XX Claim 1; Page 115-116; 119pp; English.  
 XX The present sequence is that of a novel nucleic acid encoding  
 CC human growth regulatory-like polypeptide (GRLP, see AAB82671).  
 CC The sequence was assembled using human thymus cDNA library-derived  
 CC Hyseq clone identification number 16372272 (see AAB82671) as seed,  
 CC using software programs to pull additional sequences from Hyseq's  
 CC proprietary database containing expressed sequence tag sequences,  
 CC and by gel sequencing using primers to extend both 5' and 3' ends.  
 CC The predicted protein has a mol.wt. of 14 kDa unglycosylated. GRLP  
 CC belongs to the same protein family as growth regulatory proteins,  
 CC growth factors, human melanoma derived growth regulatory protein  
 CC precursor (64% similarity and 45% identity over 111 amino acids)  
 CC or melanoma inhibitory activity, cattle cartilage-derived  
 CC retinoic acid sensitive protein (CD-RAP, 44% identity and 64%  
 CC similarity over 126 amino acids) and other retinoic acid-sensitive  
 CC proteins. GRLP polypeptides and polynucleotides of the invention  
 CC can be used in the prophylaxis, treatment (including gene therapy)  
 CC and diagnosis of disorders and diseases caused by, or involving,  
 CC cartilage development and maintenance, inhibition of melanoma cell  
 CC growth and tumours, including neuroectodermal tumours such as  
 CC gliomas. The polynucleotides can also be used to design probes  
 CC and primers, for chromosome and gene mapping, in the recombinant  
 CC production of protein, in the generation of antisense, ribozyme and  
 CC peptide-nucleic acid molecules, and to produce transgenic animals.  
 CC They may also have cytokine and cell proliferation or  
 CC differentiation activity, stem cell growth factor activity,  
 CC haematopoiesis regulating activity, tissue growth activity,  
 CC immunosuppressive or immunostimulant activity, activin/inhibin  
 CC activity, chemotactic/chemokinetic activity, haemostatic and  
 CC thrombolytic activity, use in cancer diagnosis and therapy,  
 CC drug screening, receptor/ligand activity, antiinflammatory,  
 CC activity, and treatment of leukaemia, nervous system disorders,  
 CC arthritis and inflammation.  
 XX  
 SQ Sequence 1201 BP; 357 A; 188 C; 275 G; 381 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 1-21e-74 Length: 1201  
 Score: 590.00 Matches: 110  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 22 Gaps: 0  
 US-10-019-455A-24 (1-110) x AAB26343 (1-1201)  
 Qy 1 HisGlyLePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspGluCysVal 20  
 Db 87 CATGGAATATTTATGGACCGTCTAGCTCCAAAGAGCTCTGTGCAGATGATGAGTGTGTC 146

QY 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40  
 DB 147 TATACTATTCTCTGGCTAGTGTCTCAAGAGATTATATAATGCCCGAGCTGTAGATTCTAT 206  
 QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 60  
 DB 207 AACGTTTAAAAAGGCGCAGCATCTATGTGTACTCAAGCTGGTAAAGAAATGGAGCT 266  
 QY 61 GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80  
 DB 267 GGAGAAATTTGGCTGGCAGTGTATGTGTATGATGATGCCAGGACGAGATGGAGTCTGTGGGT 326  
 QY 81 TyrPheProArgAsnLeuValLysGlnGlnArgValTyrGlnGluAlaThrLysGluVal 100  
 DB 327 TATTTCCCGCAGGAACTTGTCAAGGAAACAGCGTGTGTACCAAGGAAAGCTACCAAGGAAGTT 386  
 QY 101 ProThrThrAspIleAspPhePheCysGlu 110  
 DB 387 CCACACCGGATATTGACTTCTTCTGCGAG 416  
 RESULT 12  
 AAF59080  
 ID AAF59080 standard; DNA; 330 BP.  
 XX  
 AC AAF59080;  
 XX  
 DT 23-APR-2001 (first entry)  
 XX  
 DE Mouse MLP nucleotide sequence SEQ ID NO:25.  
 XX  
 KW MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
 KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
 KW cardiac; gene therapy; secretory cell function regulator; promoter;  
 KW inhibitor; ds.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO200102564-A1.  
 XX  
 PD 11-JAN-2001.  
 XX  
 PF 29-JUN-2000; 2000WO-JP04278.  
 XX  
 PR 30-JUN-1999; 99JP-0186718.  
 XX  
 PA (TAKE ) TAKEDA CHEM IND LTD.  
 XX  
 PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
 PI Tanaka H;  
 XX  
 DR WPI; 2001-159271/16.  
 DR P-PSDB; AAB69127.  
 XX  
 PT Safe, low-toxicity secretory cell function-regulatory protein and  
 PT encoded DNA, applicable as drugs, in diagnosis and development of  
 PT promoters and inhibitors for preventing or treating e.g. bone and joint  
 PT diseases -  
 XX  
 PS Claim 10; Page 98; 111pp; Japanese.  
 XX  
 CC The present invention describes novel MLP proteins and their encoding  
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiac  
 CC activities, and can be used in gene therapy and as secretory cell  
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
 CC the diagnosis and development of promoters and inhibitors for preventing  
 CC or treating bone and joint diseases as well as pathologic angiogenesis.  
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
 CC in the exemplification of the present invention.  
 XX  
 SQ Sequence 330 BP; 91 A; 60 C; 92 G; 87 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 2.97e-69 Length: 330